

OM protein - protein search, using sw model
Run on: July 15, 2006, 06:50:36 ; Search time 200 Seconds
(without alignments)
1645.979 Million cell updates/sec

Title: US-10-063-546-38
Perfect score: 3945
Sequence: 1 MGLGWTQGLTFLQLLLS.....LSTAFKVLPRFWMERNKK 720
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
2589679 segs, 457216429 residues
Total number of hits satisfying chosen parameters: 2589679
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database :
1: geneseq1808:*
2: geneseq1908:*
3: geneseq2008:*
4: geneseq2001a:*
5: geneseq2002a:*
6: geneseq2003a:*
7: geneseq2003bs:*
8: geneseq2004a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAV6695	standard;	protein;	720	AA.	
DE	Membrane-bound protein	PRO1344.				
PN	WO963088-A2.					
PD	09-DEC-1999.					
PA	(GETH) GENENTECH INC.					
Query Match						
Best Local Similarity	100.0%;	Score 3945;	DB 3;	Length 720;		
RESULT 2						
ID	AAU29108	standard;	protein;	720	AA.	
DE	Human PRO polypeptide sequence	#85.				
PN	WO200168848-A2.					
PD	20-SEP-2001.					
PA	(GETH) GENENTECH INC.					
Query Match						
Best Local Similarity	100.0%;	Score 3945;	DB 4;	Length 720;		
RESULT 3						
ID	AAB87544	standard;	protein;	720	AA.	
DE	Human PRO1344.					
PN	WO200116318-A2.					
PD	08-MAR-2001.					
PA	(GETH) GENENTECH INC.					
Query Match						
Best Local Similarity	100.0%;	Score 3945;	DB 4;	Length 720;		
RESULT 4						
ID	AAB65218	standard;	protein;	720	AA.	
DE	Human PRO1344 (UNQ699)	protein sequence	SRQ	ID NO:231.		
PN	WO200073454-A1.					
PD	07-DEC-2000.					
PA	(GETH) GENENTECH INC.					
Query Match						
Best Local Similarity	100.0%;	Score 3945;	DB 4;	Length 720;		
RESULT 5						
ID	ABG95869	standard;	protein;	720	AA.	
DE	Human secreted/transmembrane protein	PRO1344.				
PN	US2002119130-A1.					
PD	29-AUG-2002.					
PA	(GETH) GENENTECH INC.					
Query Match						
Best Local Similarity	100.0%;	Score 3945;	DB 5;	Length 720;		
RESULT 6						
ID	ABU58484	standard;	protein;	720	AA.	
DE	Human PRO polypeptide	#85.				

PN	US2003027272-A1.					
PD	06-FEB-2003.					
Query Match						
Best Local Similarity	100.0%;	Score 3945;	DB 6;	Length 720;		
RESULT 7						
ID	ABU88032	standard;	protein;	720	AA.	
DE	Novel human secreted and transmembrane protein	PRO1344.				
PN	US2003032127-A1.					
PD	13-FEB-2003.					
Query Match						
Best Local Similarity	100.0%;	Score 3945;	DB 6;	Length 720;		
RESULT 8						
ID	ABU84347	standard;	protein;	720	AA.	
DE	Human secreted/transmembrane protein (PRO)	#85.				
PN	US2003032112-A1.					
PD	13-FEB-2003.					
Query Match						
Best Local Similarity	100.0%;	Score 3945;	DB 6;	Length 720;		
RESULT 9						
ID	ABR66221	standard;	protein;	720	AA.	
DE	Human secreted polypeptide	PRO1344, SRQ	ID NO:170.			
PN	US2003036159-A1.					
PD	20-FEB-2003.					
Query Match						
Best Local Similarity	100.0%;	Score 3945;	DB 6;	Length 720;		
RESULT 10						
ID	ABR65611	standard;	protein;	720	AA.	
DE	Human secreted polypeptide	PRO1344, SRQ	ID NO:170.			
PN	US2003036159-A1.					
PD	20-FEB-2003.					
Query Match						
Best Local Similarity	100.0%;	Score 3945;	DB 6;	Length 720;		
RESULT 11						
ID	ABU99551	standard;	protein;	720	AA.	
DE	Human secreted/transmembrane protein (PRO)	#85.				
PN	US2003040070-A1.					
PD	27-FEB-2003.					
Query Match						
Best Local Similarity	100.0%;	Score 3945;	DB 6;	Length 720;		
RESULT 12						
ID	ABU58033	standard;	protein;	720	AA.	
DE	Human PRO polypeptide	#65.				
PN	US2003027163-A1.					
PD	06-FEB-2003.					
Query Match						
Best Local Similarity	100.0%;	Score 3945;	DB 6;	Length 720;		
RESULT 13						
ID	ABU59111	standard;	protein;	720	AA.	
DE	Novel human secreted or transmembrane protein	PRO1344.				
PN	US2002132252-A1.					
PD	19-SEP-2002.					
PA	(GETH) GENENTECH INC.					
Query Match						
Best Local Similarity	100.0%;	Score 3945;	DB 6;	Length 720;		
RESULT 14						
ID	ABU82623	standard;	protein;	720	AA.	
DE	Human secreted/transmembrane protein	PRO1344.				
PN	US2003032023-A1.					
PD	13-FEB-2003.					
Query Match						
Best Local Similarity	100.0%;	Score 3945;	DB 6;	Length 720;		
RESULT 15						
ID	ABU82790	standard;	protein;	720	AA.	
DE	Human PRO polypeptide	#85.				
PN	US2003032113-A1.					
PD	13-FEB-2003.					
Query Match						
Best Local Similarity	100.0%;	Score 3945;	DB 6;	Length 720;		
RESULT 16						
ID	ABU89911	standard;	protein;	720	AA.	
DE	Novel human secreted and transmembrane protein	PRO1344.				
PN	US2003036147-A1.					
PD	20-FEB-2003.					

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Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 17
ID ABR68160 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 18
ID ABU60542 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, #94.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 19
ID ABU96213 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 20
ID ABU92644 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 21
ID ABO08721 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 22
ID ABO02773 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 23
ID ABR74927 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 24
ID ABR94689 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 25
ID ABU13924 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH ) GENENTECH LTD.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 26
ID ABU85662 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.

Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 27
ID ABU98822 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003013151-A1.
PD 16-JAN-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 28
ID ABU98037 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 29
ID ABU91743 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 30
ID ABU89436 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 31
ID ABU86277 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 32
ID ABU67490 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 33
ID ABU80518 standard; protein; 720 AA.
DE Human PRO protein #85.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 34
ID ABU72509 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 35
ID ABU90894 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 36
ID ABO33953 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
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PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 37
ID ABR99436 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 38
ID ABR98826 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 39
ID ABO16349 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 40
ID ABR92249 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 41
ID ABO18890 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US200304925-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 42
ID ABR78311 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 43
ID ABO171970 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 44
ID ABUS5047 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 45
ID ABO00186 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 46
ID ABO11518 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.

PN US2003036124-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 47
ID ABO02163 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 48
ID ABO8737 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 49
ID ABO83432 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 50
ID ABO06233 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 51
ID ABR59269 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 52
ID ABO09331 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 53
ID ABO19195 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 54
ID ABO11213 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 55
ID ABR66831 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
RESULT 56
ID ABO16044 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040060-A1.
PD 27-FEB-2003.

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Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 57
ID ABO13750 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 58
ID ABU71524 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 59
ID ABU65653 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, SEQ ID NO:170.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 60
ID ABO07501 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 61
ID ABO03688 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 62
ID ABR67136 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 63
ID ABO15739 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 64
ID ABU56020 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, PRO1344.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 65
ID ABU72305 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 66
ID ABU65348 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 67
ID ABU95293 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 68
ID ABU71196 standard; protein; 720 AA.
DE Human PRO1344 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 69
ID ABO07806 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 70
ID ABR70047 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 71
ID ABR69380 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 72
ID ABO01521 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 73
ID ABU81323 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 74
ID ABR60120 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 75
ID ABU90978 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 76
ID ABR67855 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027269-A1.
PD 06-FEB-2003.
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Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 77
ID ABR65243 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 78
ID ABR6465 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 79
ID ABR71877 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 80
ID ABUS9258 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, #94.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 81
ID ABUS5357 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 82
ID ABUS9047 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 83
ID ABR913127 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 84
ID ABUS94983 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 85
ID ABUS9531 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 86
ID ABUS4042 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 87
ID ABUS3693 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 88
ID ABO25955 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 89
ID ABR64938 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 90
ID ABO27299 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO1344.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 91
ID ABR68770 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 92
ID ABO06586 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 93
ID ABR9131 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 94
ID ABUS7015 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 95
ID ABUS5967 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032300-A1.
PD 30-JAN-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 96
ID ABUS8254 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
```

RESULT 97
ID ABU87265 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 98
ID ABU83737 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 99
ID ABO08111 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 100
ID ABU92494 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 101
ID ABU81822 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 102
ID ABU65986 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 103
ID ABU81164 standard; protein; 720 AA.
DE Human secreted polypeptide PRO144.
PN US2003037212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 104
ID ABR59815 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 105
ID ABU94003 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 106
ID ABU98956 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032296-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 107

ID ABR66526 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 108
ID ABR90944 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 109
ID ABO53279 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 110
ID ABUS8964 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, #94.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 111
ID ABU94371 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 112
ID ABU79253 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 113
ID ABU66582 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 114
ID ABU6687 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 115
ID ABU94676 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 116
ID ABO4603 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 117

ID ABR70352 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 118
ID ABR92342 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032187-A1.
PD 30-JUN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 119
ID ABR98517 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003022301-A1.
PD 30-JUN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 120
ID ABR65916 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 121
ID ABR64633 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 122
ID ABR59407 standard; protein; 720 AA.
DE Novel human secreted or transmembrane protein PRO1109.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 123
ID ABR79558 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 124
ID ABR92949 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 125
ID ABR95908 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 126
ID ABR91128 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 127
ID ABR90221 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.

PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 128
ID ABR09636 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 129
ID ABO10908 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 130
ID ABR70962 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 131
ID ABR98281 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 132
ID ABR67570 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003022293-A1.
PD 30-JUN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 133
ID ABR91438 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 134
ID ABR9286 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 135
ID ABR64652 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 136
ID ABR69742 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 137
ID ABR80119 standard; protein; 720 AA.
DE Human PRO protein #85.
PN US2003036139-A1.

ID 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 138
ID ABU82493 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 139
ID ABU92173 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 140
ID ABU93388 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 141
ID ABO09941 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 142
ID ABO09026 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 143
ID ABU96457 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 144
ID ABU10879 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US200213463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 145
ID ABU10594 standard; protein; 720 AA.
DE Human secreted/transmembrane protein #85.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 146
ID ABU81631 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 147
ID ABU72127 standard; protein; 720 AA.

DE Human PRO polypeptide #19.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 148
ID ABU95603 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 149
ID ABU96812 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 150
ID ABR70657 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 151
ID ABO05008 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 152
ID ABO08416 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 153
ID ABU88570 standard; protein; 720 AA.
DE Human secreted and transmembrane polypeptide PRO1344.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 154
ID ABO34084 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 155
ID ABO05623 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 156
ID ABR74012 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 157

ID ABR95604 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 158
ID ABR80901 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 159
ID ABR81206 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 160
ID ABM00902 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 161
ID ABR88504 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 162
ID ABM77325 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 163
ID ABO28809 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 164
ID ABO31554 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 165
ID ABM07971 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 166
ID ABO40451 standard; protein; 720 AA.

DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 167
ID ABO35876 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 168
ID ABO44015 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 169
ID ADA77922 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 170
ID ABM24810 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 171
ID ABO03078 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036131-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 172
ID ABR90334 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040075-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 173
ID ABM17248 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 174
ID ABR94994 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 175
ID ABR95299 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 176
ID ADB17095 standard; protein; 720 AA.
DE Human transmembrane PRO polypeptide (Seqid 38).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 177
ID ABO21537 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 178
ID ABR97801 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 179
ID ABR87589 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 180
ID ABM77630 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 181
ID ABM27860 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 182
ID ABM06141 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 183
ID ABM03647 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 184
ID ABM35098 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 185

ID ABM26335 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 186
ID ABO48117 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 187
ID ABR92859 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 188
ID ABO24620 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 189
ID ADA37742 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 190
ID ABM11631 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 191
ID ABM02732 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 192
ID ABM16028 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 193
ID ABO27589 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 194
ID ABM29080 standard; protein; 720 AA.

DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 195
ID ABM07056 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 196
ID ABM21150 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 197
ID ABM09496 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 198
ID ABO41366 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 199
ID ABO36181 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 200
ID ABO43710 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 201
ID ABM76410 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003082217-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 202
ID ABM76106 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 203
ID ABM55725 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 204
ID ABM26030 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 205
ID ADA21428 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO1344.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 206
ID ABO03383 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036127-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 207
ID ABO02468 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040061-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 208
ID ABO44257 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO 1344.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 209
ID ABR90639 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036130-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 210
ID ABR73707 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 211
ID ABO16959 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 212
ID ABR94384 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044917-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 213
ID ABR75891 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044929-A1.

PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 214
ID ABR71267 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 215
ID ABR93164 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 216
ID ABR93469 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 217
ID ADA10215 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, PRO1344.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 218
ID ABR81894 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 219
ID ABO27894 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 220
ID ABO30029 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 221
ID ABO33238 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 222
ID ABO4926 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;

Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 223
ID ABO8086 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 224
ID ABO36486 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 225
ID ABO35571 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 226
ID ABO39536 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 227
ID ABO10411 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 228
ID ABO11936 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 229
ID ABO52082 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 230
ID ABO5387 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 231
ID ADA19900 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;


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RESULT 232
ID ABO23705 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 233
ID ADB17283 standard; protein; 720 AA.
DE Human transmembrane PRO polypeptide (Seqid 38).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 234
ID ADA17759 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 235
ID ABR97191 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 236
ID ABR66979 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 237
ID ABM11021 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 238
ID ABM28165 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 239
ID ABO32164 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 240
ID ABM15291 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 241
ID ABM06446 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PD 27-FEB-2003.
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PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 242
ID ABM04257 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 243
ID ABM22370 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 244
ID ABM07666 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 245
ID ABO40756 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 246
ID ABM35403 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 247
ID ABM33166 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 248
ID ABO52692 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 249
ID ABO50252 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 250
ID ABU9246 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040055-A1.
PD 27-FEB-2003.
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Query Match	100.0%;	Score 3945;	DB 6;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.8e-204;		
RESULT 251				
ID ABO04298 standard; protein; 720 AA.				
DE Human secreted/transmembrane protein (PRO) #85.				
PN US2003036164-AA.				
PD 20-FEB-2003.				
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.8e-204;		
RESULT 252				
ID ABO05928 standard; protein; 720 AA.				
DE Human secreted/transmembrane protein (PRO) #85.				
PN US2003040074-AA.				
PD 27-FEB-2003.				
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.8e-204;		
RESULT 253				
ID ABM18468 standard; protein; 720 AA.				
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.				
PN US2003054480-AA.				
PD 20-MAR-2003.				
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.8e-204;		
RESULT 254				
ID ADA27867 standard; protein; 720 AA.				
DE Human secreted/transmembrane protein PRO1344.				
PN US2003054359-AA.				
PD 20-MAR-2003.				
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.8e-204;		
RESULT 255				
ID ABR97496 standard; protein; 720 AA.				
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.				
PN US2003059885-AA.				
PD 27-MAR-2003.				
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.8e-204;		
RESULT 256				
ID ABR80596 standard; protein; 720 AA.				
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.				
PN US2003049740-AA.				
PD 13-MAR-2003.				
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.8e-204;		
RESULT 257				
ID ABM01207 standard; protein; 720 AA.				
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.				
PN US2003049770-AA.				
PD 13-MAR-2003.				
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.8e-204;		
RESULT 258				
ID ABR88809 standard; protein; 720 AA.				
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.				
PN US2003073169-AA.				
PD 17-APR-2003.				
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.8e-204;		
RESULT 259				
ID ABM13461 standard; protein; 720 AA.				
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.				
PN US2003064457-AA.				
PD 03-APR-2003.				
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.8e-204;		
RESULT 260				
ID ABM20845 standard; protein; 720 AA.				
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.				

[illegible]

RESULT 270
ID ABM02427 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US200305986-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 271
ID ABR86369 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 272
ID ABR86674 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 273
ID ABM1638 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 274
ID ABM29690 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 275
ID ABO29114 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 276
ID ABM23895 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 277
ID ABM23285 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 278
ID ABM22065 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 279

ID ABO37706 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 280
ID ABM28470 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 281
ID ABM28775 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 282
ID ABM66419 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 283
ID ABM75801 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 284
ID ABM34081 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 285
ID ABM34386 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 286
ID ABO20317 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 287
ID ABO21232 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 288
ID ABO22147 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 289
ID ADA20072 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 290
ID ABO34185 standard; protein; 720 AA.
DE Human secreted/citransembrane polypeptide PRO 1344.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 291
ID ABR96581 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 292
ID ADA94447 standard; protein; 720 AA.
DE Human secreted/citransembrane protein PRO1344.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 293
ID ABR85759 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 294
ID ABR9741 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 295
ID ABM00597 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 296
ID ABM00292 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 297
ID ABO29724 standard; protein; 720 AA.
DE Human secreted/citransembrane protein (PRO) #85.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 298
ID ABM23590 standard; protein; 720 AA.

DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 299
ID ABM29385 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 300
ID ABO38316 standard; protein; 720 AA.
DE Human secreted/citransembrane protein (PRO) #85.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 301
ID ABO45616 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 302
ID ABM20540 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 303
ID ADA81441 standard; protein; 720 AA.
DE Human secreted/citransembrane protein (PRO) #85.
PN US2003052121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 304
ID ABO16654 standard; protein; 720 AA.
DE Human secreted/citransembrane protein (PRO) #85.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 305
ID ABO18280 standard; protein; 720 AA.
DE Human secreted/citransembrane protein (PRO) #85.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 306
ID ABO22707 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 307
ID ABO23012 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003054451-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

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Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 308
ID ABR92554 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US200306446-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 309
ID ABR81511 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 310
ID ABM77935 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 311
ID ABR89724 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073171-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 312
ID ABM26640 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032121-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 313
ID ABM13766 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 314
ID ABO28504 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 315
ID ABO30334 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 316
ID ABM07361 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 317
ID ABO3952 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 318
ID ABO37096 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 319
ID ABO41671 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 320
ID ABO35266 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 321
ID ABM25115 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104540-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 322
ID ABO47507 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 323
ID ABO47812 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 324
ID ABO48422 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 325
ID ABO51472 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 326
ID ABO51777 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
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PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 327
ID ABO50557 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 328
ID ABR79681 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 329
ID ABM16943 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 330
ID ABO17975 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 331
ID ABO20927 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 332
ID ABR6886 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US200305462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 333
ID ADA38672 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 334
ID ABM12241 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US200306445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 335
ID ABM16333 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US200306449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;

RESULT 336
ID ABM24200 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 337
ID ABM14681 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US200306866-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 338
ID ABM04562 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 339
ID ABM06751 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 340
ID ABM09191 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 341
ID ABO39231 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 342
ID ABM75496 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 343
ID ABM25420 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 344
ID ABM19930 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 345
ID ABO46836 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049762-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 346
ID ABO47141 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 347
ID ADA83239 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 348
ID ABR71572 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 349
ID ABR72182 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 350
ID ABR98521 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 351
ID ABO06891 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 352
ID ABR64844 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 353
ID ABR73402 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 354
ID ABR76496 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 355
ID ABR73097 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.

PN US2003022720-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 356
ID ABM16163 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 357
ID ABO20622 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 358
ID ABO25365 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 359
ID ABO25670 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 360
ID ABR94079 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 361
ID ADA92793 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 362
ID ABR79986 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 363
ID ABM1326 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 364
ID ABO32933 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;

RESULT 365
ID ABO30639 standard; protein; 720 AA.
DE Human secreted/cytoplasmic protein (PRO) #85.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 366
ID ABO30944 standard; protein; 720 AA.
DE Human secreted/cytoplasmic protein (PRO) #85.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 367
ID ABM27250 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 368
ID ABM29995 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 369
ID ABM05531 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 370
ID ABM15596 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 371
ID ABM08581 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 372
ID ABO42281 standard; protein; 720 AA.
DE Human secreted/cytoplasmic protein (PRO) #85.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 373
ID ABO38011 standard; protein; 720 AA.
DE Human secreted/cytoplasmic protein (PRO) #85.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 374

ID ABO45921 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 375
ID ABM66724 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 376
ID ADB20282 standard; protein; 720 AA.
DE Human secreted/cytoplasmic protein (PRO) #85.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 377
ID ABM19625 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 378
ID ABO49337 standard; protein; 720 AA.
DE Human secreted/cytoplasmic protein (PRO) #85.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 379
ID ABO49642 standard; protein; 720 AA.
DE Human secreted/cytoplasmic protein (PRO) #85.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 380
ID ADA78534 standard; protein; 720 AA.
DE Human secreted/cytoplasmic protein (PRO) #85.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 381
ID ABR88199 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 382
ID ADA00369 standard; protein; 720 AA.
DE Human secreted/cytoplasmic protein (PRO) #85.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 383
ID ABM26945 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.

PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 384
ID ABM03342 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 385
ID ABO39841 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 386
ID ABO49947 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 387
ID ABO50862 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 388
ID ABO05318 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 389
ID ABR74622 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US200304924-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 390
ID ABR77101 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US200304927-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 391
ID ABM17858 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 392
ID ABR5909 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 393

ID ABO21842 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 394
ID ABO20012 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 395
ID ABO24315 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 396
ID ABR86064 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 397
ID ABM10716 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 398
ID ABM76715 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 399
ID ABR89419 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 400
ID ABM12546 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 401
ID ABM05836 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 402
ID ABO34961 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068728-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 403
ID ABM03037 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 404
ID ABM19015 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 405
ID ABM19320 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 406
ID ABM046531 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 407
ID ABO49032 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 408
ID ABR69075 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027273-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 409
ID ABR69114 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036119-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 410
ID ABR72487 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036120-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 411
ID ABR74317 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;

RESULT 412
ID ABO18585 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044921-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 413
ID ABR80291 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 414
ID ABM01512 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 415
ID ABM02122 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 416
ID ABR87284 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 417
ID ABM12851 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 418
ID ABM30605 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 419
ID ABM24505 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 420
ID ABO29419 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 421
ID ABO31249 standard; protein; 720 AA.

DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 422
ID ABM14376 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 423
ID ABM09801 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 424
ID ABO38926 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 425
ID ABM34691 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104538-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 426
ID ABO51167 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 427
ID ABO03993 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036158-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 428
ID ABO10463 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003036151-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 429
ID ABO53170 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003044806-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 430
ID ABR77706 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040057-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;

RESULT 431
ID ABR78916 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054456-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 432
ID ABO24010 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 433
ID ABR33774 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 434
ID ABM01817 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 435
ID ABM78240 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 436
ID ABR90029 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 437
ID ADA22354 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO1344.
PN US2003040473-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 438
ID ABM27555 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 439
ID ABM13156 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 440
ID ABO31859 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.

[illegible][illegible]

Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 460
ID ABM22980 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 461
ID ABM30300 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 462
ID ABM21760 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 463
ID ABM21455 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 464
ID ABM14986 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 465
ID ABO41061 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 466
ID ABO36791 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 467
ID ABO37401 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 468
ID ABM75191 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 469
ID ABM33471 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 470
ID ABO46226 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 471
ID ADA82605 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 472
ID ADB85611 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 473
ID ADB96239 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 474
ID ABM31825 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068680-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 475
ID ABM31215 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 476
ID ADB85913 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 477
ID ABM32130 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 478
ID ABM32435 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.

PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 479
ID ADB68290 standard; protein; 720 AA.
DE Human PRO1344 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 480
ID ADB68097 standard; protein; 720 AA.
DE Human PRO1344 protein.
PN US2003066600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 481
ID ABM31520 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 482
ID ABM30910 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 483
ID ADB90914 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 484
ID ADC57711 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003027754-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 485
ID ADC55075 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003045463-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 486
ID ADC11942 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003049681-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 487
ID ADC06994 standard; protein; 720 AA.
DE Human PRO1344 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 488
ID ADC56364 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003064375-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 489
ID ADC17173 standard; protein; 720 AA.
DE Mammalian PRO polypeptide (SeqID 38).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 490
ID ADC07419 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003068647-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 491
ID ADC11409 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003069403-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 492
ID ADC14871 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 493
ID ADC52366 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 494
ID ADC14531 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003082546-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 495
ID ADD08063 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003068623-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 496
ID ADC81888 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003083461-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 497
ID ADD07530 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.

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Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 498
ID ADG82421 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 499
ID ADD05643 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 500
ID ADD08601 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003073030-A1.
PD 17-APR-2003.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 501
ID ADD06850 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 502
ID ADG83097 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 503
ID ADD55204 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 504
ID ADD66042 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 505
ID ADD56162 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 506
ID ADD54600 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 507
ID ADE26754 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003087304-A1.
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PD 08-MAY-2003.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 508
ID ADE26221 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 509
ID ADF67158 standard; protein; 720 AA.
DE Human PRO1344 amino acid sequence SEQ ID NO:231.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 510
ID ADG01043 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 511
ID ADG08596 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 512
ID ADG02638 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 513
ID ADG01345 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 514
ID ADF95520 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 515
ID ADF95217 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 516
ID ADG12335 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
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RESULT 517
ID ADH24070 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 518
ID ADH34096 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 519
ID ADH2929 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 520
ID ADH23900 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 521
ID ADH08995 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 522
ID ADG85304 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 523
ID ADH24580 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 524
ID ADH37436 standard; protein; 720 AA.
DE Human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 525
ID ADH02025 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 526

ID ADH37606 standard; protein; 720 AA.
DE Human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 527
ID ADG85644 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 528
ID ADH24240 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 529
ID ADH38534 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 530
ID ADG83655 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 531
ID ADH29463 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 532
ID ADH27579 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 533
ID ADH37776 standard; protein; 720 AA.
DE Human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 534
ID ADH37953 standard; protein; 720 AA.
DE Human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 535
ID ADH57373 standard; protein; 720 AA.

DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 536
ID ADH53515 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 537
ID ADH53685 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 538
ID ADH52021 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 539
ID ADH49876 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 540
ID ADI25386 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 541
ID ADH90179 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 542
ID ADI25556 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 543
ID ADH97730 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 544
ID ADI35412 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PA (GETH) GENENTECH INC.

PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 545
ID ADI03578 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 546
ID ADI11935 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 547
ID ADH90009 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 548
ID ADH99904 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 549
ID ADH88410 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 550
ID ADI11085 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 551
ID ADI11595 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 552
ID ADH98240 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 553
ID ADH98560 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 554
ID ADH9070 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 555
ID AD105058 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 556
ID AD103408 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 557
ID AD104803 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 558
ID ADH78257 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 559
ID AD119601 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 560
ID ADH90349 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 561
ID AD103068 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 562
ID ADH77917 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
Query Match 100.0%; Score 3945; DB 7; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 563
ID ADH97900 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 564
ID AD10285 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 565
ID AD101980 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 566
ID AD103238 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 567
ID AD11425 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 568
ID AD102327 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 569
ID AD11765 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 570
ID AD105402 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 571
ID ADH79474 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
Query Match 100.0%; Score 3945; DB 7; Length 720;

RESULT 572
ID ADI19431 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 573
ID ADI05232 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 574
ID ADH79644 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 575
ID ADI01470 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 576
ID ADI01640 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 577
ID ADI01810 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 578
ID ADH79814 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 579
ID ADI04632 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 580
ID ADI02768 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 581
ID ADC52176 standard; protein; 720 AA.

ID ADH78087 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 582
ID ADI25726 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 583
ID ADI25896 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 584
ID ADK65408 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 585
ID ADH98750 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 586
ID ADH79991 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 587
ID ADL32776 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 588
ID ADM30310 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 589
ID ADL93722 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 590
ID ADC52176 standard; protein; 720 AA.

DE Novel human secreted and transmembrane protein PRO1344.
PN US200330483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 591
ID ADE74307 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003211572-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 592
ID ADE74919 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003211574-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 593
ID ADF35357 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 594
ID ADG11607 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 595
ID ADF6132 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003215909-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 596
ID ADG04403 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 597
ID ADG00563 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 598
ID ADH06608 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 599
ID ADH06438 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;

Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 600
ID ADG68859 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 601
ID ADH27749 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 602
ID ADH25090 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 603
ID ADH33722 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 604
ID ADG82819 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 605
ID ADH02365 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 606
ID ADH07972 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 607
ID ADG69369 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 608
ID ADH39190 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;

RESULT 609
ID ADH26100 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 610
ID ADG83930 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 611
ID ADH19477 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 612
ID ADG85474 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 613
ID ADH06268 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 614
ID ADH30098 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 615
ID ADH24410 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 616
ID ADH33069 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 617
ID ADG69539 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 618
ID ADH07802 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 619
ID ADG85814 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 620
ID ADH39360 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 621
ID ADH33552 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 622
ID ADH33892 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 623
ID ADH01102 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 624
ID ADG69709 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 625
ID ADH20970 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003224358-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 626
ID ADH02195 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 627
ID ADG69199 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.

PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 628
ID ADG55984 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 629
ID ADH24920 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 630
ID ADH95537 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 631
ID ADH20010 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US200319856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 632
ID ADH02535 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 633
ID ADG69029 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 634
ID ADH07632 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 635
ID ADG6154 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 636
ID ADH24750 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180908-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 637
ID ADH25798 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 638
ID ADH38364 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 639
ID ADH57203 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 640
ID ADH52191 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 641
ID ADH49557 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 642
ID ADH0519 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 643
ID ADI1255 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 644
ID ADH98920 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 645
ID ADI02150 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003190699-A1.
PD 09-OCT-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 646
ID ADH90689 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 647
ID ADJ54808 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 648
ID ADJ98564 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 649
ID ADJ98734 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 650
ID ADJ78893 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 651
ID ADJ99127 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 652
ID ADJ99297 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 653
ID ADJ98915 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 654
ID ADH79063 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 655
ID ADH79063 standard; protein; 720 AA.
DE Neoplastic disease detection protein PRO1344.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 656
ID ADM80893 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 657
ID ADM64579 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 658
ID ADM31475 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 659
ID ADM36522 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 660
ID ADM40327 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 661
ID ADM80893 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 662
ID ADN37935 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 663
ID ADY77733 standard; protein; 720 AA.
DE Neoplastic disease detection protein PRO1344.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
Query Match 100.0%; Score 3945; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;

PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 3945; DB 9; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 664
ID AEA38494 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, #133.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GERTH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 9; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 665
ID AED50165 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2005163766-A1.
PD 28-JUL-2005.
Query Match 100.0%; Score 3945; DB 9; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 666
ID AEF12564 standard; protein; 720 AA.
DE Human PRO1344 protein SEQ ID NO:38.
PN US2006008901-A1.
PD 12-JAN-2006.
PA (GERTH) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 10; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 667
ID AEF74253 standard; protein; 720 AA.
DE Human PRO1344 protein SEQ ID NO:38.
PN US2005260647-A1.
PD 24-NOV-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W L.
Query Match 100.0%; Score 3945; DB 10; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.8e-204;
RESULT 668
ID AAB70532 standard; protein; 720 AA.
DE Human PRO2 protein sequence SEQ ID NO:4.
PN WO200110902-A2.
PD 15-FEB-2001.
PA (CURA-) CURAGEN CORP.
Query Match 99.8%; Score 3939; DB 4; Length 720;
Best Local Similarity 99.7%; Pred. No. 3.8e-204;
RESULT 669
ID AAU00401 standard; protein; 720 AA.
DE Human secreted protein, POLY13.
PN WO200119856-A2.
PD 22-MAR-2001.
PA (CURA-) CURAGEN CORP.
Query Match 99.8%; Score 3939; DB 4; Length 720;
Best Local Similarity 99.7%; Pred. No. 3.8e-204;
RESULT 670
ID ADH69028 standard; protein; 720 AA.
DE Human POLYX polypeptide #13.
PN US200319858-A1.
PD 23-OCT-2003.
PA (SHIM/) SHIMKETS R A.
PA (FERN/) FERNANDES E.
PA (HERR/) HERRMANN J L.
PA (LUX/) LUX X.

PA (YANG/) YANG M.
PA (BOLD/) BOLDOG F L.
PA (SMIT/) SMITHSON G.
PA (RAST/) RASTELLI L.
Query Match 99.8%; Score 3939; DB 8; Length 720;
Best Local Similarity 99.7%; Pred. No. 3.8e-204;
RESULT 671
ID AAY68280 standard; protein; 720 AA.
DE Human TANGO 215 protein.
PN WO200018904-A2.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 99.8%; Score 3936; DB 3; Length 720;
Best Local Similarity 99.7%; Pred. No. 5.5e-204;
RESULT 672
ID ADY60612 standard; protein; 737 AA.
DE Human regeneration-associated muscle protease enzyme - SEQ ID 2.
PN JP2005073574-A.
PD 24-MAR-2005.
PA (TOKR-) ZH TOKYOTO RINSHO IGAKU SOGO KENKYUSHO.
Query Match 99.5%; Score 3926.5; DB 9; Length 737;
Best Local Similarity 97.7%; Pred. No. 1.8e-203;
RESULT 673
ID AAB85891 standard; protein; 737 AA.
DE Human serine protease-like protein (hc-PLACE1009992).
PN WO200109349-A1.
PD 08-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 99.4%; Score 3921.5; DB 4; Length 737;
Best Local Similarity 97.6%; Pred. No. 3.4e-203;
RESULT 674
ID AAB93670 standard; protein; 737 AA.
DE Human protein sequence SEQ ID NO:13202.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 99.4%; Score 3921.5; DB 4; Length 737;
Best Local Similarity 97.6%; Pred. No. 3.4e-203;
RESULT 675
ID ADI69990 standard; protein; 737 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1796.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 99.4%; Score 3921.5; DB 7; Length 737;
Best Local Similarity 97.6%; Pred. No. 3.4e-203;
RESULT 676
ID ADN04640 standard; protein; 737 AA.
DE Antipsoriatic protein sequence #505.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GERTH) GENENTECH INC.
Query Match 99.4%; Score 3921.5; DB 8; Length 737;
Best Local Similarity 97.6%; Pred. No. 3.4e-203;
RESULT 677
ID ADS85034 standard; protein; 737 AA.
DE Human atopic dermatitis-related protein sequence SeqID36.
PN WO2004031386-A1.
PD 15-APR-2004.
PA (GENO-) GENOX RES INC.
PA (UYJU-) UNIV JUJUNENDO.
Query Match 99.4%; Score 3921.5; DB 8; Length 737;
Best Local Similarity 97.6%; Pred. No. 3.4e-203;
RESULT 678
ID ADS85022 standard; protein; 737 AA.
DE Human atopic dermatitis-related protein sequence SeqID24.
PN WO2004031386-A1.
PD 15-APR-2004.
PA (GENO-) GENOX RES INC.
PA (UYJU-) UNIV JUJUNENDO.
Query Match 99.4%; Score 3921.5; DB 8; Length 737;
Best Local Similarity 97.6%; Pred. No. 3.4e-203;

RESULT 679
ID AAB85893 standard; protein; 762 AA.
DE Human serine protease-like protein (NC-PLACE1009992).
PN WO200109349-A1.
PD 08-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 99.4%; Score 3921.5; DB 4; Length 762;
Best Local Similarity 97.6%; Pred. No. 3.5e-203;
RESULT 680
ID ADY80614 standard; protein; 720 AA.
DE Mouse regeneration-associated muscle protease enzyme - SEQ ID 4.
PN JP2005073574-A.
PD 24-MAR-2005.
PA (TOKR-) ZH TOKYOTO RINSHO IGAKU SOGO KENKYUSHO.
Query Match 91.7%; Score 3617; DB 9; Length 720;
Best Local Similarity 90.3%; Pred. No. 8.3e-187;
RESULT 681
ID AAB85892 standard; protein; 720 AA.
DE Mouse serine protease-like protein (NC-PLACE1009992).
PN WO200109349-A1.
PD 08-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 91.6%; Score 3612; DB 4; Length 720;
Best Local Similarity 90.1%; Pred. No. 1.5e-186;
RESULT 682
ID AAB09927 standard; protein; 719 AA.
DE Murine TANGO 215 protein.
PN WO200018904-A2.
PD 06-APR-2000.
PA (MILL-) MILLENNium BIOTHERAPEUTICS INC.
Query Match 91.3%; Score 3602.5; DB 3; Length 719;
Best Local Similarity 90.1%; Pred. No. 5e-186;
RESULT 683
ID AAE19180 standard; protein; 649 AA.
DE Human protease, PRIS-17 protein.
PN WO200208396-A2.
PD 31-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 88.7%; Score 3500.5; DB 5; Length 649;
Best Local Similarity 90.0%; Pred. No. 1.4e-180;
RESULT 684
ID AAB70531 standard; protein; 567 AA.
DE Human PRO1 protein sequence SEQ ID NO:2.
PN WO200110902-A2.
PD 15-FEB-2001.
PA (CURA-) CURAGEN CORP.
Query Match 78.3%; Score 3089.5; DB 4; Length 567;
Best Local Similarity 99.5%; Pred. No. 1.7e-158;
RESULT 685
ID AAB49533 standard; protein; 570 AA.
DE Clone HEPPEY75.
PN WO200061774-A2.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 74.7%; Score 2946.5; DB 3; Length 570;
Best Local Similarity 96.8%; Pred. No. 8.7e-151;
RESULT 686
ID ADR41485 standard; protein; 551 AA.
DE Human CD-like molecule HSDXF41, SEQ ID NO:284.
PN WO200226930-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 74.6%; Score 2944; DB 5; Length 551;
Best Local Similarity 99.3%; Pred. No. 1.2e-150;
RESULT 687
ID AAM41706 standard; protein; 499 AA.
DE Human polypeptide SEQ ID NO 6637.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 65.3%; Score 2577.5; DB 4; Length 499;
Best Local Similarity 96.6%; Pred. No. 5.8e-131;
RESULT 688

ID AAE20817 standard; protein; 455 AA.
DE Human gene 5 encoded secreted protein HSLGU75, SEQ ID NO:79.
PN WO200218435-A1.
PD 07-MAR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 61.2%; Score 2413; DB 5; Length 455;
Best Local Similarity 99.3%; Pred. No. 3.9e-122;
RESULT 689
ID ABG64652 standard; protein; 455 AA.
DE Human albumin fusion protein #1327.
PN WO20017137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 61.2%; Score 2413; DB 5; Length 455;
Best Local Similarity 99.3%; Pred. No. 3.9e-122;
RESULT 690
ID ADL77919 standard; protein; 455 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1401.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 61.2%; Score 2413; DB 8; Length 455;
Best Local Similarity 99.3%; Pred. No. 3.9e-122;
RESULT 691
ID ADL06662 standard; protein; 417 AA.
DE Human 3T3 cell conversion promoter FP938.
PN CN1403477-A.
PD 19-MAR-2003.
PA (SHAN-) SHANGHAI XINSHIJI GENE TECHN DEV CO LTD.
Query Match 52.2%; Score 2059; DB 7; Length 417;
Best Local Similarity 95.6%; Pred. No. 4.2e-103;
RESULT 692
ID AAM39920 standard; protein; 359 AA.
DE Human polypeptide SEQ ID NO 3065.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 48.4%; Score 1909; DB 4; Length 359;
Best Local Similarity 100.0%; Pred. No. 4.4e-95;
RESULT 693
ID AAM39957 standard; protein; 359 AA.
DE Human polypeptide SEQ ID NO 3102.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 48.4%; Score 1909; DB 4; Length 359;
Best Local Similarity 100.0%; Pred. No. 4.4e-95;
RESULT 694
ID AAE20797 standard; protein; 323 AA.
DE Human gene 5 encoded secreted protein HSLGU75, SEQ ID NO:59.
PN WO200218435-A1.
PD 07-MAR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 43.3%; Score 1708.5; DB 5; Length 323;
Best Local Similarity 94.1%; Pred. No. 2.5e-84;
RESULT 695
ID ABG64653 standard; protein; 323 AA.
DE Human albumin fusion protein #1328.
PN WO20017137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 43.3%; Score 1708.5; DB 5; Length 323;
Best Local Similarity 94.1%; Pred. No. 2.5e-84;
RESULT 696
ID ADL77920 standard; protein; 323 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1402.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 43.3%; Score 1708.5; DB 8; Length 323;
Best Local Similarity 94.1%; Pred. No. 2.5e-84;

RESULT 697
ID AAM24485 standard; protein; 234 AA.
DE Human EST encoded protein seq ID NO: 2010.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 29.8%; Score 1175.5; DB 4; Length 234;
Best Local Similarity 91.4%; Pred. No. 9.5e-56;
RESULT 698
ID ABP72332 standard; protein; 1019 AA.
DE Horseshoe crab Factor C.
PN WO2003002976-A2.
PD 09-JAN-2003.
PA (WHIK) BIOMHITTAKER INC.
Query Match 17.0%; Score 672; DB 6; Length 1019;
Best Local Similarity 25.6%; Pred. No. 4.9e-28;
RESULT 699
ID AAM3394 standard; protein; 1019 AA.
DE Singapore horseshoe crab factor C proenzyme (CrFC 21) .
PN SG42456-A1.
PD 15-AUG-1997.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 2; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.2e-27;
RESULT 700
ID AAY05750 standard; protein; 1019 AA.
DE Horseshoe crab Factor C.
PN WO9915676-A1.
PD 01-APR-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 2; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.2e-27;
RESULT 701
ID AAM94302 standard; protein; 1019 AA.
DE Horseshoe crab Factor C protein #2.
PN US5858706-A.
PD 12-JAN-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 2; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.2e-27;
RESULT 702
ID AAY42490 standard; protein; 1019 AA.
DE Recombinant N-terminally truncated Horseshoe crab Factor C protein.
PN US5985590-A.
PD 16-NOV-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 3; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.2e-27;
RESULT 703
ID AAB60935 standard; protein; 1019 AA.
DE Horseshoe crab recombinant Factor C #2.
PN WO200127289-A2.
PD 19-APR-2001.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 4; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.2e-27;
RESULT 704
ID ABP72334 standard; protein; 1019 AA.
DE Horseshoe crab Factor C.
PN WO2003002976-A2.
PD 09-JAN-2003.
PA (WHIK) BIOMHITTAKER INC.
Query Match 16.9%; Score 665; DB 6; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.2e-27;
RESULT 705
ID ADM39099 standard; protein; 1019 AA.
DE Southeast Asian horseshoe crab Factor C.
PN WO2005003163-A1.
PD 13-JAN-2005.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 9; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.2e-27;
RESULT 706

ID AAM3393 standard; protein; 1083 AA.
DE Singapore horseshoe crab factor C proenzyme (CrFC 26) .
PN SG42456-A1.
PD 15-AUG-1997.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 2; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1.2e-27;
RESULT 707
ID AAY05749 standard; protein; 1083 AA.
DE Horseshoe crab Factor C.
PN WO9915676-A1.
PD 01-APR-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 2; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1.2e-27;
RESULT 708
ID AAM94301 standard; protein; 1083 AA.
DE Horseshoe crab Factor C protein #1.
PN US5858706-A.
PD 12-JAN-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 2; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1.2e-27;
RESULT 709
ID AAY42489 standard; protein; 1083 AA.
DE Horseshoe crab recombinant Factor C protein.
PN US5985590-A.
PD 16-NOV-1999.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 3; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1.2e-27;
RESULT 710
ID AAB60934 standard; protein; 1083 AA.
DE Horseshoe crab recombinant Factor C #1.
PN WO200127289-A2.
PD 19-APR-2001.
PA (UYSI-) UNIV SINGAPORE NAT.
Query Match 16.9%; Score 665; DB 4; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1.2e-27;
RESULT 711
ID ABP72333 standard; protein; 1083 AA.
DE Horseshoe crab Factor C.
PN WO2003002976-A2.
PD 09-JAN-2003.
PA (WHIK) BIOMHITTAKER INC.
Query Match 16.9%; Score 665; DB 6; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1.2e-27;
RESULT 712
ID AAM41743 standard; protein; 146 AA.
DE Human polypeptide SRQ ID NO 6674.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 16.8%; Score 662; DB 4; Length 146;
Best Local Similarity 85.4%; Pred. No. 2.8e-28;
RESULT 713
ID AAY11743 standard; protein; 103 AA.
DE Human 5' EST secreted protein SEQ ID NO: 343.
PN WO9906550-A2.
PD 11-FEB-1999.
PA (GBST) GENSET.
Query Match 14.7%; Score 580; DB 2; Length 103;
Best Local Similarity 97.1%; Pred. No. 5.3e-24;
RESULT 714
ID AEP13693 standard; protein; 699 AA.
DE Human MBL-associated serine protease 1 (MASP-1) protein.
PN WO2005123776-A1.
PD 29-DEC-2005.
PA (OMER-) OMEROS CORP.
Query Match 12.1%; Score 478; DB 10; Length 699;
Best Local Similarity 24.6%; Pred. No. 9.8e-18;
RESULT 715

ID AEB26839 standard; protein; 680 AA.
DE Human MASP-1 protein, SEQ ID NO: 6 #2.
PN US2005158297-A1.
PD 21-JUL-2005.
PA (JENS//) JENSENIUS J C.
PA (THIE//) THIEL S.
Query Match 12.1%; Score 476; DB 9; Length 680;
Best Local Similarity 24.6%; Pred. No. 1.2e-17;
RESULT 716
ID ADE87459 standard; protein; 699 AA.
DE Human MBL-associated serine protease-1 protein.
PN EP1344533-A1.
PD 17-SEP-2003.
PA (NATI-) NATIMMUNE AS.
Query Match 12.1%; Score 476; DB 7; Length 699;
Best Local Similarity 24.6%; Pred. No. 1.3e-17;
RESULT 717
ID ADJ91028 standard; protein; 699 AA.
DE Human mannosyl binding lectin amino acid sequence SEQ ID NO:14.
PN WO2004024925-A2.
PD 25-MAR-2004.
PA (NATI-) NATIMMUNE AS.
Query Match 12.0%; Score 475; DB 8; Length 699;
Best Local Similarity 24.6%; Pred. No. 1.4e-17;
RESULT 718
ID AEM83722 standard; protein; 698 AA.
DE Human diagnostic and therapeutic protein SEQ ID NO:3971.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 12.0%; Score 474.5; DB 8; Length 698;
Best Local Similarity 24.4%; Pred. No. 1.5e-17;
RESULT 719
ID AAB85060 standard; protein; 728 AA.
DE Human serine protease MASP-3 polypeptide.
PN WO200140451-A2.
PD 07-JUN-2001.
PA (JENS//) JENSENIUS J C.
PA (THIE//) THIEL S.
Query Match 11.9%; Score 471; DB 4; Length 728;
Best Local Similarity 25.0%; Pred. No. 2.4e-17;
RESULT 720
ID AEB26835 standard; protein; 679 AA.
DE Human MASP-1 protein, SEQ ID NO: 6 #1.
PN US2005158297-A1.
PD 21-JUL-2005.
PA (JENS//) JENSENIUS J C.
PA (THIE//) THIEL S.
Query Match 11.9%; Score 469.5; DB 9; Length 679;
Best Local Similarity 24.4%; Pred. No. 2.7e-17;
RESULT 721
ID ADE87461 standard; protein; 728 AA.
DE Human MBL-associated serine protease-4 protein.
PN EP1344533-A1.
PD 17-SEP-2003.
PA (NATI-) NATIMMUNE AS.
Query Match 11.9%; Score 468; DB 7; Length 728;
Best Local Similarity 25.0%; Pred. No. 3.5e-17;
RESULT 722
ID ADJ91027 standard; protein; 728 AA.
DE Human mannosyl binding lectin amino acid sequence SEQ ID NO:13.
PN WO2004024925-A2.
PD 25-MAR-2004.
PA (NATI-) NATIMMUNE AS.
Query Match 11.9%; Score 468; DB 8; Length 728;
Best Local Similarity 25.0%; Pred. No. 3.5e-17;
RESULT 723
ID AAB47559 standard; protein; 728 AA.
DE Protease PRS-1.
PN WO200171004-A2.
PD 27-SEP-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 11.7%; Score 461; DB 4; Length 728;

Best Local Similarity 24.9%; Pred. No. 8.4e-17;
RESULT 724
ID AAG80756 standard; protein; 707 AA.
DE Murine C1r protein.
PN KR200107614-A.
PD 20-AUG-2001.
PA (BIOC-) BIO CLUE & SOLUTION CO LTD.
PA (KIMT/) KIM T Y.
Query Match 10.9%; Score 429; DB 5; Length 707;
Best Local Similarity 22.3%; Pred. No. 4.3e-15;
RESULT 725
ID AEF03476 standard; protein; 670 AA.
DE Mature rat MASP-2.
PN WO2005123128-A2.
PD 29-DEC-2005.
PA (OMER-) OMEROS CORP.
PA (UYLE-) UNIV LEICESTER.
Query Match 10.7%; Score 423; DB 10; Length 670;
Best Local Similarity 24.1%; Pred. No. 8.6e-15;
RESULT 726
ID AEF03475 standard; protein; 685 AA.
DE Full length rat MASP-2.
PN WO2005123128-A2.
PD 29-DEC-2005.
PA (OMER-) OMEROS CORP.
PA (UYLE-) UNIV LEICESTER.
Query Match 10.7%; Score 423; DB 10; Length 685;
Best Local Similarity 24.1%; Pred. No. 8.8e-15;
RESULT 727
ID AEF03473 standard; protein; 670 AA.
DE Mature murine MASP-2.
PN WO2005123128-A2.
PD 29-DEC-2005.
PA (OMER-) OMEROS CORP.
PA (UYLE-) UNIV LEICESTER.
Query Match 10.4%; Score 412; DB 10; Length 670;
Best Local Similarity 21.4%; Pred. No. 3.4e-14;
RESULT 728
ID AEF03472 standard; protein; 685 AA.
DE Full length murine MASP-2.
PN WO2005123128-A2.
PD 29-DEC-2005.
PA (OMER-) OMEROS CORP.
PA (UYLE-) UNIV LEICESTER.
Query Match 10.4%; Score 412; DB 10; Length 685;
Best Local Similarity 21.4%; Pred. No. 3.5e-14;
RESULT 729
ID AEB26836 standard; protein; 688 AA.
DE Human C1r-associated serine protease, C1r SEQ ID NO: 7.
PN US2005158297-A1.
PD 21-JUL-2005.
PA (JENS//) JENSENIUS J C.
PA (THIE//) THIEL S.
Query Match 10.2%; Score 403.5; DB 9; Length 688;
Best Local Similarity 22.9%; Pred. No. 9.9e-14;
RESULT 730
ID ABB50288 standard; protein; 705 AA.
DE Complement component 1 r ovarian tumour marker protein, SEQ ID NO:66.
PN WO20017517-A2.
PD 11-OCT-2001.
PA (USSH-) US DBPT HEALTH & HUMAN SERVICES.
Query Match 10.2%; Score 403.5; DB 4; Length 705;
Best Local Similarity 22.9%; Pred. No. 1e-13;
RESULT 731
ID AAG80757 standard; protein; 705 AA.
DE Human C1r protein.
PN KR200107614-A.
PD 20-AUG-2001.
PA (BIOC-) BIO CLUE & SOLUTION CO LTD.
PA (KIMT/) KIM T Y.
Query Match 10.2%; Score 403.5; DB 5; Length 705;
Best Local Similarity 22.9%; Pred. No. 1e-13;
RESULT 732

ID ADP65211 standard; protein; 705 AA.
DE Human complement component 1, r subcomponent.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
ID AEB26831 standard; protein; 686 AA.
DE Human mannan binding lectin-associated serine protease-2, SEQ ID NO: 2.
PN US2005158297-A1.
PD 21-JUL-2005.
PA (JENS/) JENSENIUS J C.
PA (THIE/) THIEL S.
Query Match 10.2%; Score 401.5; DB 9; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.3e-13;
RESULT 743
ID AEB13349 standard; protein; 705 AA.
DE Complement component C1r SEQ ID NO 14.
PN WO2005061537-A2.
PD 07-JUL-2005.
PA (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEIT.
PA (VAEC-) VAECGENE BIOTECH GMBH.
Query Match 10.2%; Score 403.5; DB 9; Length 705;
Best Local Similarity 22.9%; Pred. No. 1e-13;
RESULT 734
ID AED74704 standard; protein; 705 AA.
DE Human placental protein SEQ ID NO:1532.
PN US2005255114-A1.
PD 17-NOV-2005.
PA (NUVE-) NUVELO INC.
Query Match 10.2%; Score 403.5; DB 9; Length 705;
Best Local Similarity 22.9%; Pred. No. 1e-13;
RESULT 735
ID ADU18123 standard; protein; 704 AA.
DE Human candidate osteoarthritis marker protein - SEQ ID 154.
PN WO2004092413-A2.
PD 28-OCT-2004.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS PHARMA GMBH.
Query Match 10.2%; Score 403; DB 8; Length 704;
Best Local Similarity 22.5%; Pred. No. 1.1e-13;
RESULT 736
ID ABG31619 standard; protein; 686 AA.
DE Human mannan-binding lectin associated serine protease-2 protein.
PN US2002082208-A1.
PD 27-JUN-2002.
PA (JENS/) JENSENIUS J C.
PA (THIE/) THIEL S.
Query Match 10.2%; Score 401.5; DB 5; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.3e-13;
RESULT 737
ID AAB14564 standard; protein; 686 AA.
DE Human MASP-2 protein.
PN WO200206460-A2.
PD 24-JAN-2002.
PA (JENS/) JENSENIUS J C.
PA (THIE/) THIEL S.
Query Match 10.2%; Score 401.5; DB 5; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.3e-13;
RESULT 738
ID ABG32115 standard; protein; 686 AA.
DE Mannan-binding lectin associated serine protease-2 (MASP-2).
PN US2002082209-A1.
PD 27-JUN-2002.
PA (JENS/) JENSENIUS J C.
PA (THIE/) THIEL S.
Query Match 10.2%; Score 401.5; DB 5; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.3e-13;
RESULT 739
ID ADL91025 standard; protein; 686 AA.
DE Human mannosid binding lectin amino acid sequence SEQ ID NO:11.
PN WO2004024925-A2.
PD 25-MAR-2004.
PA (NATI-) NATIMMUNE AS.
Query Match 10.2%; Score 401.5; DB 8; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.3e-13;
RESULT 740
ID AEA17053 standard; protein; 686 AA.
DE Alzheimer's disease associated protein #6.
PN US2005123962-A1.
PD 09-JUN-2005.

PA (AGYT-) AGY THERAPEUTICS INC.
Query Match 10.2%; Score 401.5; DB 9; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.3e-13;
RESULT 741
ID AEB26831 standard; protein; 686 AA.
DE Human mannan binding lectin-associated serine protease-2, SEQ ID NO: 2.
PN US2005158297-A1.
PD 21-JUL-2005.
PA (JENS/) JENSENIUS J C.
PA (THIE/) THIEL S.
Query Match 10.2%; Score 401.5; DB 9; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.3e-13;
RESULT 742
ID AEP03426 standard; protein; 686 AA.
DE Full length MASP-2.
PN WO2005123128-A2.
PD 29-DEC-2005.
PA (OMER-) OMEROS CORP.
PA (UYLE-) UNIV LEICESTER.
Query Match 10.2%; Score 401.5; DB 10; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.3e-13;
RESULT 743
ID AEF13655 standard; protein; 686 AA.
DE Human MBL-associated serine protease 2 (MASP-2) protein.
PN WO2005123776-A1.
PD 29-DEC-2005.
PA (OMER-) OMEROS CORP.
PA (UYLE-) UNIV LEICESTER.
Query Match 10.2%; Score 401.5; DB 10; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.3e-13;
RESULT 744
ID AAB14568 standard; protein; 686 AA.
DE Human MASP-2 protein, alternative version.
PN WO200206460-A2.
PD 24-JAN-2002.
PA (JENS/) JENSENIUS J C.
PA (THIE/) THIEL S.
Query Match 10.2%; Score 400.5; DB 5; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.4e-13;
RESULT 745
ID ADE87460 standard; protein; 686 AA.
DE Human MBL-associated serine protease-2 protein.
PN EP1344533-A1.
PD 17-SEP-2003.
PA (NATI-) NATIMMUNE AS.
Query Match 10.2%; Score 400.5; DB 7; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.4e-13;
RESULT 746
ID ADV50598 standard; protein; 686 AA.
DE Human mannan-binding lectin serine protease 2 (MASP2) protein.
PN WO2004106384-A1.
PD 09-DEC-2004.
PA (NATI-) NATIMMUNE AS.
Query Match 10.2%; Score 400.5; DB 9; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.4e-13;
RESULT 747
ID ADY62954 standard; protein; 686 AA.
DE human mitogen activated serine protease-2 (MASP-2).
PN WO2005024013-A1.
PD 17-MAR-2005.
PA (NATI-) NATIMMUNE AS.
Query Match 10.2%; Score 400.5; DB 9; Length 686;
Best Local Similarity 22.7%; Pred. No. 1.4e-13;
RESULT 748
ID ADQ27010 standard; protein; 671 AA.
DE Human MASP-2 mature polypeptide.
PN WO2004050907-A2.
PD 17-JUN-2004.
PA (UYAA-) UNIV AARHUS.
PA (AARH) AARHUS AMT.
Query Match 10.1%; Score 399.5; DB 8; Length 671;
Best Local Similarity 22.8%; Pred. No. 1.6e-13;
RESULT 749

ID AEB26838 standard; protein; 671 AA.
DE Human mature MASP-2 protein (residues 16-686).
PN US2005158297-A1.
PD 21-JUL-2005.
PA (JENS//) JENSENIUS J C.
PA (THIE//) THIEL S.
Query Match 10.1%; Score 399.5; DB 9; Length 671;
Best Local Similarity 22.8%; Pred. No. 1.6e-13;
RESULT 750
ID AEF03427 standard; protein; 671 AA.
DE Mature MASP-2.
PN WO2005123128-A2.
PD 29-DEC-2005.
PA (OMER-) OMEROS CORP.
PA (UYLE-) UNIV LEICESTER.
Query Match 10.1%; Score 399.5; DB 10; Length 671;
Best Local Similarity 22.8%; Pred. No. 1.6e-13;
RESULT 751
ID AEF13656 standard; protein; 671 AA.
DE Human MBL-associated serine protease 2 (MASP-2) mature protein.
PN WO200512376-A1.
PD 29-DEC-2005.
PA (OMER-) OMEROS CORP.
PA (UYLE-) UNIV LEICESTER.
Query Match 10.1%; Score 399.5; DB 10; Length 671;
Best Local Similarity 22.8%; Pred. No. 1.6e-13;
RESULT 752
ID AAE14565 standard; peptide; 671 AA.
DE Human mature MASP-2 protein.
PN WO200206460-A2.
PD 24-JAN-2002.
PA (JENS//) JENSENIUS J C.
PA (THIE//) THIEL S.
Query Match 10.1%; Score 398.5; DB 5; Length 671;
Best Local Similarity 22.8%; Pred. No. 1.8e-13;
RESULT 753
ID AEC95282 standard; protein; 604 AA.
DE Enteropeptidase, SEQ ID 5.
PN JP2005253325-A.
PD 22-SEP-2005.
PA (UYHO-) UNIV HOKKAIDO.
Query Match 9.4%; Score 369.5; DB 9; Length 604;
Best Local Similarity 24.3%; Pred. No. 6e-12;
RESULT 754
ID AEC95280 standard; protein; 1036 AA.
DE Enteropeptidase, SEQ ID 3.
PN JP2005253325-A.
PD 22-SEP-2005.
PA (UYHO-) UNIV HOKKAIDO.
Query Match 9.4%; Score 369.5; DB 9; Length 1036;
Best Local Similarity 24.3%; Pred. No. 9.9e-12;
RESULT 755
ID ADX26355 standard; protein; 694 AA.
DE Novel cell pain response detection method-related mouse protein SeqID701.
PN WO2005014849-A2.
PD 17-FEB-2005.
PA (EURO-) EUROCELTIQUE SA.
Query Match 9.2%; Score 364; DB 9; Length 694;
Best Local Similarity 22.1%; Pred. No. 1.3e-11;
RESULT 756
ID ADE56422 standard; protein; 694 AA.
DE Rat Protein BAA25797, SEQ ID NO 2275.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 8.6%; Score 340.5; DB 7; Length 694;
Best Local Similarity 21.2%; Pred. No. 2.5e-10;
RESULT 757
ID ADE83526 standard; protein; 694 AA.
DE Rat Protein BAA25797, SEQ ID NO 11123.
PN WO2003016475-A2.
PD 27-FEB-2003.

PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 8.6%; Score 340.5; DB 7; Length 694;
Best Local Similarity 21.2%; Pred. No. 2.5e-10;
RESULT 758
ID ADX26430 standard; protein; 694 AA.
DE Novel cell pain response detection method-related rat protein SeqID776.
PN WO2005014849-A2.
PD 17-FEB-2005.
PA (EURO-) EUROCELTIQUE SA.
Query Match 8.6%; Score 340.5; DB 9; Length 694;
Best Local Similarity 21.2%; Pred. No. 2.5e-10;
RESULT 759
ID ADE56418 standard; protein; 695 AA.
DE Rat Protein D88250, SEQ ID NO 2271.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 8.6%; Score 340.5; DB 7; Length 695;
Best Local Similarity 21.2%; Pred. No. 2.5e-10;
RESULT 760
ID ADD45338 standard; protein; 695 AA.
DE Rat Protein D88250, SEQ ID NO 10771.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 8.6%; Score 340.5; DB 7; Length 695;
Best Local Similarity 21.2%; Pred. No. 2.5e-10;
RESULT 761
ID AAB43579 standard; protein; 760 AA.
DE Human cancer associated protein sequence SEQ ID NO:1024.
PN WO200505350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.5%; Score 336; DB 3; Length 760;
Best Local Similarity 21.7%; Pred. No. 4.7e-10;
RESULT 762
ID AEB26837 standard; protein; 673 AA.
DE Human C1q-associated serine protease, C1s SEQ ID NO: 8.
PN US2005158297-A1.
PD 21-JUL-2005.
PA (JENS//) JENSENIUS J C.
PA (THIE//) THIEL S.
Query Match 8.5%; Score 334; DB 9; Length 673;
Best Local Similarity 21.7%; Pred. No. 5.4e-10;
RESULT 763
ID ADD45340 standard; protein; 688 AA.
DE Human Protein Q9UCV3, SEQ ID NO 10773.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 8.5%; Score 334; DB 7; Length 688;
Best Local Similarity 21.7%; Pred. No. 5.5e-10;
RESULT 764
ID ADE56420 standard; protein; 688 AA.
DE Human Protein Q9UCV3, SEQ ID NO 2273.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 8.5%; Score 334; DB 7; Length 688;
Best Local Similarity 21.7%; Pred. No. 5.5e-10;
RESULT 765
ID ADE65315 standard; protein; 688 AA.
DE Human complement c1s component precursor (c1 esterase).
PN WO200307827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 8.5%; Score 334; DB 7; Length 688;
Best Local Similarity 21.7%; Pred. No. 5.5e-10;

RESULT 766
ID ADJ5392 standard; protein; 688 AA.
DE Marker gene related amino acid sequence SEQ ID NO:644.
PN EPI394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match
Best Local Similarity 8.5%; Score 334; DB 8; Length 688;
Pred. No. 5.5e-10;
RESULT 767
ID ADJ1020 standard; protein; 688 AA.
DE Human mannose binding lectin amino acid sequence SEQ ID NO:6.
PN WO2004024925-A2.
PD 25-MAR-2004.
PA (NATI-) NATIMUNE AS.
Query Match
Best Local Similarity 8.5%; Score 334; DB 8; Length 688;
Pred. No. 5.5e-10;
RESULT 768
ID ABM61337 standard; protein; 688 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO2660, SEQ:3453.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 8.5%; Score 334; DB 8; Length 688;
Pred. No. 5.5e-10;
RESULT 769
ID ADU06459 standard; protein; 688 AA.
DE Novel bronchial cancer-associated human protein SeqID683.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
Query Match
Best Local Similarity 8.5%; Score 334; DB 8; Length 688;
Pred. No. 5.5e-10;
RESULT 770
ID ADX6285 standard; protein; 688 AA.
DE Novel cell pain response detection method-related human protein SeqID631.
PN WO2005014849-A2.
PD 17-FEB-2005.
PA (EURO-) EUROCELTICUE SA.
Query Match
Best Local Similarity 8.5%; Score 334; DB 9; Length 688;
Pred. No. 5.5e-10;
RESULT 771
ID ADZ80432 standard; protein; 688 AA.
DE Mature complement C1s (C1 esterase) SEQ ID NO 45.
PN WO2005040422-A2.
PD 06-MAY-2005.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS PHARMA GMBH.
Query Match
Best Local Similarity 8.5%; Score 334; DB 9; Length 688;
Pred. No. 5.5e-10;
RESULT 772
ID AED74705 standard; protein; 688 AA.
DE Human placental protein SEQ ID NO:1533.
PN US2005255114-A1.
PD 17-NOV-2005.
PA (NUVE-) NUVELO INC.
Query Match
Best Local Similarity 8.5%; Score 334; DB 9; Length 688;
Pred. No. 5.5e-10;
RESULT 773
ID ADI16884 standard; protein; 855 AA.
DE Human NOVX protein homologue SeqID 420.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 8.4%; Score 332; DB 5; Length 855;
Pred. No. 8.6e-10;
RESULT 774
ID ADI16818 standard; protein; 855 AA.
DE Human NOVX protein homologue SeqID 354.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.

Query Match
Best Local Similarity 8.4%; Score 332; DB 5; Length 855;
Pred. No. 8.6e-10;
RESULT 775
ID AEF27702 standard; protein; 855 AA.
DE Human prostetamin, SEQ:132.
PN US2006009634-A1.
PD 12-JAN-2006.
PA (KEKU/) KEKUDA R.
PA (ALSO/) ALSOBROOK J.
PA (TCHE/) TCHERNEV V.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTER K.
PA (PATT/) PATTERJUN M.
PA (GROS/) GROSSE W.
PA (LEPL/) LEPLER D.
PA (BURG/) BURGESS C.
PA (VERN/) VERNET C.
PA (LILL/) LI L.
PA (GORM/) GORMAN L.
PA (EDIN/) EDINGER S.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (WALT/) WALYANKAR U.
PA (ROTH/) ROTHENBERG M.
PA (STON/) STONE D.
PA (BOLD/) BOLDOLF F.
PA (GUOX/) GUO X.
PA (SHEN/) SHENOV S.
PA (ANDE/) ANDERSON D.
PA (PADI/) PADIGARU M.
PA (TAUP/) TAUPIER R.
PA (MILL/) MILLER C.
PA (EISE/) EISEN A.
Query Match
Best Local Similarity 8.4%; Score 332; DB 10; Length 855;
Pred. No. 8.6e-10;
RESULT 776
ID AAE06940 standard; protein; 1019 AA.
DE Human enterokinase protein.
PN WO200157194-A2.
PD 09-AUG-2001.
PA (CORV-) CORVAS INT INC.
Query Match
Best Local Similarity 8.4%; Score 331.5; DB 4; Length 1019;
Pred. No. 1.1e-09;
RESULT 777
ID ADA83985 standard; protein; 1019 AA.
DE Human PRSS7 protein.
PN WO2002103028-A2.
PD 27-DEC-2002.
PA (BIOM-) BIOMEDICAL CENT.
Query Match
Best Local Similarity 8.4%; Score 331.5; DB 6; Length 1019;
Pred. No. 1.1e-09;
RESULT 778
ID ADI10400 standard; protein; 1019 AA.
DE Human cell surface protease #16.
PN WO200295007-A2.
PD 28-NOV-2002.
PA (CORV-) CORVAS INT INC.
Query Match
Best Local Similarity 8.4%; Score 331.5; DB 7; Length 1019;
Pred. No. 1.1e-09;
RESULT 779
ID ADU46924 standard; protein; 1019 AA.
DE Human transmembrane serine protease (MTSP)-related polypeptide #6.
PN US2004001801-A1.
PD 01-JAN-2004.
PA (CORV-) CORVAS INT INC.
Query Match
Best Local Similarity 8.4%; Score 331.5; DB 8; Length 1019;
Pred. No. 1.1e-09;
RESULT 780
ID ADU70437 standard; protein; 1019 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID2243.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.

PA (BUCK-) BUCK INST AGE RES.
Query Match 8.4%; Score 330.5; DB 7; Length 1019;
Best Local Similarity 22.9%; Pred. No. 1.2e-09;
RESULT 781
ID ADJ70480 standard; protein; 3389 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID2286.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 8.4%; Score 329.5; DB 7; Length 3389;
Best Local Similarity 20.8%; Pred. No. 4.3e-09;
RESULT 782
ID AEE02790 standard; protein; 3566 AA.
DE Human S-100 beta binding protein, SEQ ID NO:33.
PN WO2005106473-A1.
PD 10-NOV-2005.
PA (ONOV) ONO PHARM CO LTD.
Query Match 8.4%; Score 329.5; DB 9; Length 3566;
Best Local Similarity 20.8%; Pred. No. 4.5e-09;
RESULT 783
ID ADH72216 standard; protein; 3567 AA.
DE Human protein of the invention NOV54b SEQ ID NO:1112.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.4%; Score 329.5; DB 8; Length 3567;
Best Local Similarity 20.8%; Pred. No. 4.5e-09;
RESULT 784
ID AAR13623 standard; protein; 460 AA.
DE Human protein C zymogen SC.
PN EP443875-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.
Query Match 8.3%; Score 329; DB 2; Length 460;
Best Local Similarity 25.5%; Pred. No. 7e-10;
RESULT 785
ID ABG76507 standard; protein; 1274 AA.
DE DNA encoding protein modification and maintenance molecule #11.
PN WO200260942-A2.
PD 08-AUG-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 8.3%; Score 328.5; DB 5; Length 1274;
Best Local Similarity 20.8%; Pred. No. 1.9e-09;
RESULT 786
ID AAU11815 standard; protein; 1783 AA.
DE Cancer and neurogenesis associated gene, variant 5G-3V3.
PN WO200190354-A1.
PD 29-NOV-2001.
PA (UTLE-) UNIV LEEDS.
Query Match 8.3%; Score 328.5; DB 5; Length 1783;
Best Local Similarity 20.8%; Pred. No. 2.7e-09;
RESULT 787
ID AAU11813 standard; protein; 1800 AA.
DE Cancer and neurogenesis associated gene, variant 5G-3V1.
PN WO200190354-A1.
PD 29-NOV-2001.
PA (UTLE-) UNIV LEEDS.
Query Match 8.3%; Score 328.5; DB 5; Length 1800;
Best Local Similarity 20.8%; Pred. No. 2.7e-09;
RESULT 788
ID AAU11812 standard; protein; 1826 AA.
DE Cancer and neurogenesis associated gene.
PN WO200190354-A1.
PD 29-NOV-2001.
PA (UTLE-) UNIV LEEDS.
Query Match 8.3%; Score 328.5; DB 5; Length 1826;
Best Local Similarity 20.8%; Pred. No. 2.7e-09;
RESULT 789
ID AAU11814 standard; protein; 2008 AA.
DE Cancer and neurogenesis associated gene, variant 5G-3V2.
PN WO200190354-A1.
PD 29-NOV-2001.
PA (REGC) UNIV CALIFORNIA.

PA (UTLE-) UNIV LEEDS.
Query Match 8.3%; Score 328.5; DB 5; Length 2008;
Best Local Similarity 20.8%; Pred. No. 3e-09;
RESULT 790
ID AAU11817 standard; protein; 2306 AA.
DE Cancer and neurogenesis associated gene, variant 5R23V2.
PN WO200190354-A1.
PD 29-NOV-2001.
PA (UTLE-) UNIV LEEDS.
Query Match 8.3%; Score 328.5; DB 5; Length 2306;
Best Local Similarity 20.8%; Pred. No. 3.4e-09;
RESULT 791
ID AAU11816 standard; protein; 2352 AA.
DE Cancer and neurogenesis associated gene, variant 5R-3V2.
PN WO200190354-A1.
PD 29-NOV-2001.
PA (UTLE-) UNIV LEEDS.
Query Match 8.3%; Score 328.5; DB 5; Length 2352;
Best Local Similarity 20.8%; Pred. No. 3.4e-09;
RESULT 792
ID AAB19551 standard; protein; 683 AA.
DE Human matrixase (truncated form).
PN WO200053232-A1.
PD 14-SEP-2000.
PA (GROU) UNIV GEORGETOWN.
Query Match 8.3%; Score 328; DB 3; Length 683;
Best Local Similarity 21.4%; Pred. No. 1.2e-09;
RESULT 793
ID AAY90284 standard; protein; 762 AA.
DE Human peptidase, HPEP-1 protein sequence.
PN WO200042201-A2.
PD 20-JUL-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 8.3%; Score 328; DB 3; Length 762;
Best Local Similarity 21.4%; Pred. No. 1.3e-09;
RESULT 794
ID AAM25628 standard; protein; 851 AA.
DE Human protein sequence SEQ ID NO:1143.
PN WO200153455-A2.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.3%; Score 328; DB 4; Length 851;
Best Local Similarity 21.6%; Pred. No. 1.4e-09;
RESULT 795
ID AAB11428 standard; peptide; 851 AA.
DE Human membrane-type Ser kinase homologue, SEQ ID NO:1798.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.3%; Score 328; DB 4; Length 851;
Best Local Similarity 21.6%; Pred. No. 1.4e-09;
RESULT 796
ID ADO55145 standard; protein; 853 AA.
DE Protein #47 with increased gene expression in renal cell carcinoma.
PN WO2004032842-A2.
PD 22-APR-2004.
PA (VAND-) VAN ANDEL INST.
Query Match 8.3%; Score 328; DB 8; Length 853;
Best Local Similarity 21.4%; Pred. No. 1.4e-09;
RESULT 797
ID AAB19552 standard; protein; 855 AA.
DE Human matrixase.
PN WO200053232-A1.
PD 14-SEP-2000.
PA (GROU) UNIV GEORGETOWN.
Query Match 8.3%; Score 328; DB 3; Length 855;
Best Local Similarity 21.4%; Pred. No. 1.4e-09;
RESULT 798
ID AAB35465 standard; protein; 855 AA.
DE Human membrane-type serine protease MT-SPI.
PN WO200123524-A2.
PD 05-APR-2001.
PA (REGC) UNIV CALIFORNIA.

Query Match 8.3%; Score 328; DB 4; Length 855;
Best Local Similarity 21.4%; Pred. No. 1.4e-09;
RESULT 799
ID ADI16817 standard; protein; 855 AA.
DE Human NOVX protein homologue SegID 353.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.3%; Score 328; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 1.4e-09;
RESULT 800
ID ADI16883 standard; protein; 855 AA.
DE Human NOVX protein homologue SegID 419.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.3%; Score 328; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 1.4e-09;
RESULT 801
ID ADI16876 standard; protein; 855 AA.
DE Human NOVX protein homologue SegID 412.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.3%; Score 328; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 1.4e-09;
RESULT 802
ID ADN39867 standard; protein; 855 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C237.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 8.3%; Score 328; DB 7; Length 855;
Best Local Similarity 21.4%; Pred. No. 1.4e-09;
RESULT 803
ID ADN04754 standard; protein; 855 AA.
DE Antiproteolytic protein sequence #558.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match 8.3%; Score 328; DB 8; Length 855;
Best Local Similarity 21.4%; Pred. No. 1.4e-09;
RESULT 804
ID ADP23334 standard; protein; 855 AA.
DE PRO polypeptide SEQ ID NO:428.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH-) GENENTECH INC.
Query Match 8.3%; Score 328; DB 8; Length 855;
Best Local Similarity 21.4%; Pred. No. 1.4e-09;
RESULT 805
ID AD866721 standard; protein; 863 AA.
DE Human prostatic carcinoma derived protein SEQ ID 233 #3.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILAJ/) PILARSKY C.
Query Match 8.3%; Score 328; DB 8; Length 863;
Best Local Similarity 21.4%; Pred. No. 1.4e-09;
RESULT 806
ID AD866379 standard; protein; 863 AA.
DE Human prostatic carcinoma derived protein SEQ ID 233 #2.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILAJ/) PILARSKY C.
Query Match 8.3%; Score 328; DB 8; Length 863;

Best Local Similarity 21.4%; Pred. No. 1.4e-09;
RESULT 807
ID AAB58274 standard; protein; 449 AA.
DE Lung cancer associated polypeptide sequence SEQ ID 612.
PN WO200055180-A2.
PD 21-SEP-2000.
PA (HDMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 8.3%; Score 327.5; DB 3; Length 449;
Best Local Similarity 23.3%; Pred. No. 8.3e-10;
RESULT 808
ID ADL64961 standard; protein; 688 AA.
DE Human complement component 1 protein, CIS.
PN US2004033582-A1.
PD 19-FEB-2004.
PA (EDMO/) EDMONDS M.
PA (HUTL/) HUT L.
PA (PERR/) PERRONE M.
PA (POWE/) POWELL J R.
PA (RAMA/) RAMANATHAN C S.
PA (SWAN/) SWANSON B.
PA (TSUC/) TSUCHIHASHI Z.
PA (ZERR/) ZERBA K.
Query Match 8.3%; Score 327; DB 8; Length 688;
Best Local Similarity 21.7%; Pred. No. 1.3e-09;
RESULT 809
ID ADI16508 standard; protein; 757 AA.
DE Human NOVX protein to treat human pathological conditions SegID44.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.3%; Score 327; DB 5; Length 757;
Best Local Similarity 21.6%; Pred. No. 1.4e-09;
RESULT 810
ID AAY06671 standard; protein; 855 AA.
DE Tumor antigen derived gene-15 (TAG-15) protein.
PN WO9942120-A1.
PD 26-AUG-1999.
PA (UYAR-) UNIV ARKANSAS.
Query Match 8.3%; Score 327; DB 2; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.6e-09;
RESULT 811
ID AAB98500 standard; protein; 855 AA.
DE Human TAG-15.
PN WO200129056-A1.
PD 26-APR-2001.
PA (UYAR-) UNIV ARKANSAS.
Query Match 8.3%; Score 327; DB 4; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.6e-09;
RESULT 812
ID AAE06930 standard; protein; 855 AA.
DE Human membrane-type serine protease (MTSP) 1.
PN WO200157194-A2.
PD 09-AUG-2001.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 4; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.6e-09;
RESULT 813
ID AA022929 standard; protein; 855 AA.
DE Type II transmembrane serine protease 1 protein SEQ ID NO 2.
PN WO200272786-A2.
PD 19-SEP-2002.
PA (CORV-) CORVAS INT INC.
Query Match 8.3%; Score 327; DB 5; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.6e-09;
RESULT 814
ID ADI16816 standard; protein; 855 AA.
DE Human NOVX protein homologue SegID 352.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.3%; Score 327; DB 5; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.6e-09;

RESULT 815
ID AD116882 standard; protein; 855 AA.
DE Human NOVX protein homologue SeqID 418.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 8.3%; Score 327; DB 5; Length 855;
Pred. No. 1.6e-09;
RESULT 816
ID AD116875 standard; protein; 855 AA.
DE Human NOVX protein homologue SeqID 411.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 8.3%; Score 327; DB 5; Length 855;
Pred. No. 1.6e-09;
RESULT 817
ID AB556619 standard; protein; 855 AA.
DE Human membrane-type serine protease MTSP1 protein SEQ ID NO:2.
PN WO200292841-A2.
PD 21-NOV-2002.
PA (CORV-) CORVAS INT INC.
Query Match
Best Local Similarity 8.3%; Score 327; DB 6; Length 855;
Pred. No. 1.6e-09;
RESULT 818
ID AAO30146 standard; protein; 855 AA.
DE Human membrane-type serine protease MTSP1 protein.
PN WO2003044179-A2.
PD 30-MAY-2003.
PA (CORV-) CORVAS INT INC.
Query Match
Best Local Similarity 8.3%; Score 327; DB 6; Length 855;
Pred. No. 1.6e-09;
RESULT 819
ID AAE29820 standard; protein; 855 AA.
DE Human membrane-type serine protease 1 (MTSP1).
PN WO200277267-A2.
PD 03-OCT-2002.
PA (CORV-) CORVAS INT INC.
Query Match
Best Local Similarity 8.3%; Score 327; DB 6; Length 855;
Pred. No. 1.6e-09;
RESULT 820
ID AAB29791 standard; protein; 855 AA.
DE Human membrane-type serine protease, MTSP1.
PN WO200277263-A2.
PD 03-OCT-2002.
PA (CORV-) CORVAS INT INC.
Query Match
Best Local Similarity 8.3%; Score 327; DB 6; Length 855;
Pred. No. 1.6e-09;
RESULT 821
ID ABP72376 standard; protein; 855 AA.
DE Transmembrane serine protease 1 (MTSP1).
PN WO2003004681-A2.
PD 16-JAN-2003.
PA (CORV-) CORVAS INT INC.
Query Match
Best Local Similarity 8.3%; Score 327; DB 6; Length 855;
Pred. No. 1.6e-09;
RESULT 822
ID ADB97551 standard; protein; 855 AA.
DE Human MTSP1, SEQ ID NO:2.
PN WO2003031585-A2.
PD 17-APR-2003.
PA (CORV-) CORVAS INT INC.
Query Match
Best Local Similarity 8.3%; Score 327; DB 7; Length 855;
Pred. No. 1.6e-09;
RESULT 823
ID AD110371 standard; protein; 855 AA.
DE Human cell surface protease #1.
PN WO200295007-A2.
PD 28-NOV-2002.
PA (CORV-) CORVAS INT INC.
Query Match
Best Local Similarity 8.3%; Score 327; DB 7; Length 855;
Pred. No. 1.6e-09;
RESULT 824

ID ADG65326 standard; protein; 855 AA.
DE Human MTSP1.
PN WO2003104394-A2.
PD 18-DEC-2003.
PA (DENND-) DENNDREON SAN DIEGO LLC.
Query Match
Best Local Similarity 8.3%; Score 327; DB 8; Length 855;
Pred. No. 1.6e-09;
RESULT 825
ID AD128861 standard; protein; 855 AA.
DE Human matricipase (MTSP1) serine protease.
PN WO2004005471-A2.
PD 15-JAN-2004.
PA (DENND-) DENNDREON SAN DIEGO LLC.
Query Match
Best Local Similarity 8.3%; Score 327; DB 8; Length 855;
Pred. No. 1.6e-09;
RESULT 826
ID ADJ46895 standard; protein; 855 AA.
DE Human transmembrane serine protease (MTSP) polypeptide #1.
PN US2004001801-A1.
PD 01-JAN-2004.
PA (CORV-) CORVAS INT INC.
Query Match
Best Local Similarity 8.3%; Score 327; DB 8; Length 855;
Pred. No. 1.6e-09;
RESULT 827
ID AED61724 standard; protein; 855 AA.
DE Human membrane-type serine protease 1.
PN WO2005100556-A2.
PD 27-OCT-2005.
PA (CATV-) CATALYST BIOSCIENCES.
Query Match
Best Local Similarity 8.3%; Score 327; DB 9; Length 855;
Pred. No. 1.6e-09;
RESULT 828
ID AER05739 standard; protein; 855 AA.
DE Wild type human membrane-type serine protease 1 (MT-SPL).
PN WO2005110453-A2.
PD 24-NOV-2005.
PA (CATV-) CATALYST BIOSCIENCES.
Query Match
Best Local Similarity 8.3%; Score 327; DB 9; Length 855;
Pred. No. 1.6e-09;
RESULT 829
ID AAE20788 standard; protein; 3095 AA.
DE Rat C3b/C4b complement receptor like protein.
PN WO200210199-A2.
PD 07-FEB-2002.
PA (AMGE-) AMGEN INC.
Query Match
Best Local Similarity 8.2%; Score 324; DB 5; Length 3095;
Pred. No. 7.8e-09;
RESULT 830
ID ADN42162 standard; protein; 757 AA.
DE Human novel protein NOV 8.
PN US2004033493-A1.
PD 19-FEB-2004.
PA (TCHE/) TCHERNEV V T.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATR/) PATTURAJAN M.
PA (SHIM/) SHIMKETS R A.
PA (LILU/) LI T.
PA (GANG/) GANGOLLI E A.
PA (PADI/) PADIGARU M.
PA (ANDE/) ANDERSON D W.
PA (RAST/) RASTELI L.
PA (MILL/) MILLER C E.
PA (GBRL/) GERLACH V.
PA (TAUP/) TAUPIER R J.
PA (GUSE/) GUSEV V Y.
PA (COLM/) COLMAN S D.
PA (WOLE/) WOLENC A R.
PA (PENR/) PENR C E A.
PA (FURT/) FURTAK K.
PA (GROS/) GROSSE W M.
PA (ALSO/) ALSOBROOK J P.
PA (LEPL/) LEPLLEY D M.

PA (RIEG/) RIEGER D K.
PA (BURG/) BURGESS C E.
Query Match 8.2%; Score 323; DB 8; Length 757;
Best Local Similarity 21.6%; Pred. No. 2.4e-09;
RESULT 831
ID ADH71146 standard; protein; 3130 AA.
DE Human protein of the invention NOV4f SEQ ID NO:42.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 321; DB 8; Length 3130;
Best Local Similarity 22.6%; Pred. No. 1.1e-08;
RESULT 832
ID ADH71144 standard; protein; 3483 AA.
DE Human protein of the invention NOV4e SEQ ID NO:40.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 321; DB 8; Length 3483;
Best Local Similarity 22.6%; Pred. No. 1.3e-08;
RESULT 833
ID ADH71136 standard; protein; 3546 AA.
DE Human protein of the invention NOV4a SEQ ID NO:32.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 321; DB 8; Length 3546;
Best Local Similarity 22.6%; Pred. No. 1.3e-08;
RESULT 834
ID AAE20787 standard; protein; 3069 AA.
DE Human C3b/C4b complement receptor like protein #1.
PN WO200210199-A2.
PD 07-FEB-2002.
PA (AMGE-) AMGEN INC.
Query Match 8.1%; Score 320.5; DB 5; Length 3069;
Best Local Similarity 20.7%; Pred. No. 1.2e-08;
RESULT 835
ID AAE20789 standard; protein; 3100 AA.
DE Human C3b/C4b complement receptor like protein #2.
PN WO200210199-A2.
PD 07-FEB-2002.
PA (AMGE-) AMGEN INC.
Query Match 8.1%; Score 320.5; DB 5; Length 3100;
Best Local Similarity 20.7%; Pred. No. 1.2e-08;
RESULT 836
ID AAU99088 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant G383N/G385T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.1%; Score 319.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 2.1e-09;
RESULT 837
ID AAU99080 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L349N/D351T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.1%; Score 319.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 2.1e-09;
RESULT 838
ID ADG83836 standard; protein; 455 AA.
DE Rough scale snake venom protease.
PN WO2003082914-A1.
PD 09-OCT-2003.
PA (UYOU) UNIV QUEENSLAND.
Query Match 8.1%; Score 319.5; DB 8; Length 455;
Best Local Similarity 23.4%; Pred. No. 2.3e-09;
RESULT 839
ID AAU99078 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant I348N/G350T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.1%; Score 318.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 2.4e-09;
RESULT 840
ID ADH71142 standard; protein; 2612 AA.
DE Human protein of the invention NOV4d SEQ ID NO:38.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 318; DB 8; Length 2612;
Best Local Similarity 22.6%; Pred. No. 1.4e-08;
RESULT 841
ID ABG79169 standard; protein; 2669 AA.
DE Human cub and sushi domain containing protein #2.
PN WO200264791-A2.
PD 22-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 318; DB 5; Length 2669;
Best Local Similarity 22.6%; Pred. No. 1.4e-08;
RESULT 842
ID ADH71140 standard; protein; 2669 AA.
DE Human protein of the invention NOV4c SEQ ID NO:36.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 318; DB 8; Length 2669;
Best Local Similarity 22.6%; Pred. No. 1.4e-08;
RESULT 843
ID ABG79168 standard; protein; 3104 AA.
DE Human cub and sushi domain containing protein #1.
PN WO200264791-A2.
PD 22-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 318; DB 5; Length 3104;
Best Local Similarity 22.6%; Pred. No. 1.6e-08;
RESULT 844
ID ADH71168 standard; protein; 3104 AA.
DE Human protein of the invention NOV4g SEQ ID NO:64.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 318; DB 8; Length 3104;
Best Local Similarity 22.6%; Pred. No. 1.6e-08;
RESULT 845
ID ADH71166 standard; protein; 3104 AA.
DE Human protein of the invention NOV4p SEQ ID NO:62.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 318; DB 8; Length 3104;
Best Local Similarity 22.6%; Pred. No. 1.6e-08;
RESULT 846
ID ADH71138 standard; protein; 3104 AA.
DE Human protein of the invention NOV4b SEQ ID NO:34.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 318; DB 8; Length 3104;
Best Local Similarity 22.6%; Pred. No. 1.6e-08;
RESULT 847
ID AAU99006 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D189N/K191T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 317.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 2.7e-09;
RESULT 848
ID AAU99066 standard; protein; 419 AA.

DE Human Protein C zymogen protein mutant T315N/V317T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 317.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 2.7e-09;
RESULT 849
ID ADN28524 standard; protein; 421 AA.
DE Human protein C variant #2.
PN WO2004113385-A1.
PD 29-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 317.5; DB 9; Length 421;
Best Local Similarity 24.7%; Pred. No. 2.7e-09;
RESULT 850
ID AEA20987 standard; protein; 627 AA.
DE Novel human polypeptide SEQ ID NO 1681.
PN WO2005049806-A2.
PD 02-JUN-2005.
PA (NIVE-) NIVELO INC.
Query Match 8.0%; Score 317.5; DB 9; Length 627;
Best Local Similarity 21.3%; Pred. No. 3.9e-09;
RESULT 851
ID AAR57283 standard; protein; 798 AA.
DE Bovine enterokinase.
PN WO9416083-A1.
PD 21-JUL-1994.
PA (GEMV-) GENETICS INST INC.
Query Match 8.0%; Score 317.5; DB 2; Length 798;
Best Local Similarity 24.6%; Pred. No. 4.9e-09;
RESULT 852
ID AAE20900 standard; protein; 3069 AA.
DE Human C3b/C4b complement receptor like protein #1, alternative version.
PN WO200210199-A2.
PD 07-FEB-2002.
PA (AMGE-) AMGEN INC.
Query Match 8.0%; Score 317.5; DB 5; Length 3069;
Best Local Similarity 20.7%; Pred. No. 1.7e-08;
RESULT 853
ID AAE20901 standard; protein; 3100 AA.
DE Human C3b/C4b complement receptor like protein #2, alternative version.
PN WO200210199-A2.
PD 07-FEB-2002.
PA (AMGE-) AMGEN INC.
Query Match 8.0%; Score 317.5; DB 5; Length 3100;
Best Local Similarity 20.7%; Pred. No. 1.7e-08;
RESULT 854
ID AAU99076 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant M338N/S340T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 316.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 3e-09;
RESULT 855
ID AAU99022 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K217N/L219T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 316.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 3e-09;
RESULT 856
ID AAU99026 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L220N/R222T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.

Query Match 8.0%; Score 315.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 3.4e-09;
RESULT 857
ID AAU99081 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D351N/Q353S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 315.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 3.4e-09;
RESULT 858
ID AAU99071 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S336N/M338S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 315.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 3.4e-09;
RESULT 859
ID AAU99087 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant G383N/G385S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 315.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 3.4e-09;
RESULT 860
ID AAU99079 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L349N/D351S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 315.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 3.4e-09;
RESULT 861
ID AAR62653 standard; protein; 461 AA.
DE Human Protein C.
PN US5358932-A.
PD 25-OCT-1994.
PA (ZYMO-) ZYMOGENETICS INC.
Query Match 8.0%; Score 315.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 3.8e-09;
RESULT 862
ID AAR35760 standard; protein; 419 AA.
DE Protein C (PC).
PN WO9309804-A1.
PD 27-MAY-1993.
PA (SCRI-) SCRIPPS RES INST.
Query Match 8.0%; Score 314.5; DB 2; Length 419;
Best Local Similarity 23.3%; Pred. No. 3.9e-09;
RESULT 863
ID AAU99053 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant R306N/K308S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 314.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 3.9e-09;
RESULT 864
ID AAU99007 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S190N/K192S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 314.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 3.9e-09;
RESULT 865

ID AAU99077 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant I348N/G350S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 314.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 3.9e-09;
RESULT 866
ID AAU99043 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L296N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 314.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 3.9e-09;
RESULT 867
ID ADG83832 standard; protein; 454 AA.
DE Red belly black snake venom protease.
PN WO2003082914-A1.
PD 09-OCT-2003.
PA (UYOU) UNIV QUEBENSISLAND.
Query Match 8.0%; Score 314.5; DB 8; Length 454;
Best Local Similarity 23.0%; Pred. No. 4.2e-09;
RESULT 868
ID ADM7504 standard; protein; 461 AA.
DE Human protein C variant #2 amino acid sequence.
PN WO2003106666-A2.
PD 24-DEC-2003.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 8.0%; Score 314.5; DB 8; Length 461;
Best Local Similarity 24.5%; Pred. No. 4.3e-09;
RESULT 869
ID ADW28523 standard; protein; 420 AA.
DE Human protein C variant #1.
PN WO200413385-A1.
PD 29-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
PA (MAXY-) MAXYGEN APS.
Query Match 8.0%; Score 314; DB 9; Length 420;
Best Local Similarity 24.5%; Pred. No. 4.2e-09;
RESULT 870
ID AAE23083 standard; protein; 855 AA.
DE Eptchin protein.
PN WO200203787-A2.
PD 17-JAN-2002.
PA (DELT-) DELTAGEN INC.
Query Match 8.0%; Score 314; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 8.1e-09;
RESULT 871
ID ADI16819 standard; protein; 855 AA.
DE Murine NOVX protein homologue Segid 355.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.0%; Score 314; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 8.1e-09;
RESULT 872
ID ADI16877 standard; protein; 855 AA.
DE Murine NOVX protein homologue Segid 413.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.0%; Score 314; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 8.1e-09;
RESULT 873
ID AAW72753 standard; protein; 419 AA.
DE Primary structure of activated human protein C.
PN EP875563-A2.
PD 04-NOV-1998.
PA (ELIL) LILLY & CO ELI.

Query Match 7.9%; Score 313.5; DB 2; Length 419;
Best Local Similarity 23.3%; Pred. No. 4.4e-09;
RESULT 874
ID AAU99005 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D189N/K191S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 313.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 4.4e-09;
RESULT 875
ID AAU99025 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L220N/R222S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 313.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.4e-09;
RESULT 876
ID AAU99065 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant T315N/V317S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 313.5; DB 5; Length 419;
Best Local Similarity 24.3%; Pred. No. 4.4e-09;
RESULT 877
ID AAU99016 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D214N/S216T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 313.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 4.4e-09;
RESULT 878
ID AAU99023 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K218N/L220S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 313.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 4.4e-09;
RESULT 879
ID AAR13083 standard; protein; 509 AA.
DE PAP-I-protein C fusion construct.
PN WO9109953-A.
PD 11-JUL-1991.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 7.9%; Score 313; DB 2; Length 509;
Best Local Similarity 23.5%; Pred. No. 5.6e-09;
RESULT 880
ID ADI16820 standard; protein; 855 AA.
DE Rat NOVX protein homologue Segid 356.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.9%; Score 313; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 9.1e-09;
RESULT 881
ID ADI16881 standard; protein; 855 AA.
DE Rat NOVX protein homologue Segid 417.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.9%; Score 313; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 9.1e-09;
RESULT 882
ID ADI16878 standard; protein; 855 AA.

DE Rat NOVX protein homologue Segid 414.
PN WO200258649-A2.
PD 06-SEP-2002.
PA (CUNA-) CUPAGEN CORP.
Query Match 7.9%; Score 313; DB 5; Length 855;
Best Local Similarity 21.4%; Pred. No. 9.1e-09;
RESULT 883
ID AAU99072 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S336N/M338T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5e-09;
RESULT 884
ID AAU99097 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D189N/K191N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 5e-09;
RESULT 885
ID AAU99009 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K191N/K193S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 5e-09;
RESULT 886
ID AAU99064 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant R312N/R314T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 5e-09;
RESULT 887
ID AAU99069 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V334N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5e-09;
RESULT 888
ID AAU99082 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D351N/Q353T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5e-09;
RESULT 889
ID AAU99096 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant M338A.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5e-09;
RESULT 890
ID AAU99091 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L387N/M389S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5e-09;
RESULT 891
ID AAU99024 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K218N/L220T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5e-09;
RESULT 892
ID AAU99048 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant H303N/S305T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.3%; Pred. No. 5e-09;
RESULT 893
ID AAU99067 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant F316N/L318S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5e-09;
RESULT 894
ID AAU99075 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant M338N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5e-09;
RESULT 895
ID AAU99092 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L387N/M389T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5e-09;
RESULT 896
ID AAU99011 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K192N/L194S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5e-09;
RESULT 897
ID AAU99032 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S250N/S252T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5e-09;
RESULT 898
ID ADM77507 standard; protein; 461 AA.
DE Human protein C variant #5 amino acid sequence.
PN WO200310666-A2.
PD 24-DEC-2003.

PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 8; Length 461;
Best Local Similarity 24.3%; Pred. No. 5.5e-09;
RESULT 909
ID ADW77505 standard; protein; 461 AA.
DE Human protein C variant #3 amino acid sequence.
PN WO2003106666-A2.
PD 24-DEC-2003.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 312.5; DB 8; Length 461;
Best Local Similarity 24.5%; Pred. No. 5.5e-09;
RESULT 900
ID AAB82677 standard; protein; 419 AA.
DE Human protein C derivative (H100/S11G/Q32E/N33D/L194S).
PN WO200157193-A2.
PD 09-AUG-2001.
PA (ELILY) LILLY & CO ELI.
Query Match 7.9%; Score 312; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.3e-09;
RESULT 901
ID AAR13537 standard; protein; 460 AA.
DE Human Protein C zymogen N.
PN EP443875-A.
PD 28-AUG-1991.
PA (ELILY) LILLY & CO ELI.
Query Match 7.9%; Score 312; DB 2; Length 460;
Best Local Similarity 24.7%; Pred. No. 5.8e-09;
RESULT 902
ID ADG68330 standard; protein; 467 AA.
DE Coastal taipan venom protease.
PN WO2003082914-A1.
PD 09-OCT-2003.
PA (UYOU) UNIV QUEENSLAND.
Query Match 7.9%; Score 312; DB 8; Length 467;
Best Local Similarity 23.0%; Pred. No. 5.9e-09;
RESULT 903
ID ABP60993 standard; protein; 1031 AA.
DE Novel human protein. SEQ ID 80.
PN WO200250105-A1.
PD 27-JUN-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
Query Match 7.9%; Score 312; DB 5; Length 1031;
Best Local Similarity 22.6%; Pred. No. 1.2e-08;
RESULT 904
ID AAU99008 standard; protein; 419 AA.
DE Human protein C zymogen protein mutant S190N/K192T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 5.6e-09;
RESULT 905
ID AAU99039 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant T254N/N256S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.6e-09;
RESULT 906
ID AAU99047 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant H303N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.6e-09;
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.6e-09;
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.6e-09;

Best Local Similarity 24.3%; Pred. No. 5.6e-09;
RESULT 907
ID AAU99070 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V334N/S336T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.6e-09;
RESULT 908
ID AAU99017 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E215N/K217S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.6e-09;
RESULT 909
ID AAU99044 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L296N/T298S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.6e-09;
RESULT 910
ID AAU99014 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K193N/A195T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.6e-09;
RESULT 911
ID AAU99031 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S250N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.6e-09;
RESULT 912
ID AAU99057 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K308N/A310S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.6e-09;
RESULT 913
ID AAU99054 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant R306N/K308T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.6e-09;
RESULT 914
ID AAU99095 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D214A.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.6e-09;
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.6e-09;

RESULT 915
ID AAU99015 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D214N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 5.6e-09;
RESULT 916
ID AAP81205 standard; protein; 461 AA.
DE Human Protein C.
PN EP266190-A.
PD 04-MAY-1988.
PA (ZYMO-) ZYMOGENETICS INC.
Query Match 7.9%; Score 311.5; DB 1; Length 461;
Best Local Similarity 24.5%; Pred. No. 6.2e-09;
RESULT 917
ID AAR13539 standard; protein; 461 AA.
DE Human Protein C zymogen LIN.
PN EP443875-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 311.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 6.2e-09;
RESULT 918
ID AAR13997 standard; protein; 461 AA.
DE Human protein C zymogen Q329.
PN EP443874-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 311.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 6.2e-09;
RESULT 919
ID ADM77503 standard; protein; 461 AA.
DE Human protein C variant #1 amino acid sequence.
PN WO2003106666-A2.
PD 24-DEC-2003.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 311.5; DB 8; Length 461;
Best Local Similarity 24.5%; Pred. No. 6.2e-09;
RESULT 920
ID AAB82678 standard; protein; 419 AA.
DE Human protein C derivative (H10Q/S11G/Q32E/N33D/L194S).
PN WO200157193-A2.
PD 09-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 311; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 6e-09;
RESULT 921
ID AAB82675 standard; protein; 419 AA.
DE Human protein C derivative (S11G/Q32E/N33D/L194S).
PN WO200157193-A2.
PD 09-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 311; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 6e-09;
RESULT 922
ID ADX39090 standard; protein; 446 AA.
DE Rat factor VII.
PN WO2005014775-A2.
PD 17-FEB-2005.
PA (UFL) UNIV FLORIDA RES FOUND INC.
Query Match 7.9%; Score 311; DB 9; Length 446;
Best Local Similarity 23.3%; Pred. No. 6.4e-09;
RESULT 923
ID ADC40013 standard; protein; 409 AA.
DE Human activated protein C-related protein #2.
PN WO2003075834-A2.
PD 18-SEP-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 7; Length 409;

Best Local Similarity 24.5%; Pred. No. 6.3e-09;
RESULT 924
ID ADC40012 standard; protein; 410 AA.
DE Human activated protein C-related protein #1.
PN WO2003075834-A2.
PD 18-SEP-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 7; Length 410;
Best Local Similarity 24.5%; Pred. No. 6.3e-09;
RESULT 925
ID AAY56803 standard; protein; 415 AA.
DE Truncated human protein C polypeptide.
PN WO963070-A1.
PD 09-DEC-1999.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 3; Length 415;
Best Local Similarity 24.5%; Pred. No. 6.3e-09;
RESULT 926
ID AAB82673 standard; protein; 419 AA.
DE Wild-type human protein C.
PN WO200157193-A2.
PD 09-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 927
ID AAB36896 standard; protein; 419 AA.
DE Human protein C derivative 3.
PN WO200066754-A1.
PD 09-NOV-2000.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 928
ID AAB36894 standard; protein; 419 AA.
DE Human protein C derivative 1.
PN WO200066754-A1.
PD 09-NOV-2000.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 929
ID AAE08625 standard; protein; 419 AA.
DE Human mature wild type protein C.
PN WO200159084-A1.
PD 16-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 930
ID AAU99063 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant R312N/R314S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 931
ID AAU99012 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K192N/L194T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 932
ID AAU99050 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S304N/R306T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.

PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 933
ID AAU99010 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K191N/K193T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 6.4e-09;
RESULT 934
ID AAU99040 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant T254N/N256T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 935
ID AAU99060 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E309N/K311T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 936
ID AAU99055 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E307N/E309S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 937
ID AAU99056 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E307N/E309T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 938
ID AAU99059 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E309N/K311S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 939
ID AAU99002 standard; protein; 419 AA.
DE Human Protein C zymogen protein.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 940
ID AAU99051 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S305N/E307S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 941
ID AAU99052 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S305N/E307T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 942
ID ABR55547 standard; protein; 419 AA.
DE Amino acid sequence of mature human protein C (PC).
PN FR2831170-A1.
PD 25-APR-2003.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 6; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 943
ID AD40014 standard; protein; 419 AA.
DE Human activated protein C-related protein #3.
PN WO2003075834-A2.
PD 18-SEP-2003.
PA (ELIL) LILLY & CO ELI.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 7; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 944
ID ADO18786 standard; protein; 419 AA.
DE Mature human zymogen-like protein C.
PN WO200404190-A2.
PD 27-MAY-2004.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 8; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 945
ID ADW28521 standard; protein; 419 AA.
DE Human protein C.
PN WO2004113385-A1.
PD 29-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 310.5; DB 9; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 946
ID ADY52283 standard; protein; 419 AA.
DE Human activated protein C (APC).
PN WO2005023308-A1.
PD 17-MAR-2005.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
PA (MAXY-) MAXYGEN APS.
Query Match 7.9%; Score 310.5; DB 9; Length 419;
Best Local Similarity 24.5%; Pred. No. 6.4e-09;
RESULT 947
ID ADG83834 standard; protein; 453 AA.
DE Mainland tiger snake venom protease.
PN WO2003082914-A1.
PD 09-OCT-2003.
PA (UYOU) UNIV QUEENSLAND.
Query Match 7.9%; Score 310.5; DB 8; Length 453;
Best Local Similarity 22.8%; Pred. No. 6.9e-09;
RESULT 948
ID AAP81104 standard; protein; 460 AA.
DE Sequence of human protein C.
PN JP63263083-A.
PD 31-OCT-1988.
PA (FAKH) HOECHST JAPAN LTD.
Query Match 7.9%; Score 310.5; DB 1; Length 460;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 949
ID AAW25086 standard; protein; 460 AA.
DE Human protein C.

PN W09720043-A1.
PD 05-JUN-1997.
PA (ZYMO) ZYMOGENETICS INC.
PN (PLT-) PPL THERAPEUTICS.
Query Match 7.9%; Score 310.5; DB 2; Length 460;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 950
ID AAF60001 standard; protein; 461 AA.
DE Sequence of polypeptide with human protein C activity.
PN EPI91606-A.
PD 20-AUG-1996.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 1; Length 461;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 951
ID AAF70085 standard; protein; 461 AA.
DE Human Protein C.
PN EPI15548-A.
PD 25-MAR-1987.
PA (ZYMO) ZYMOGENETICS INC.
PN (UNIM) UNIV WASHINGTON.
Query Match 7.9%; Score 310.5; DB 1; Length 461;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 952
ID AAF90401 standard; protein; 461 AA.
DE Zymogen form of human protein C.
PN EPI23149-A.
PD 05-JUL-1999.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 1; Length 461;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 953
ID AAR13622 standard; protein; 461 AA.
DE Human protein C.
PN W0912320-A.
PD 22-AUG-1991.
PA (ZYMO) ZYMOGENETICS INC.
PN (TEIJ) TEIJUN LTD.
Query Match 7.9%; Score 310.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 954
ID AAR13081 standard; protein; 461 AA.
DE Human protein C.
PN W09109953-A.
PD 11-JUL-1991.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 7.9%; Score 310.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 955
ID AAR13074 standard; protein; 461 AA.
DE Protein C precursor.
PN W09109951-A.
PD 11-JUL-1991.
PA (ZYMO) ZYMOGENETICS INC.
PN (TEIJ) TEIJUN LTD.
Query Match 7.9%; Score 310.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 956
ID AAR34295 standard; protein; 461 AA.
DE Protein C.
PN JF05064588-A.
PD 19-MAR-1993.
PA (TEIJ) TEIJUN LTD.
Query Match 7.9%; Score 310.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 957
ID AAW02600 standard; protein; 461 AA.
DE Human protein C.
PN US551650-A.
PD 14-MAY-1996.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 7.9%; Score 310.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 7e-09;

RESULT 958
ID AAY49561 standard; protein; 461 AA.
DE Human lecithin cholesterol acyltransferase protein sequence.
PN W0950454-A2.
PD 07-OCT-1999.
PA (WHEH) WHITEHEAD INST BIOMEDICAL RES.
Query Match 7.9%; Score 310.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 959
ID AAB82674 standard; protein; 461 AA.
DE Wild-type human protein C.
PN W0200157193-A2.
PD 09-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 4; Length 461;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 960
ID AAB36895 standard; protein; 461 AA.
DE Human protein C derivative 2.
PN W0200066754-A1.
PD 09-NOV-2000.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 4; Length 461;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 961
ID AAE08626 standard; protein; 461 AA.
DE Human wild type protein C.
PN W0200159084-A1.
PD 16-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.9%; Score 310.5; DB 4; Length 461;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 962
ID AAU95001 standard; protein; 461 AA.
DE Human protein C precursor protein.
PN W0200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PN (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 5; Length 461;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 963
ID ADW77502 standard; protein; 461 AA.
DE Human protein C wild-type amino acid sequence.
PN W02002106666-A2.
PD 24-DEC-2003.
PA (MAXY-) MAXYGEN APS.
PN (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 8; Length 461;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 964
ID ADO18787 standard; protein; 461 AA.
DE Human zymogen-like protein C.
PN W02004044190-A2.
PD 27-MAY-2004.
PA (MAXY-) MAXYGEN APS.
PN (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 8; Length 461;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 965
ID ADW28520 standard; protein; 461 AA.
DE Human protein C precursor.
PN W02004113385-A1.
PD 29-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.9%; Score 310.5; DB 9; Length 461;
Best Local Similarity 24.5%; Pred. No. 7e-09;
RESULT 966
ID ADW28522 standard; protein; 461 AA.
DE Human protein C precursor I39R/K mutant.
PN W02004113385-A1.
PD 29-DEC-2004.

PA (MAXY-) MAXYGEN HOLDINGS LTD.
PA (MAXY-) MAXYGEN APS.
Query Match
Best Local Similarity 24.5%; Score 310.5; DB 9; Length 461;
PD 28-AUG-1991.
RESULT 967
ID AED96684 standard; protein; 461 AA.
DE Human C-reactive protein (CRP) associated marker SEQ ID NO 866.
PN WO2005107364-A2.
PD 17-NOV-2005.
PA (COMP-) COMPUEN LTD.
PA (COHE/) COHEN Y.
Query Match
Best Local Similarity 24.5%; Score 310.5; DB 9; Length 461;
PD 09-NOV-2000.
RESULT 968
ID AEE72258 standard; protein; 461 AA.
DE Human target protein #99.
PN WO2005119262-A2.
PD 15-DEC-2005.
PA (GALA-) GALAPAGOS GENOMICS NV.
Query Match
Best Local Similarity 24.5%; Score 310.5; DB 10; Length 461;
PD 23-FEB-2006.
RESULT 969
ID AEG02811 standard; protein; 461 AA.
DE Human Protein C.
PN WO2006018204-A1.
PD 23-FEB-2006.
PA (ZLBB-) ZLB BEHRING GMBH.
Query Match
Best Local Similarity 24.5%; Score 310.5; DB 10; Length 461;
PD 23-FEB-2006.
RESULT 970
ID AEC01736 standard; protein; 506 AA.
DE PC-GPI cassette protein.
PN WO2005073375-A1.
PD 11-AUG-2005.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 24.5%; Score 310.5; DB 9; Length 506;
PD 11-AUG-2005.
RESULT 971
ID AEC01741 standard; protein; 507 AA.
DE PCUNAC-GPI-4Stop cassette.
PN WO2005073375-A1.
PD 11-AUG-2005.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 24.5%; Score 310.5; DB 9; Length 507;
PD 11-AUG-2005.
RESULT 972
ID AEC01737 standard; protein; 507 AA.
DE PC-UGAC-GPI-4Stop cassette protein.
PN WO2005073375-A1.
PD 11-AUG-2005.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 24.5%; Score 310.5; DB 9; Length 507;
PD 11-AUG-2005.
RESULT 973
ID AAB82676 standard; protein; 419 AA.
DE Human protein C derivative (S11G/Q32E/N33D/L194S/T254S).
PN WO200157193-A2.
PD 09-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 24.5%; Score 310; DB 4; Length 419;
PD 09-AUG-2001.
RESULT 974
ID AAB08630 standard; protein; 419 AA.
DE Human protein C derivative #4.
PN WO200159084-A1.
PD 16-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 24.5%; Score 310; DB 4; Length 419;
PD 16-AUG-2001.
RESULT 975

ID AAR13538 standard; protein; 460 AA.
DE Human Protein C zymogen FN.
PN EP443875-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 24.7%; Score 310; DB 2; Length 460;
PD 28-AUG-1991.
RESULT 976
ID AAB36897 standard; protein; 419 AA.
DE Human protein C derivative 4.
PN WO20006754-A1.
PD 09-NOV-2000.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 24.5%; Score 309.5; DB 4; Length 419;
PD 09-NOV-2000.
RESULT 977
ID AAB36898 standard; protein; 419 AA.
DE Human protein C derivative 5.
PN WO20006754-A1.
PD 09-NOV-2000.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 24.5%; Score 309.5; DB 4; Length 419;
PD 09-NOV-2000.
RESULT 978
ID AAU99018 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E215N/K217T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match
Best Local Similarity 24.4%; Score 309.5; DB 5; Length 419;
PD 25-APR-2002.
RESULT 979
ID AAU99033 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K251N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 24.5%; Score 309.5; DB 5; Length 419;
PD 25-APR-2002.
RESULT 980
ID AAU99013 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K193N/A195S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match
Best Local Similarity 24.4%; Score 309.5; DB 5; Length 419;
PD 25-APR-2002.
RESULT 981
ID AAU99068 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant F316N/L318T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match
Best Local Similarity 24.4%; Score 309.5; DB 5; Length 419;
PD 25-APR-2002.
RESULT 982
ID AAU99062 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant A310N/R312T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 24.8%; Score 309.5; DB 5; Length 419;
PD 25-APR-2002.
RESULT 983
ID AAU99020 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S216N/K218T.
PN WO200232461-A2.
PD 25-APR-2002.

PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 309.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 7.2e-09;
RESULT 984
ID AAU99035 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S252N.
PD WO200232461-A2.
PN 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 309.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 7.2e-09;
RESULT 985
ID AAU99085 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E357N/D359S.
PD WO200232461-A2.
PN 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 309.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 7.2e-09;
RESULT 986
ID AAU99058 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K308N/A310T.
PD WO200232461-A2.
PN 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 309.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 7.2e-09;
RESULT 987
ID AAU99019 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S216N/K218S.
PD WO200232461-A2.
PN 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 309.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 7.2e-09;
RESULT 988
ID AAU99094 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant H388N/Y390T.
PD WO200232461-A2.
PN 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 309.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 7.2e-09;
RESULT 989
ID AAU99089 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L386N/H388S.
PD WO200232461-A2.
PN 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 309.5; DB 5; Length 419;
Best Local Similarity 24.7%; Pred. No. 7.2e-09;
RESULT 990
ID AAU99070 standard; protein; 461 AA.
DE Human Protein C.
PD EP19312-A.
PN 07-JUN-1989.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 309.5; DB 1; Length 461;
Best Local Similarity 24.5%; Pred. No. 7.9e-09;
RESULT 991
ID AAR13540 standard; protein; 461 AA.
DE Human Protein C zymogen FLIN.
PD EP43875-A.
PN 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 309.5; DB 2; Length 461;
Best Local Similarity 24.5%; Pred. No. 7.9e-09;
RESULT 992
ID AD16874 standard; protein; 799 AA.
DE Murine NOXA protein homologue Segid 410.
PD WO200268649-A2.
PN 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.8%; Score 309.5; DB 5; Length 799;
Best Local Similarity 21.6%; Pred. No. 1.3e-08;
RESULT 993
ID AD16880 standard; protein; 799 AA.
DE Murine NOXA protein homologue Segid 416.
PD WO200268649-A2.
PN 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.8%; Score 309.5; DB 5; Length 799;
Best Local Similarity 21.6%; Pred. No. 1.3e-08;
RESULT 994
ID AAE08627 standard; protein; 419 AA.
DE Human protein C derivative #1.
PD WO200159084-A1.
PN 16-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 309; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 7.7e-09;
RESULT 995
ID AAE08629 standard; protein; 419 AA.
DE Human protein C derivative #3.
PD WO200159084-A1.
PN 16-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 309; DB 4; Length 419;
Best Local Similarity 24.5%; Pred. No. 7.7e-09;
RESULT 996
ID AAU99049 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S304N/R306S.
PD WO200232461-A2.
PN 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 7.7e-09;
RESULT 997
ID AAU99061 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant A310N/R312S.
PD WO200232461-A2.
PN 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.1%; Pred. No. 8.2e-09;
RESULT 998
ID AAU99090 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant L386N/H388T.
PD WO200232461-A2.
PN 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 8.2e-09;
RESULT 999
ID AAU99086 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E357N/D359T.
PD WO200232461-A2.
PN 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 8.2e-09;
RESULT 1000
ID AAU99036 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S252N/T254S.
PD WO200232461-A2.

PD 25-APR-2002.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Beet Local Similarity 24.5%; Pred. No. 8.2e-09;
RESULT 1001
ID AAU99045 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant Y302N.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Beet Local Similarity 24.5%; Pred. No. 8.2e-09;
RESULT 1002
ID AAU99034 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K251N/T253S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 308.5; DB 5; Length 419;
Beet Local Similarity 24.5%; Pred. No. 8.2e-09;
RESULT 1003
ID ADM77506 standard; protein; 461 AA.
DE Human protein C variant #4 amino acid sequence.
PN WO2003106666-A2.
PD 24-DEC-2003.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 308.5; DB 8; Length 461;
Beet Local Similarity 24.5%; Pred. No. 9e-09;
RESULT 1004
ID AAE08628 standard; protein; 419 AA.
DE Human protein C derivative #2.
PN WO200159084-A1.
PD 16-AUG-2001.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 308; DB 4; Length 419;
Beet Local Similarity 24.5%; Pred. No. 8.7e-09;
RESULT 1005
ID AAU99084 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant R352N/D354T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 307.5; DB 5; Length 419;
Beet Local Similarity 24.6%; Pred. No. 9.3e-09;
RESULT 1006
ID AAU99021 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K217N/L219S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 307.5; DB 5; Length 419;
Beet Local Similarity 24.4%; Pred. No. 9.3e-09;
RESULT 1007
ID AAU99046 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant Y302N/S304T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 307.5; DB 5; Length 419;
Beet Local Similarity 24.5%; Pred. No. 9.3e-09;
RESULT 1008
ID AAU99093 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant H388N/Y390S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.

PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 307.5; DB 5; Length 419;
Beet Local Similarity 24.7%; Pred. No. 9.3e-09;
RESULT 1009
ID AAU99083 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant R352N/D354S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 306.5; DB 5; Length 419;
Beet Local Similarity 24.5%; Pred. No. 1.1e-08;
RESULT 1010
ID AAU99074 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V339T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 306.5; DB 5; Length 419;
Beet Local Similarity 24.4%; Pred. No. 1.1e-08;
RESULT 1011
ID AAU99003 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D172N/K174S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.8%; Score 306.5; DB 5; Length 419;
Beet Local Similarity 24.4%; Pred. No. 1.1e-08;
RESULT 1012
ID AAR13585 standard; protein; 461 AA.
DE Human protein C zymogen Q313.
PN EP443874-A.
PD 28-AUG-1991.
PA (ELIL) LILLY & CO ELI.
Query Match 7.8%; Score 306.5; DB 2; Length 461;
Beet Local Similarity 24.1%; Pred. No. 1.1e-08;
RESULT 1013
ID ABM63654 standard; protein; 495 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3903.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.8%; Score 306.5; DB 8; Length 495;
Beet Local Similarity 24.8%; Pred. No. 1.2e-08;
RESULT 1014
ID AED96686 standard; protein; 495 AA.
DE Human C-reactive protein (CRP) associated marker SEQ ID NO 868.
PN WO2005107364-A2.
PD 17-NOV-2005.
PA (COMP-) COMPUGEN LTD.
PA (COHE/) COHEN Y.
Query Match 7.8%; Score 306.5; DB 9; Length 495;
Beet Local Similarity 24.8%; Pred. No. 1.2e-08;
RESULT 1015
ID AAU99004 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D172N/K174T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.7%; Score 305.5; DB 5; Length 419;
Beet Local Similarity 24.4%; Pred. No. 1.2e-08;
RESULT 1016
ID AAU99073 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V339S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.7%; Score 305.5; DB 5; Length 419;
Beet Local Similarity 24.4%; Pred. No. 1.2e-08;

RESULT 1017
ID AEA20109 standard; protein; 667 AA.
DE Novel human polypeptide SEQ ID NO 803.
PN WO2005049806-A2.
PD 02-JUN-2005.
PA (NOVE-) NOVELO INC.
Query Match 7.7%; Score 305; DB 9; Length 667;
Best Local Similarity 20.8%; Pred. No. 2e-08;
RESULT 1018
ID AEG02812 standard; protein; 419 AA.
DE Mature Protein C polypeptide.
PN WO2006018204-A1.
PD 23-FEB-2006.
PA (ZIBB-) ZLB BEHRING GMBH.
Query Match 7.7%; Score 304.5; DB 10; Length 419;
Best Local Similarity 24.9%; Pred. No. 1.3e-08;
RESULT 1019
ID AAR13582 standard; protein; 461 AA.
DE Human protein C zymogen Q097.
PN EP443874-A.
PD 28-AUG-1991.
PA (ELIL-) LILLY & CO ELI.
Query Match 7.7%; Score 304.5; DB 2; Length 461;
Best Local Similarity 24.4%; Pred. No. 1.5e-08;
RESULT 1020
ID AAR13584 standard; protein; 461 AA.
DE Human protein C zymogen Q248.
PN EP443874-A.
PD 28-AUG-1991.
PA (ELIL-) LILLY & CO ELI.
Query Match 7.7%; Score 304.5; DB 2; Length 461;
Best Local Similarity 24.4%; Pred. No. 1.5e-08;
RESULT 1021
ID AAU99037 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant T253N/D255S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.7%; Score 302.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 1.7e-08;
RESULT 1022
ID AAU99028 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V243N/V245T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.7%; Score 302.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 1.7e-08;
RESULT 1023
ID AAU99027 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V243N/V245S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.6%; Score 301.5; DB 5; Length 419;
Best Local Similarity 24.5%; Pred. No. 2e-08;
RESULT 1024
ID AAU99038 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant T253N/D255T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.6%; Score 301.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 2e-08;
RESULT 1025
ID AAP93714 standard; protein; 461 AA.
DE Hybrid protein of protein-C and Factor-X.
PN EP296413-A.
PD 28-DEC-1988.

PA (FASH) HOECHST JAPAN LTD.
Query Match 7.6%; Score 301.5; DB 1; Length 461;
Best Local Similarity 24.7%; Pred. No. 2.1e-08;
RESULT 1026
ID ADX39098 standard; protein; 681 AA.
DE Mouse factor VII mutant.
PN WO2005014775-A2.
PD 17-FEB-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 7.6%; Score 301.5; DB 9; Length 681;
Best Local Similarity 22.3%; Pred. No. 3.1e-08;
RESULT 1027
ID ADX39094 standard; protein; 446 AA.
DE Mouse factor VII.
PN WO2005014775-A2.
PD 17-FEB-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 7.6%; Score 300.5; DB 9; Length 446;
Best Local Similarity 22.3%; Pred. No. 2.3e-08;
RESULT 1028
ID AAU99041 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D255N/D257S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.6%; Score 299.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 2.5e-08;
RESULT 1029
ID ADX39097 standard; protein; 443 AA.
DE Rabbit factor VII.
PN WO2005014775-A2.
PD 17-FEB-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 7.6%; Score 299.5; DB 9; Length 443;
Best Local Similarity 24.0%; Pred. No. 2.6e-08;
RESULT 1030
ID AAU99029 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V245N/P247S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.6%; Score 298.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 2.8e-08;
RESULT 1031
ID AAU99030 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant V245N/P247T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.6%; Score 298.5; DB 5; Length 419;
Best Local Similarity 24.4%; Pred. No. 2.8e-08;
RESULT 1032
ID AAU99042 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant D255N/D257T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Query Match 7.6%; Score 298.5; DB 5; Length 419;
Best Local Similarity 24.2%; Pred. No. 2.8e-08;
RESULT 1033
ID ADX39092 standard; protein; 433 AA.
DE Danio factor VII.
PN WO2005014775-A2.
PD 17-FEB-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 7.6%; Score 298.5; DB 9; Length 433;
Best Local Similarity 23.0%; Pred. No. 2.9e-08;
RESULT 1034
ID ADB65750 standard; protein; 397 AA.

DE Human protein encoded by clone UTRU20087070.
PN EPI30459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (RENS-) RES ASSOC BIOTECHNOLOGY.
Query Match 7.6%; Score 298; DB 7; Length 397;
Best Local Similarity 24.1%; Pred. No. 2.9e-08;
RESULT 1035
ID AD117268 standard; protein; 230 AA.
DE Polypeptide homologous to a human NOVX domain SegID 804.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.5%; Score 296; DB 5; Length 230;
Best Local Similarity 32.3%; Pred. No. 2.2e-08;
RESULT 1036
ID AD117276 standard; protein; 230 AA.
DE Polypeptide homologous to a human NOVX domain SegID 812.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.5%; Score 296; DB 5; Length 230;
Best Local Similarity 32.3%; Pred. No. 2.2e-08;
RESULT 1037
ID ADU93075 standard; protein; 230 AA.
DE Trypsin-like serine protease protein - SEQ ID 66.
PN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO/) ALSOBROOK J P.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PART/) PARTURAJAN M.
PA (LEPL/) LEPLER D M.
PA (BURG/) BURGESS C E.
PA (SHIM/) SHIMKETS R A.
PA (GROS/) GROSSE W M.
PA (SZEK/) SZEKERES E S.
PA (VERN/) VERNET C A M.
PA (LILU/) LI L.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOG F L.
PA (GORM/) GORMAN L.
PA (GANG/) GANGOLLI E A.
PA (FERN/) FERNANDES E R.
PA (RIEG/) RIEGER D K.
PA (BDIN/) EDINGER S R.
PA (GUNT/) GUNTHER E.
PA (MILL/) MILLET I.
PA (SCIO/) SCIORE P.
PA (BLIE/) BLIERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Query Match 7.5%; Score 296; DB 7; Length 230;
Best Local Similarity 32.3%; Pred. No. 2.2e-08;
RESULT 1038
ID AEF27705 standard; protein; 230 AA.
DE Trypsin-like serine protease consensus sequence, SEQ:135.
PN US2006009634-A1.
PD 12-JAN-2006.
PA (KERU/) KERUDA R.
PA (ALSO/) ALSOBROOK J.
PA (TCHE/) TCHERNEV V.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K.
PA (PART/) PARTURAJAN M.
PA (GROS/) GROSSE W.
PA (LEPL/) LEPLER D.
PA (BURG/) BURGESS C.
PA (VERN/) VERNET C.
PA (LILU/) LI L.
PA (GORM/) GORMAN L.

PA (EDIN/) EDINGER S.
PA (SCIO/) SCIORE P.
PA (BLIE/) BLIERMAN K.
PA (MALI/) MALYANKAR U.
PA (ROTH/) ROTHENBERG M.
PA (STON/) STONE D.
PA (BOLD/) BOLDOG F.
PA (GUOX/) GUO X.
PA (SHEN/) SHENOY S.
PA (ANDE/) ANDERSON D.
PA (PADI/) PADIGARU M.
PA (TAUP/) TAUPIER R.
PA (MILL/) MILLER C.
PA (EISE/) EISEN A.
Query Match 7.5%; Score 296; DB 10; Length 230;
Best Local Similarity 32.3%; Pred. No. 2.2e-08;
RESULT 1039
ID AEG02859 standard; protein; 451 AA.
DE Factor VII/X fusion protein SEQ ID NO:53.
PN WO2006018204-A1.
PD 23-FEB-2006.
PA (ZILB-) ZILB BEHRING GMBH.
Query Match 7.5%; Score 296; DB 10; Length 451;
Best Local Similarity 25.2%; Pred. No. 4.1e-08;
RESULT 1040
ID ADM64351 standard; protein; 527 AA.
DE Mutant human plasminogen activator protein - SEQ ID 3.
PN CN1526726-A.
PD 08-SEP-2004.
PA (LIBB/) LI B.
Query Match 7.5%; Score 296; DB 8; Length 527;
Best Local Similarity 23.4%; Pred. No. 4.8e-08;
RESULT 1041
ID ABG21442 standard; protein; 932 AA.
DE Novel human diagnostic protein #21433.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.5%; Score 296; DB 4; Length 932;
Best Local Similarity 21.0%; Pred. No. 8.1e-08;
RESULT 1042
ID ADX39096 standard; protein; 425 AA.
DE Chicken factor VII.
PN WO2005014775-A2.
PD 17-FEB-2005.
PA (UYFL-) UNIV FLORIDA RES FOUND INC.
Query Match 7.5%; Score 295; DB 9; Length 425;
Best Local Similarity 23.4%; Pred. No. 4.4e-08;
RESULT 1043
ID AAR09290 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator analogue GF6 (Ieu 66, Asp 67, Thr 68, Gln 117).
PN WO8912681-A.
PD 28-DEC-1989.
PA (BRI-) BRIT BIO-TECHN LTD.
Query Match 7.5%; Score 294; DB 2; Length 562;
Best Local Similarity 23.3%; Pred. No. 6.5e-08;
RESULT 1044
ID ADX39099 standard; protein; 407 AA.
DE Bovine factor VII.
PN WO2005014775-A2.
PD 17-FEB-2005.
PA (UYFL-) UNIV FLORIDA RES FOUND INC.
Query Match 7.4%; Score 293.5; DB 9; Length 407;
Best Local Similarity 24.1%; Pred. No. 5.1e-08;
RESULT 1045
ID ABU12065 standard; protein; 986 AA.
DE Human NOVI2a CG92293-01 protein SEQ ID 50.
PN WO200281625-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.4%; Score 293; DB 6; Length 986;
Best Local Similarity 23.1%; Pred. No. 1.2e-07;

RESULT 1046
ID AAR70903 standard; protein; 527 AA.
DE Human t-PA variant (N103,A432,A434).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.4%; Score 292; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 7.9e-08;
RESULT 1047
ID AAR70895 standard; protein; 527 AA.
DE Human t-PA variant (N103,A331,A332).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.4%; Score 292; DB 2; Length 527;
Best Local Similarity 23.5%; Pred. No. 7.9e-08;
RESULT 1048
ID ADN03787 standard; protein; 516 AA.
DE Antiposrotatic protein sequence #90.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.4%; Score 291.5; DB 8; Length 516;
Best Local Similarity 23.1%; Pred. No. 8.2e-08;
RESULT 1049
ID ABR80985 standard; protein; 516 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO81669, SEQ:2539.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.4%; Score 291.5; DB 8; Length 516;
Best Local Similarity 23.1%; Pred. No. 8.2e-08;
RESULT 1050
ID ADO39246 standard; protein; 516 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 909.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.4%; Score 291.5; DB 8; Length 516;
Best Local Similarity 23.1%; Pred. No. 8.2e-08;
RESULT 1051
ID AAR13921 standard; protein; 522 AA.
DE Delta (466-470) tPA variant with H432A and R434A subctns.
PN WO9113149-A.
PD 05-SEP-1991.
PA (GETH) GENENTECH INC.
Query Match 7.4%; Score 291.5; DB 2; Length 522;
Best Local Similarity 22.7%; Pred. No. 8.3e-08;
RESULT 1052
ID AAP70475 standard; protein; 564 AA.
DE Sequence of tissue plasminogen (TPA) analogue.
PN WO8703906-A.
PD 02-JUL-1987.
PA (UPJO) UPJOHN CO.
PA (MARO/) MAROTTI K R.
Query Match 7.4%; Score 291.5; DB 1; Length 564;
Best Local Similarity 22.9%; Pred. No. 8.9e-08;
RESULT 1053
ID AAG83838 standard; protein; 376 AA.
DE Rough scale snake venom prothrombin activator, trocarin.
PN WO2003082914-A1.
PD 09-OCT-2003.
PA (UYOU) UNIV QUEENSLAND.
Query Match 7.4%; Score 291; DB 8; Length 376;
Best Local Similarity 22.2%; Pred. No. 6.5e-08;
RESULT 1054
ID AAP60614 standard; protein; 516 AA.
DE Plasmid pDAP3 encoded sequence.
PN JP61139386-A.
PD 26-JUN-1986.
PA (TOYJ) TOYO SODA MFG CO LTD.
PA (SAGA) SAGAMI CHEM RES CENTRE.
PA (CENG) CENTRAL GLASS CO LTD.

PA (HODO) HODOGAYA CHEM IND CO LTD.
Query Match 7.4%; Score 290.5; DB 1; Length 516;
Best Local Similarity 23.1%; Pred. No. 9.3e-08;
RESULT 1055
ID AAP70257 standard; protein; 516 AA.
DE Sequence of human tissue plasminogen activator (TPA) and leader.
PN EP231883-A.
PD 12-AUG-1987.
PA (SAGA) SAGAMI CHEM RES CENTRE.
PA (NIPS) NIPPON SODA CO.
PA (CENG) CENTRAL GLASS CO LTD.
PA (TOYJ) TOYO SODA MFG CO LTD.
PA (NISC) NISSAN CHEM IND LTD.
PA (NISC) NISSAN CHEMICAL INDS KK.
Query Match 7.4%; Score 290.5; DB 1; Length 516;
Best Local Similarity 23.1%; Pred. No. 9.3e-08;
RESULT 1056
ID AAR70878 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N103,D184,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.4%; Score 290; DB 2; Length 483;
Best Local Similarity 23.3%; Pred. No. 9.3e-08;
RESULT 1057
ID AAR70885 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N103,D184,E275,1277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.4%; Score 290; DB 2; Length 483;
Best Local Similarity 23.3%; Pred. No. 9.3e-08;
RESULT 1058
ID AAR70894 standard; protein; 527 AA.
DE Human t-PA variant (N103,A303,A304).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.4%; Score 290; DB 2; Length 527;
Best Local Similarity 24.0%; Pred. No. 1e-07;
RESULT 1059
ID ADW64350 standard; protein; 527 AA.
DE Mutant human plasminogen activator protein - SEQ ID 2.
PN CN1526726-A.
PD 06-SEP-2004.
PA (LIBB/) LI B.
Query Match 7.4%; Score 290; DB 8; Length 527;
Best Local Similarity 23.2%; Pred. No. 1e-07;
RESULT 1060
ID ADL00357 standard; protein; 520 AA.
DE Human tissue type plasminogen activator (h-tpa) mutant polypeptide.
PN CN1397564-A.
PD 19-FEB-2003.
PA (LIBB/) LI B.
Query Match 7.3%; Score 289.5; DB 7; Length 520;
Best Local Similarity 23.2%; Pred. No. 1.1e-07;
RESULT 1061
ID AAR12340 standard; protein; 559 AA.
DE T-PA variant contg. fibrinectin for thrombosis lysis (1).
PN JP03061482-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.3%; Score 289.5; DB 2; Length 559;
Best Local Similarity 22.2%; Pred. No. 1.1e-07;
RESULT 1062
ID AAR22664 standard; protein; 564 AA.
DE tPA analogue KK2A.
PN US5106741-A.
PD 21-APR-1992.
PA (UPJO) UPJOHN CO.
Query Match 7.3%; Score 289.5; DB 2; Length 564;
Best Local Similarity 23.4%; Pred. No. 1.1e-07;
RESULT 1063

ID AAE06934 standard; protein; 658 AA.
DE Human membrane-type serine protease (MTSP) 4-S splice variant.
PN WO200157194-A2.
PD 09-AUG-2001.
PA (CORV-) CORVAS INT INC.
Query Match 7.3%; Score 289.5; DB 4; Length 658;
Best Local Similarity 22.7%; Pred. No. 1.3e-07;
RESULT 1064

ID AD110379 standard; protein; 658 AA.
DE Human cell surface protease #5.
PN WO200295007-A2.
PD 28-NOV-2002.
PA (CORV-) CORVAS INT INC.
Query Match 7.3%; Score 289.5; DB 7; Length 658;
Best Local Similarity 22.7%; Pred. No. 1.3e-07;
RESULT 1065

ID AD146903 standard; protein; 658 AA.
DE Human transmembrane serine protease (MTSP) polypeptide #5.
PN US2004001801-A1.
PD 01-JAN-2004.
PA (CORV-) CORVAS INT INC.
Query Match 7.3%; Score 289.5; DB 8; Length 658;
Best Local Similarity 22.7%; Pred. No. 1.3e-07;
RESULT 1066

ID AAE06933 standard; protein; 802 AA.
DE Human membrane-type serine protease (MTSP) 4-L splice variant.
PN WO200157194-A2.
PD 09-AUG-2001.
PA (CORV-) CORVAS INT INC.
Query Match 7.3%; Score 289.5; DB 4; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.6e-07;
RESULT 1067

ID AD110377 standard; protein; 802 AA.
DE Human cell surface protease #4.
PN WO200295007-A2.
PD 28-NOV-2002.
PA (CORV-) CORVAS INT INC.
Query Match 7.3%; Score 289.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.6e-07;
RESULT 1068

ID AD146901 standard; protein; 802 AA.
DE Human transmembrane serine protease (MTSP) polypeptide #4.
PN US2004001801-A1.
PD 01-JAN-2004.
PA (CORV-) CORVAS INT INC.
Query Match 7.3%; Score 289.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.6e-07;
RESULT 1069

ID AAR21598 standard; protein; 527 AA.
DE tPA variant - T103N, D236A, D238A, K240A.
PN WO9202612-A.
PD 20-FEB-1992.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 289; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.1e-07;
RESULT 1070

ID AAR09217 standard; protein; 529 AA.
DE t-PA insertion variant 1304 HH.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 289; DB 2; Length 529;
Best Local Similarity 23.4%; Pred. No. 1.1e-07;
RESULT 1071

ID AAB85076 standard; peptide; 296 AA.
DE Amino acid sequence of MASP-1 polypeptide.
PN WO200140451-A2.
PD 07-JUN-2001.
PA (JENS/) JENSENIUS J C.
Query Match 7.3%; Score 288.5; DB 4; Length 296;
Best Local Similarity 29.3%; Pred. No. 7.1e-08;
RESULT 1072

ID AAY41710 standard; protein; 802 AA.
DE Human PRO618 protein sequence.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 2; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1073

ID AAB44266 standard; protein; 802 AA.
DE Human PRO618 (UNQ354) protein sequence SEQ ID NO:169.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 3; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1074

ID AAB24052 standard; protein; 802 AA.
DE Human PRO618 protein sequence SEQ ID NO:24.
PN WO200053754-A1.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 3; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1075

ID AAB82755 standard; protein; 802 AA.
DE Amino acid sequence of novel human protease #54.
PN WO200200860-A2.
PD 03-JAN-2002.
PA (SUGEN) SUGEN INC.
Query Match 7.3%; Score 288.5; DB 5; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1076

ID ABO25212 standard; protein; 802 AA.
DE Novel human secreted and transmembrane protein PRO618.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1077

ID ABO72218 standard; protein; 802 AA.
DE Novel human secreted and transmembrane protein PRO618.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1078

ID ABB84898 standard; protein; 802 AA.
DE Human secreted and transmembrane polypeptide PRO618.
PN US200217553-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1079

ID ABB61096 standard; protein; 802 AA.
DE Human PRO618 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1080

ID ABB80365 standard; protein; 802 AA.
DE Human secreted/transmembrane protein PRO618.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1081

ID ADA24708 standard; protein; 802 AA.

DE Novel human secreted and transmembrane protein PRO618.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1082
ID ABO19667 standard; protein; 802 AA.
DE Novel human secreted and transmembrane protein PRO618.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1083
ID ADA12369 standard; protein; 802 AA.
DE Human secreted/transmembrane polypeptide PRO618.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1084
ID ABO19558 standard; protein; 802 AA.
DE Novel human secreted and transmembrane polypeptide #26.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1085
ID ADB73675 standard; protein; 802 AA.
DE Human PRO polypeptide #26.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1086
ID ADB73691 standard; protein; 802 AA.
DE Human PRO polypeptide #26.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1087
ID ADC43817 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1088
ID ADC61577 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1089
ID ADC63541 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1090
ID ADC66641 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1091
ID ADC68765 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1092
ID ADC62825 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1093
ID ADC67890 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1094
ID ADC41210 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1095
ID ADC67265 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1096
ID ADC62201 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1097
ID ADC41834 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1098
ID ADB49203 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US200306744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1099
ID ADB35257 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003203434-A1.
PD 30-OCT-2003.

PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 7; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1100
ID ADEL6371 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
FN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 7; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1101
ID ADD72986 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
FN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 7; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1102
ID ADD72344 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
FN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 7; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1103
ID ADEL6995 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
FN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 7; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1104
ID ADF47009 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
FN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 7; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1105
ID ADG52766 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
FN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 7; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1106
ID ADG60086 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
FN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 7; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1107
ID ADI60846 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
FN US2003077700-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 7; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1108
ID ADA8503 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
FN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 7; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.8e-07;

Query Match
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1109
ID ADH9604 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
FN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLMAN K J.
PA (KJAV/) KJAVAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1110
ID ADF61244 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
FN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1111
ID ADF39936 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
FN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1112
ID ADF45732 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
FN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1113
ID ADF24128 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
FN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;
Query Match
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1114
ID ADF40560 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
FN US2003199021-A1.
PD 23-OCT-2003.


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Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1133
ID ADH25391 standard; protein; 802 AA.
DE Human neurotrophin homologue related protein sequence SEQ ID NO:169.
PN EP386931-A1.
PD 04-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1134
ID ADM17168 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1135
ID ADL07002 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1136
ID ADT91615 standard; protein; 802 AA.
DE Human PRO618 protein sequence.
PN AU2002317529-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1137
ID ADU50124 standard; protein; 802 AA.
DE PRO618, SEQ ID 169.
PN US2004233964-A1.
PD 11-NOV-2004.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1138
ID ADW49403 standard; protein; 802 AA.
DE PRO618 protein, SEQ ID 169.
PN US2005014226-A1.
PD 20-JAN-2005.
PA (ASHK ) ASHKENAZI A J.
PA (BAKE ) BAKER K P.
PA (BOTS ) BOTSTEIN D.
PA (DESN ) DESNOYERS L.
PA (EATO ) EATON D L.
PA (FERR ) FERRARA N.
PA (FLIV ) FLIVAROFF E.
PA (FONG ) FONG S.
PA (GAOW ) GAO W.
PA (GERB ) GERBER H.
PA (GERR ) GERRITSEN M E.
PA (GODD ) GODDARD A.
PA (GODO ) GODOWSKI P J.
PA (GRIM ) GRIMALDI J C.
PA (GURN ) GURNEY A L.
PA (HILL ) HILLAN K J.
PA (KLJA ) KLJAVIN I J.
PA (KUOS ) KUO S S.
PA (NAPI ) NAPIER M A.
PA (PANJ ) PAN J.
PA (PAON ) PAONI N F.
PA (ROYM ) ROY M A.
PA (SHEL ) SHELTON D L.
PA (STEW ) STEWART T A.
PA (TUMA ) TUMAS D.
PA (WILL ) WILLIAMS P M.
PA (WOOD ) WOOD W I.

Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1139
ID ADZ52064 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2005084935-A1.
PD 21-APR-2005.
PA (ASHK ) ASHKENAZI A J.
PA (BAKE ) BAKER K P.
PA (BOTS ) BOTSTEIN D.
PA (DESN ) DESNOYERS L.
PA (EATO ) EATON D L.
PA (FERR ) FERRARA N.
PA (FLIV ) FLIVAROFF E.
PA (FONG ) FONG S.
PA (GAOW ) GAO W.
PA (GERB ) GERBER H.
PA (GERR ) GERRITSEN M E.
PA (GODD ) GODDARD A.
PA (GODO ) GODOWSKI P J.
PA (GRIM ) GRIMALDI J C.
PA (GURN ) GURNEY A L.
PA (HILL ) HILLAN K J.
PA (KLJA ) KLJAVIN I J.
PA (KUOS ) KUO S S.
PA (NAPI ) NAPIER M A.
PA (PANJ ) PAN J.
PA (PAON ) PAONI N F.
PA (ROYM ) ROY M A.
PA (SHEL ) SHELTON D L.
PA (STEW ) STEWART T A.
PA (TUMA ) TUMAS D.
PA (WILL ) WILLIAMS P M.
PA (WOOD ) WOOD W I.
Query Match 7.3%; Score 288.5; DB 9; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1140
ID AED47892 standard; protein; 802 AA.
DE Human PRO618 amino acid sequence.
PN US2005227342-A1.
PD 13-OCT-2005.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 9; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1141
ID AAB98507 standard; protein; 902 AA.
DE Murine epithin.
PN WO200129056-A1.
PD 26-APR-2001.
PA (UYAR ) UNIV ARKANSAS.
Query Match 7.3%; Score 288.5; DB 4; Length 902;
Best Local Similarity 21.4%; Pred. No. 2e-07;
RESULT 1142
ID AAU80517 standard; protein; 902 AA.
DE Mouse epithilin-like serine protease.
PN WO200196378-A2.
PD 20-DEC-2001.
PA (FARB ) BAYER AG.
Query Match 7.3%; Score 288.5; DB 5; Length 902;
Best Local Similarity 21.4%; Pred. No. 2e-07;
RESULT 1143
ID AAU77549 standard; protein; 902 AA.
DE Murine type II membrane serine protease, epithin.
PN WO200212461-A2.
PD 14-FEB-2002.
PA (FARB ) BAYER AG.
Query Match 7.3%; Score 288.5; DB 5; Length 902;
Best Local Similarity 21.4%; Pred. No. 2e-07;
RESULT 1144
ID AAR05489 standard; protein; 527 AA.
DE tPA024 precursor protein.
PN EP373896-A.
PD 20-JUN-1990.
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PA (YAMA) YAMANOUCHI PHARM CO LTD.
PA (YAMA) NIPPON STEEL CORP.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.6%; Pred. No. 1.3e-07;
RESULT 1145
ID AAR21599 standard; protein; 527 AA.
DE tPA variant - N117Q, D236A, D238A, K240A.
PN WO9202612-A.
PD 20-FEB-1992.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.3e-07;
RESULT 1146
ID AAR20220 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-012.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.3e-07;
RESULT 1147
ID AAR20219 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-011.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.3e-07;
RESULT 1148
ID AAR20217 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-009.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.3e-07;
RESULT 1149
ID AAR20218 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-010.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 1.3e-07;
RESULT 1150
ID AAR70901 standard; protein; 527 AA.
DE Human t-PA variant (N103, A416, A417, A418).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.5%; Pred. No. 1.3e-07;
RESULT 1151
ID AAR70904 standard; protein; 527 AA.
DE Human t-PA variant (N103, A440).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 288; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.3e-07;
RESULT 1152
ID AAY49558 standard; protein; 356 AA.
DE Human protein C protein sequence.
PN WO950454-A2.
PD 07-OCT-1999.
PA (WHEB) WHITEHEAD INST BIOMEDICAL RES.
Query Match 7.3%; Score 287.5; DB 2; Length 356;
Best Local Similarity 24.5%; Pred. No. 9.5e-08;
RESULT 1153
ID AAM52187 standard; protein; 406 AA.
DE Human FVII mutant K143N/N145T/R315N/V317T.
PN WO200158935-A2.
PD 16-AUG-2001.
PA (GETH) GENENTECH INC.

PA (MAXY-) MAXYGEN APS.
Query Match 7.3%; Score 287.5; DB 4; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.1e-07;
RESULT 1154
ID AD56078 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant K143N/ N145T/ R230N/ A232T.
PN WO200400366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.3%; Score 287.5; DB 8; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.1e-07;
RESULT 1155
ID ADV44720 standard; protein; 406 AA.
DE Human factor VII mutant K143N/N145T/R315N/V317T.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.3%; Score 287.5; DB 9; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.1e-07;
RESULT 1156
ID ADY74310 standard; protein; 406 AA.
DE Human Factor VII variant polypeptide #253.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.3%; Score 287.5; DB 9; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.1e-07;
RESULT 1157
ID AEP15066 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #35.
PN WO2005023916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.3%; Score 287.5; DB 10; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.1e-07;
RESULT 1158
ID AAR13918 standard; protein; 522 AA.
DE Delta (466-470) tPA variant with K146A, H417A and E418A substns.
PN WO9113149-A.
PD 05-SEP-1991.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287.5; DB 2; Length 522;
Best Local Similarity 22.9%; Pred. No. 1.4e-07;
RESULT 1159
ID ABR43952 standard; protein; 795 AA.
DE Human PROS18.
PN WO200231111-A2.
PD 18-APR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 7.3%; Score 287.5; DB 5; Length 795;
Best Local Similarity 22.7%; Pred. No. 2e-07;
RESULT 1160
ID ADC83828 standard; protein; 467 AA.
DE Coastal taipan venom protease.
PN WO2003082914-A1.
PD 09-OCT-2003.
PA (UTQU) UNIV QUEENSLAND.
Query Match 7.3%; Score 287; DB 8; Length 467;
Best Local Similarity 22.5%; Pred. No. 1.3e-07;
RESULT 1161
ID AAR70879 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44, N103, S184, E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.3e-07;
RESULT 1162
ID AAR70883 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44, N103, K210, E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.

Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.3e-07;
RESULT 1163
ID AAR70884 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.3e-07;
RESULT 1164
ID AAR70886 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,S184,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.3e-07;
RESULT 1165
ID AAR70877 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.3e-07;
RESULT 1166
ID AAR70887 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,K213,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.3e-07;
RESULT 1167
ID AAR70881 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,R210,A211,R212,R213,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.3e-07;
RESULT 1168
ID AAR70882 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,R252,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.3e-07;
RESULT 1169
ID AAR70889 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,R252,E275,O277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.3e-07;
RESULT 1170
ID AAR70888 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,R210,A211,R212,R213,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.3e-07;
RESULT 1171
ID AAR70890 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,K210,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.3e-07;
RESULT 1172
ID AAR70880 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,K213,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.3e-07;
RESULT 1173
ID AAR70907 standard; protein; 527 AA.
DE Human t-PA variant (N103,A460,A462).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.5e-07;
RESULT 1174
ID AAR70874 standard; protein; 527 AA.
DE Human t-PA variant (N67,N103).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.5e-07;
RESULT 1175
ID AAR70892 standard; protein; 527 AA.
DE Human t-PA variant (N103,A283,A287).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.5e-07;
RESULT 1176
ID AAM52182 standard; protein; 406 AA.
DE Human FVII mutant K143N/N145T.
PN WO200158935-A2.
PD 16-AUG-2001.
PA (MAXY-) MAXYGEN APS.
Query Match 7.3%; Score 286.5; DB 4; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.2e-07;
RESULT 1177
ID ADU56073 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant K143N/ N145T.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.3%; Score 286.5; DB 8; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.2e-07;
RESULT 1178
ID ADO10589 standard; protein; 406 AA.
DE Human factor VII/VIII protein mutant #25.
PN WO2004029091-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.3%; Score 286.5; DB 8; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.2e-07;
RESULT 1179
ID ADVA4715 standard; protein; 406 AA.
DE Human factor VII mutant K143N/N145T.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.3%; Score 286.5; DB 9; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.2e-07;
RESULT 1180
ID ADY74305 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #248.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.3%; Score 286.5; DB 9; Length 406;

Best Local Similarity 23.4%; Pred. No. 1.3e-07;
RESULT 1172
ID AAR70880 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N103,K213,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 483;
Best Local Similarity 23.4%; Pred. No. 1.3e-07;
RESULT 1173
ID AAR70907 standard; protein; 527 AA.
DE Human t-PA variant (N103,A460,A462).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.5e-07;
RESULT 1174
ID AAR70874 standard; protein; 527 AA.
DE Human t-PA variant (N67,N103).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.5e-07;
RESULT 1175
ID AAR70892 standard; protein; 527 AA.
DE Human t-PA variant (N103,A283,A287).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 287; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 1.5e-07;
RESULT 1176
ID AAM52182 standard; protein; 406 AA.
DE Human FVII mutant K143N/N145T.
PN WO200158935-A2.
PD 16-AUG-2001.
PA (MAXY-) MAXYGEN APS.
Query Match 7.3%; Score 286.5; DB 4; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.2e-07;
RESULT 1177
ID ADU56073 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant K143N/ N145T.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.3%; Score 286.5; DB 8; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.2e-07;
RESULT 1178
ID ADO10589 standard; protein; 406 AA.
DE Human factor VII/VIII protein mutant #25.
PN WO2004029091-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.3%; Score 286.5; DB 8; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.2e-07;
RESULT 1179
ID ADVA4715 standard; protein; 406 AA.
DE Human factor VII mutant K143N/N145T.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.3%; Score 286.5; DB 9; Length 406;
Best Local Similarity 23.0%; Pred. No. 1.2e-07;
RESULT 1180
ID ADY74305 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #248.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.3%; Score 286.5; DB 9; Length 406;

Best Local Similarity 23.0%; Pred. No. 1.2e-07;
 RESULT 1181
 ID AEP15046 standard; protein; 406 AA.
 DE Variant human coagulation Factor VII protein #15.
 PN WO2005123916-A2.
 PD 29-DEC-2005.
 PA (NOVO) NOVO NORDISK HEALTH CARE AG.
 Query Match 7.3%; Score 286.5; DB 10; Length 406;
 Best Local Similarity 23.0%; Pred. No. 1.2e-07;
 RESULT 1182
 ID ADG63826 standard; protein; 467 AA.
 DE Brown snake venom protease.
 PN WO2003082914-A1.
 PD 09-OCT-2003.
 PA (UNIV) UNIV QUEENSLAND.
 Query Match 7.3%; Score 286.5; DB 8; Length 467;
 Best Local Similarity 22.2%; Pred. No. 1.4e-07;
 RESULT 1183
 ID AAR14486 standard; protein; 522 AA.
 DE Delta (466-470) CPA variant with Y67N substitution.
 PN WO9113149-A.
 PD 05-SEP-1991.
 PA (GENET) GENENTECH INC.
 Query Match 7.3%; Score 286.5; DB 2; Length 522;
 Best Local Similarity 22.7%; Pred. No. 1.5e-07;
 RESULT 1184
 ID AAR44816 standard; protein; 527 AA.
 DE Human CPA variant (N67,N103).
 PN US5270198-A.
 PD 14-DEC-1993.
 PA (GENET) GENENTECH INC.
 Query Match 7.2%; Score 286; DB 2; Length 527;
 Best Local Similarity 23.2%; Pred. No. 1.7e-07;
 RESULT 1185
 ID AAR44812 standard; protein; 527 AA.
 DE Human CPA variant N103.
 PN US5270198-A.
 PD 14-DEC-1993.
 PA (GENET) GENENTECH INC.
 Query Match 7.2%; Score 286; DB 2; Length 527;
 Best Local Similarity 23.2%; Pred. No. 1.7e-07;
 RESULT 1186
 ID AAR70868 standard; protein; 527 AA.
 DE Human t-PA variant (N67,A432,A434).
 PN US5385732-A.
 PD 31-JAN-1995.
 PA (GENET) GENENTECH INC.
 Query Match 7.2%; Score 286; DB 2; Length 527;
 Best Local Similarity 23.2%; Pred. No. 1.7e-07;
 RESULT 1187
 ID AAR70860 standard; protein; 527 AA.
 DE Human t-PA variant (N67,A331,A332).
 PN US5385732-A.
 PD 31-JAN-1995.
 PA (GENET) GENENTECH INC.
 Query Match 7.2%; Score 286; DB 2; Length 527;
 Best Local Similarity 23.4%; Pred. No. 1.7e-07;
 RESULT 1188
 ID AAR70900 standard; protein; 527 AA.
 DE Human t-PA variant (N103,A410).
 PN US5385732-A.
 PD 31-JAN-1995.
 PA (GENET) GENENTECH INC.
 Query Match 7.2%; Score 286; DB 2; Length 527;
 Best Local Similarity 23.1%; Pred. No. 1.7e-07;
 RESULT 1189
 ID AAR09220 standard; protein; 529 AA.
 DE t-PA insertion variant 1304H, 1305H.
 PN WO9002798-A.
 PD 22-MAR-1990.
 PA (GENET) GENENTECH INC.
 Query Match 7.2%; Score 286; DB 2; Length 529;
 Best Local Similarity 23.2%; Pred. No. 1.7e-07;
 RESULT 1190
 ID AAR70449 standard; protein; 530 AA.
 DE Sequence encoded by of synthetic gene for mature human tissue plasminogen activator (tPA).
 PN WO8705934-A.
 PD 08-OCT-1987.
 PA (CREA/) CREA R.
 Query Match 7.2%; Score 286; DB 1; Length 530;
 Best Local Similarity 22.9%; Pred. No. 1.7e-07;
 RESULT 1191
 ID AAR12342 standard; protein; 561 AA.
 DE T-PA with -ve charged finger and/or kringle domain (1).
 PN JP03061483-A.
 PD 18-MAR-1991.
 PA (FUJ) FUJISAWA PHARM CO LTD.
 Query Match 7.2%; Score 286; DB 2; Length 561;
 Best Local Similarity 22.1%; Pred. No. 1.8e-07;
 RESULT 1192
 ID AAR09289 standard; protein; 562 AA.
 DE Sequence of tissue plasminogen activator analogue BMT12 (Aap 67, Thr 68).
 PN WO8912681-A.
 PD 28-DEC-1989.
 PA (BRBI-) BRIT BIO-TECHN LTD.
 Query Match 7.2%; Score 286; DB 2; Length 562;
 Best Local Similarity 23.3%; Pred. No. 1.8e-07;
 RESULT 1193
 ID AAR70880 standard; protein; 527 AA.
 DE Thrombolytic proteins 1-9-11 having t-PA activity and R275 is deleted or replaced and containing a modified N-linked glycosylation site.
 PN WO8704722-A.
 PD 13-AUG-1987.
 PA (GENY) GENETICS INST INC.
 Query Match 7.2%; Score 285.5; DB 1; Length 527;
 Best Local Similarity 23.1%; Pred. No. 1.8e-07;
 RESULT 1194
 ID AAP91683 standard; protein; 527 AA.
 DE Sequence of tissue plasminogen activator (tPA).
 PN WO8911531-A.
 PD 30-NOV-1989.
 PA (GENET) GENENTECH INC.
 Query Match 7.2%; Score 285; DB 1; Length 527;
 Best Local Similarity 23.2%; Pred. No. 1.9e-07;
 RESULT 1195
 ID AAR09270 standard; protein; 527 AA.
 DE t-PA variant H331A, H332A.
 PN WO9002798-A.
 PD 22-MAR-1990.
 PA (GENET) GENENTECH INC.
 Query Match 7.2%; Score 285; DB 2; Length 527;
 Best Local Similarity 23.2%; Pred. No. 1.9e-07;
 RESULT 1196
 ID AAR09278 standard; protein; 527 AA.
 DE t-PA variant H432A, R434A.
 PN WO9002798-A.
 PD 22-MAR-1990.
 PA (GENET) GENENTECH INC.
 Query Match 7.2%; Score 285; DB 2; Length 527;
 Best Local Similarity 23.0%; Pred. No. 1.9e-07;
 RESULT 1197
 ID ADW64349 standard; protein; 527 AA.
 DE Mutant human plasminogen activator protein - SEQ ID 1.
 PN CN1526726-A.
 PD 08-SEP-2004.
 PA (LIBB/) LI B.
 Query Match 7.2%; Score 285; DB 8; Length 527;
 Best Local Similarity 23.0%; Pred. No. 1.9e-07;
 RESULT 1198
 ID AAP71449 standard; protein; 528 AA.
 DE Modified human tissue plasminogen activator.
 PN EP238304-A.
 PD 23-SEP-1987.

PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 285; DB 1; Length 528;
Best Local Similarity 23.4%; Pred. No. 1.9e-07;
RESULT 1199
ID AAR3148 standard; protein; 556 AA.
DE Human t-PA variant contg. fibrinectin for thrombosis lysis (2).
PN JP03061482-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.2%; Score 285; DB 2; Length 556;
Best Local Similarity 21.9%; Pred. No. 2e-07;
RESULT 1200
ID AAB11710 standard; protein; 264 AA.
DE Human serine protease BSSP5 (hbssps) SEQ ID NO:2.
PN WO200031243-A1.
PD 02-JUN-2000.
PA (FUSO) FUSO PHARM IND LTD.
Query Match 7.2%; Score 284.5; DB 3; Length 264;
Best Local Similarity 28.0%; Pred. No. 1e-07;
RESULT 1201
ID AAP1961 standard; protein; 518 AA.
DE Sequence of des 1-44E75 t-PA mutant.
PN WO8909266-A.
PD 05-OCT-1989.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284.5; DB 1; Length 518;
Best Local Similarity 22.9%; Pred. No. 2e-07;
RESULT 1202
ID ABM64749 standard; protein; 629 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4998.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.2%; Score 284.5; DB 8; Length 629;
Best Local Similarity 19.5%; Pred. No. 2.4e-07;
RESULT 1203
ID ABM62817 standard; protein; 629 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3066.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.2%; Score 284.5; DB 8; Length 629;
Best Local Similarity 19.5%; Pred. No. 2.4e-07;
RESULT 1204
ID AAR70851 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,D184,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 483;
Best Local Similarity 23.1%; Pred. No. 2e-07;
RESULT 1205
ID AAR70844 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,D184,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 483;
Best Local Similarity 23.1%; Pred. No. 2e-07;
RESULT 1206
ID AAR44809 standard; protein; 527 AA.
DE Human tPA variant (N65, S67).
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 527;
Best Local Similarity 23.1%; Pred. No. 2.1e-07;
RESULT 1207
ID AAR70908 standard; protein; 527 AA.
DE Human t-PA variant (N103,A477).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.

Query Match 7.2%; Score 284; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 2.1e-07;
RESULT 1208
ID AAR70859 standard; protein; 527 AA.
DE Human t-PA variant (N67,A303,A304).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 527;
Best Local Similarity 23.8%; Pred. No. 2.1e-07;
RESULT 1209
ID AAR70893 standard; protein; 527 AA.
DE Human t-PA variant (N103,A296,A297,A298,A299).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 527;
Best Local Similarity 23.5%; Pred. No. 2.1e-07;
RESULT 1210
ID AAR70891 standard; protein; 527 AA.
DE Human t-PA variant (N103,A267).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 284; DB 2; Length 527;
Best Local Similarity 23.7%; Pred. No. 2.1e-07;
RESULT 1211
ID AAP70474 standard; protein; 562 AA.
DE Sequence of tissue plasminogen (TPA) analogue.
PN WO8703906-A.
PD 02-JUL-1987.
PA (UPJO) UPJOHN CO.
Query Match 7.2%; Score 284; DB 1; Length 562;
Best Local Similarity 23.7%; Pred. No. 2.3e-07;
RESULT 1212
ID AAR09286 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator analogue BBNT5 (Ser 67, Ser 68).
PN WO8912681-A.
PD 28-DEC-1989.
PA (BRBI-) BRIT BIO-TECHN LTD.
Query Match 7.2%; Score 284; DB 2; Length 562;
Best Local Similarity 23.1%; Pred. No. 2.3e-07;
RESULT 1213
ID AAR23807 standard; protein; 562 AA.
DE t-PA (Tyr 297) mutant.
PN WO9206203-A.
PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 7.2%; Score 284; DB 2; Length 562;
Best Local Similarity 23.2%; Pred. No. 2.3e-07;
RESULT 1214
ID ABB8068 standard; protein; 406 AA.
DE Human coagulation factor VII mutant polypeptide L305V/M306D/D309S.
PN WO200183725-A1.
PD 08-NOV-2001.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.2%; Score 283.5; DB 5; Length 406;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1215
ID ABG73125 standard; protein; 406 AA.
DE Human coagulation factor VII mutant polypeptide L305V/M306D/D309S.
PN WO200277218-A1.
PD 03-OCT-2002.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.2%; Score 283.5; DB 6; Length 406;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1216
ID ADJ55852 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant L305V/ M306D/ D309S.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.

Query Match 7.2%; Score 283.5; DB 8; Length 406;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1217
ID ADY44489 standard; protein: 406 AA.
DE Human factor VII mutant L305V/M306D/D309S.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.2%; Score 283.5; DB 9; Length 406;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1218
ID ADY74078 standard; protein: 406 AA.
DE Human Factor VII variant polypeptide #21.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.2%; Score 283.5; DB 9; Length 406;
Best Local Similarity 22.7%; Pred. No. 1.8e-07;
RESULT 1219
ID ADE83543 standard; protein: 482 AA.
DE Rat Protein NP 058639, SEQ ID NO 11161.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.2%; Score 283.5; DB 7; Length 482;
Best Local Similarity 22.8%; Pred. No. 2.1e-07;
RESULT 1220
ID AAR13917 standard; peptide: 522 AA.
DE Delta (466-470) tPA variant with K236A, H237A, R298A and R299A
DE substitutions.
PN WO9113149-A.
PD 05-SEP-1991.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 283.5; DB 2; Length 522;
Best Local Similarity 22.8%; Pred. No. 2.2e-07;
RESULT 1221
ID AAP90169 standard; peptide: 571 AA.
DE Tissue plasminogen activator mutant 2G.
PN WO8907146-A.
PD 10-AUG-1989.
PA (INTEG) INTEG GENETICS INC.
Query Match 7.2%; Score 283.5; DB 1; Length 571;
Best Local Similarity 22.4%; Pred. No. 2.4e-07;
RESULT 1222
ID ADM20190 standard; protein: 407 AA.
DE Human factor VII (FVII) protein variant sequence #28.
PN WO2004111242-A1.
PD 23-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.2%; Score 283; DB 9; Length 407;
Best Local Similarity 22.2%; Pred. No. 1.9e-07;
RESULT 1223
ID AAR09257 standard; protein: 483 AA.
DE t-PA variant d1-44, N184D, I210R, G211A, K212R, V213R, T252R, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 283; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.2e-07;
RESULT 1224
ID AAR09269 standard; protein: 527 AA.
DE t-PA variant E303A, R304A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 283; DB 2; Length 527;
Best Local Similarity 23.7%; Pred. No. 2.4e-07;
RESULT 1225
ID AAR44810 standard; protein: 527 AA.
DE Human tPA variant (N65, T67).
PN US5270198-A.

PD 14-DEC-1993.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 283; DB 2; Length 527;
Best Local Similarity 23.1%; Pred. No. 2.4e-07;
RESULT 1226
ID AAR44817 standard; protein: 527 AA.
DE Human tPA variant (N67, A296, A297, A298, A299).
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 283; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 2.4e-07;
RESULT 1227
ID AAR44814 standard; protein: 527 AA.
DE Human tPA variant (N105, T107).
PN US5270198-A.
PD 14-DEC-1993.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 283; DB 2; Length 527;
Best Local Similarity 23.6%; Pred. No. 2.4e-07;
RESULT 1228
ID AAR70899 standard; protein: 527 AA.
DE Human t-PA variant (N103, A408).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 283; DB 2; Length 527;
Best Local Similarity 22.9%; Pred. No. 2.4e-07;
RESULT 1229
ID AAR12341 standard; protein: 560 AA.
DE T-PA variant contg. fibronectin for thrombolytic lysis (3).
PN JP03061482-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.2%; Score 283; DB 2; Length 560;
Best Local Similarity 22.1%; Pred. No. 2.5e-07;
RESULT 1230
ID AAR12367 standard; protein: 561 AA.
DE T-PA with -ve charged finger and/or kringle domain (7).
PN JP03061483-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.2%; Score 283; DB 2; Length 561;
Best Local Similarity 22.1%; Pred. No. 2.5e-07;
RESULT 1231
ID ADM42867 standard; protein: 925 AA.
DE Human corin protein deletion region 569-1042.
PN WO2004111225-A1.
PD 23-DEC-2004.
PA (SCHD) SCHERING AG.
Query Match 7.2%; Score 283; DB 9; Length 925;
Best Local Similarity 20.5%; Pred. No. 4.1e-07;
RESULT 1232
ID AEG02852 standard; protein: 436 AA.
DE Factor VII/IX fusion protein SEQ ID NO:46.
PN WO2006018204-A1.
PD 23-FEB-2006.
PA (ZLBB-) ZLB BEHRING GMBH.
Query Match 7.2%; Score 282.5; DB 10; Length 436;
Best Local Similarity 24.2%; Pred. No. 2.1e-07;
RESULT 1233
ID AEG02835 standard; peptide: 436 AA.
DE Factor VII/IX fusion protein SEQ ID NO:29.
PN WO2006018204-A1.
PD 23-FEB-2006.
PA (ZLBB-) ZLB BEHRING GMBH.
Query Match 7.2%; Score 282.5; DB 10; Length 436;
Best Local Similarity 24.2%; Pred. No. 2.1e-07;
RESULT 1234
ID AAR09231 standard; protein: 524 AA.
DE t-PA deletion variant d297-299.
PN WO9002798-A.
PD 22-MAR-1990.

PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282.5; DB 2; Length 524;
Best Local Similarity 22.8%; Pred. No. 2.5e-07;
RESULT 1235
ID ADM20177 standard; protein: 406 AA.
DE Human factor VII (FVII) protein variant sequence #15.
PN WO200411242-A1.
PD 23-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
PA (MAXY-) MAXYGEN APS.
Query Match 7.1%; Score 282; DB 9; Length 406;
Best Local Similarity 22.1%; Pred. No. 2.1e-07;
RESULT 1236
ID AAR09246 standard; protein: 483 AA.
DE t-PA variant d1-44, N184D, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 483;
Best Local Similarity 23.0%; Pred. No. 2.5e-07;
RESULT 1237
ID AAR09254 standard; protein: 483 AA.
DE t-PA variant d1-44, I210R, G211H, K212Q, V213K, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 483;
Best Local Similarity 22.8%; Pred. No. 2.5e-07;
RESULT 1238
ID AAR09230 standard; protein: 525 AA.
DE t-PA deletion variant d297-298.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 525;
Best Local Similarity 23.4%; Pred. No. 2.7e-07;
RESULT 1239
ID AAR09255 standard; protein: 527 AA.
DE t-PA variant I210R, G211H, K212Q, V213K, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 527;
Best Local Similarity 22.8%; Pred. No. 2.7e-07;
RESULT 1240
ID AAR21600 standard; protein: 527 AA.
DE tPA variant - E94A, D95A, T102N.
PN WO9202612-A.
PD 20-FEB-1992.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 2.7e-07;
RESULT 1241
ID AAR70866 standard; protein: 527 AA.
DE Human t-PA variant (N67,A416,A417,A418).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 2.7e-07;
RESULT 1242
ID AAR70902 standard; protein: 527 AA.
DE Human t-PA variant (N103,A426,A427,A429,A430).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 2.7e-07;
RESULT 1243
ID AAR70869 standard; protein: 527 AA.
DE Human t-PA variant (N67,A440).
PN US5385732-A.
PD 31-JAN-1995.

PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 282; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 2.7e-07;
RESULT 1244
ID AAB82582 standard; protein: 562 AA.
DE Tissue plasminogen activator with S-119 subseq for M and QG196-98 subseq
DE for NGT.
PN JF63230083-A.
PD 26-SEP-1988.
PA (EISA) EISAI CO LTD.
Query Match 7.1%; Score 282; DB 1; Length 562;
Best Local Similarity 23.2%; Pred. No. 2.9e-07;
RESULT 1245
ID AAR09287 standard; protein: 562 AA.
DE Sequence of tissue plasminogen activator analogue BBNT6 (Thr 67, Asp 68).
PN WO8912681-A.
PD 28-DEC-1989.
PA (BRBI-) BRIT BIO-TECHN LTD.
Query Match 7.1%; Score 282; DB 2; Length 562;
Best Local Similarity 23.1%; Pred. No. 2.9e-07;
RESULT 1246
ID AAR23808 standard; protein: 562 AA.
DE t-PA (Glu 298) mutant.
PN WO9206203-A.
PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 7.1%; Score 282; DB 2; Length 562;
Best Local Similarity 23.5%; Pred. No. 2.9e-07;
RESULT 1247
ID AAR23810 standard; protein: 562 AA.
DE t-PA (Gly 301) mutant.
PN WO9206203-A.
PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 7.1%; Score 282; DB 2; Length 562;
Best Local Similarity 23.6%; Pred. No. 2.9e-07;
RESULT 1248
ID AAB84869 standard; protein: 406 AA.
DE Mutant blood coagulant factor VII (FVII-30).
PN JP2001061479-A.
PD 13-MAR-2001.
PA (KAGA) ZH KAGAKU & KESSEI RYOH KENKYUSHO.
Query Match 7.1%; Score 281.5; DB 4; Length 406;
Best Local Similarity 22.8%; Pred. No. 2.3e-07;
RESULT 1249
ID AAM52185 standard; protein: 406 AA.
DE Human FVII mutant G291N.
PN WO200158935-A2.
PD 16-AUG-2001.
PA (MAXY-) MAXYGEN APS.
Query Match 7.1%; Score 281.5; DB 4; Length 406;
Best Local Similarity 22.8%; Pred. No. 2.3e-07;
RESULT 1250
ID AAO30584 standard; protein: 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/V158D/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1251
ID AAO30626 standard; protein: 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/V158T/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1252
ID AAO30582 standard; protein: 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/V158T/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.

PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1253
ID ADJ56067 standard; protein; 406 AA.
DE Human factor VII protein mutant F374Y/ V158T/ M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1254
ID ADJ56072 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1255
ID ADJ56068 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/V158D/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1256
ID ADJ55926 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1257
ID ADJ55927 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1258
ID ADJ55915 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1259
ID ADJ55970 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ K316Q/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1260
ID ADJ56063 standard; protein; 406 AA.
DE Human factor VII protein mutant F374Y/ V158D/ M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1261
ID ADJ55959 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant M298Q/ L305V/ K316Q/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.

Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1262
ID ADJ56067 standard; protein; 406 AA.
DE Human factor VII protein mutant F374Y/ V158T/ M298Q/ L305V/ S314E/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1263
ID ADJ55971 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ K316Q/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1264
ID ADJ56033 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ S314E/ M298Q/ L305V/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1265
ID ADJ56076 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant G291N.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1266
ID ADJ56085 standard; protein; 406 AA.
DE Human factor VII/VIIa protein mutant #21.
PN WO2004029091-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN APS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.8%; Pred. No. 2.3e-07;
RESULT 1267
ID ADJ56062 standard; protein; 406 AA.
DE Human factor VII/VIIa protein mutant #62.
PN WO2004029091-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN APS.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.8%; Pred. No. 2.3e-07;
RESULT 1268
ID ADJ512886 standard; protein; 406 AA.
DE Human factor VII G237L mutant.
PN WO2004083361-A2.
PD 30-SEP-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.6%; Pred. No. 2.3e-07;
RESULT 1269
ID ADJ512886 standard; protein; 406 AA.
DE Human factor VII G237L mutant.
PN WO2004083361-A2.
PD 30-SEP-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 281.5; DB 8; Length 406;
Best Local Similarity 22.6%; Pred. No. 2.3e-07;
RESULT 1270
ID ADJ44466 standard; protein; 406 AA.
DE Human factor VII mutant S314E/L305V/V158T/K337A/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1271
ID ADJ444707 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/V158D/M298QV/S314E/K337A/L305V.
PN WO2004110469-A2.

PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1271
ID ADVA4568 standard; protein; 406 AA.
DE Human factor VII mutant S314E/L305V/V158D/K337A/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1272
ID ADVA4718 standard; protein; 406 AA.
DE Human factor VII mutant G291N.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.8%; Pred. No. 2.3e-07;
RESULT 1273
ID ADVA4610 standard; protein; 406 AA.
DE Human factor VII mutant K316Q/L305V/V158T/K337A/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1274
ID ADVA4612 standard; protein; 406 AA.
DE Human factor VII mutant K316Q/L305V/V158D/K337A/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1275
ID ADVA4673 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/L305V/M298Q/K337A/S314E.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1276
ID ADVA4556 standard; protein; 406 AA.
DE Human factor VII mutant S314E/L305V/K337A/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1277
ID ADVA4704 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/V158T/S314E/M298Q/K337A/L305V.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1278
ID ADVA4600 standard; protein; 406 AA.
DE Human factor VII mutant K316Q/L305V/K337A/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1279
ID ADY74145 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #88.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1280
ID ADY74296 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #239.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1281
ID ADY74155 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #98.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1282
ID ADY74262 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #205.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1283
ID ADY74293 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #236.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1284
ID ADY74189 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #132.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1285
ID ADY74308 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #251.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.8%; Pred. No. 2.3e-07;
RESULT 1286
ID ADY74201 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #144.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1287
ID ADY74157 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #100.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1288
ID ADY74199 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #142.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.

Query Match 7.1%; Score 281.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1289
ID AEF1516 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #85.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1290
ID AEF1512 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #91.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1291
ID AEF15072 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #41.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1292
ID AEF15160 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #129.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1293
ID AEF15083 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #52.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1294
ID AEF15124 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #53.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1295
ID AEF15157 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #126.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 281.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.3e-07;
RESULT 1296
ID AAR09233 standard; protein; 522 AA.
DE t-PA deletion variant d297-301.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GENETH) GENENTECH INC.
Query Match 7.1%; Score 281.5; DB 2; Length 522;
Best Local Similarity 23.4%; Pred. No. 2.9e-07;
RESULT 1297
ID AAR13919 standard; protein; 522 AA.
DE Delta (466-470) tPA variant with E426A, R427A, K429A and E430A substitutions.
PN WO9113149-A.
PD 05-SEP-1991.
PA (GENETH) GENENTECH INC.

Query Match 7.1%; Score 281.5; DB 2; Length 522;
Best Local Similarity 22.7%; Pred. No. 2.9e-07;
RESULT 1298
ID AAR09239 standard; protein; 524 AA.
DE t-PA deletion variant d300-302.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GENETH) GENENTECH INC.
Query Match 7.1%; Score 281.5; DB 2; Length 524;
Best Local Similarity 23.2%; Pred. No. 2.9e-07;
RESULT 1299
ID AAR12366 standard; protein; 562 AA.
DE T-PA with -ve charged finger and/or kringle domain (5).
PN JP03061483-A.
PD 18-MAR-1991.
PA (FUJII) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 281.5; DB 2; Length 562;
Best Local Similarity 21.9%; Pred. No. 3.1e-07;
RESULT 1300
ID ADM20189 standard; protein; 407 AA.
DE Human factor VII (FVII) protein variant sequence #27.
PN WO2004111242-A1.
PD 23-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 281; DB 9; Length 407;
Best Local Similarity 22.2%; Pred. No. 2.4e-07;
RESULT 1301
ID AAR09249 standard; protein; 483 AA.
DE t-PA variant d1-44, I210R, G211A, K212R, V213K, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GENETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.3%; Pred. No. 2.8e-07;
RESULT 1302
ID AAR70855 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N67,S184,E275).
PN US3385732-A.
PD 31-JAN-1995.
PA (GENETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.8e-07;
RESULT 1303
ID AAR70845 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N67,S184,E275).
PN US3385732-A.
PD 31-JAN-1995.
PA (GENETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.8e-07;
RESULT 1304
ID AAR70848 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N67,R252,E275).
PN US3385732-A.
PD 31-JAN-1995.
PA (GENETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.8e-07;
RESULT 1305
ID AAR70849 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N67,K210,E275).
PN US3385732-A.
PD 31-JAN-1995.
PA (GENETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.8e-07;
RESULT 1306
ID AAR70854 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N67,R252,E275,I277).
PN US3385732-A.
PD 31-JAN-1995.
PA (GENETH) GENENTECH INC.

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Query Match          7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.8e-07;
RESULT 1307
ID AAR70843 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match          7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.8e-07;
RESULT 1308
ID AAR70846 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,K213,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match          7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.8e-07;
RESULT 1309
ID AAR79144 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,S184,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match          7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.8e-07;
RESULT 1310
ID AAR70850 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match          7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.8e-07;
RESULT 1311
ID AAR70852 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,K213,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match          7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.2%; Pred. No. 2.8e-07;
RESULT 1312
ID AAR70847 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,R210,A211,R212,R213,E275).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match          7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.0%; Pred. No. 2.8e-07;
RESULT 1313
ID AAR70853 standard; protein; 483 AA.
DE Human tissue PA variant (delta1-44,N67,R210,A211,R212,R213,E275,I277).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match          7.1%; Score 281; DB 2; Length 483;
Best Local Similarity 23.0%; Pred. No. 2.8e-07;
RESULT 1314
ID AAR60518 standard; protein; 487 AA.
DE Cattle Factor-Xa.
PN WO9418227-A2.
PD 18-AUG-1994.
PA (DENZ-) DENZYME APS.
Query Match          7.1%; Score 281; DB 2; Length 487;
Best Local Similarity 22.5%; Pred. No. 2.9e-07;
RESULT 1315
ID AAW76216 standard; protein; 488 AA.
DE Human Factor X protein.
PN WO9838317-A1.
PD 03-SEP-1998.
PA (IMMO ) IMMUONO AG.
Query Match          7.1%; Score 281; DB 2; Length 488;
Best Local Similarity 23.2%; Pred. No. 3.1e-07;
RESULT 1316
ID AAW76217 standard; protein; 488 AA.
DE Human Factor X protein analogue.
PN WO9838317-A1.
PD 03-SEP-1998.
PA (IMMO ) IMMUONO AG.
Query Match          7.1%; Score 281; DB 2; Length 488;
Best Local Similarity 22.6%; Pred. No. 2.9e-07;
RESULT 1317
ID AAW76218 standard; protein; 488 AA.
DE Human Factor X protein.
PN WO9838318-A1.
PD 03-SEP-1998.
PA (IMMO ) IMMUONO AG.
Query Match          7.1%; Score 281; DB 2; Length 488;
Best Local Similarity 24.0%; Pred. No. 2.9e-07;
RESULT 1318
ID AAB70411 standard; protein; 488 AA.
DE Human factor X protein sequence SEQ ID NO:2.
PN WO200110896-A2.
PD 15-FEB-2001.
PA (BAXT ) BAXTER AG.
Query Match          7.1%; Score 281; DB 4; Length 488;
Best Local Similarity 24.0%; Pred. No. 2.9e-07;
RESULT 1319
ID AAR60502 standard; protein; 492 AA.
DE Serine protease for fusion protein cleavage.
PN WO9418227-A2.
PD 18-AUG-1994.
PA (DENZ-) DENZYME APS.
Query Match          7.1%; Score 281; DB 2; Length 492;
Best Local Similarity 22.5%; Pred. No. 2.9e-07;
RESULT 1320
ID AAR9238 standard; protein; 525 AA.
DE t-PA deletion variant d300-301.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Query Match          7.1%; Score 281; DB 2; Length 525;
Best Local Similarity 22.8%; Pred. No. 3.1e-07;
RESULT 1321
ID AAR9276 standard; protein; 527 AA.
DE t-PA variant K416A, H417A, E418A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Query Match          7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 3.1e-07;
RESULT 1322
ID AAR9279 standard; protein; 527 AA.
DE t-PA variant R440A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Query Match          7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.1e-07;
RESULT 1323
ID AAR70875 standard; protein; 527 AA.
DE Human t-PA variant (N60,N103).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match          7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 3.1e-07;
RESULT 1324
ID AAR70876 standard; protein; 527 AA.
DE Human t-PA variant (N60,N67,N103).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match          7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 3.1e-07;
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RESULT 1325
ID AAR70857 standard; protein; 527 AA.
DE Human t-PA variant (N67,A283,A287).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 3.1e-07;
RESULT 1326
ID AAR70898 standard; protein; 527 AA.
DE Human t-PA variant (N103,A364,A365,A366).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 3.1e-07;
RESULT 1327
ID AAR70906 standard; protein; 527 AA.
DE Human t-PA variant (N103,A449,A453).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 3.1e-07;
RESULT 1328
ID AAR70872 standard; protein; 527 AA.
DE Human t-PA variant (N67,A460,A462).
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 3.1e-07;
RESULT 1329
ID AAR70842 standard; protein; 527 AA.
DE Wild type tissue plasminogen activator protein.
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 281; DB 2; Length 527;
Best Local Similarity 23.2%; Pred. No. 3.1e-07;
RESULT 1330
ID AAR13150 standard; protein; 558 AA.
DE T-PA with -ve charged finger and/or kringle domain (3).
PN JF03061483-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 281; DB 2; Length 558;
Best Local Similarity 23.0%; Pred. No. 3.2e-07;
RESULT 1331
ID AAR13152 standard; protein; 559 AA.
DE T-PA with -ve charged finger and/or kringle domain (6).
PN JF03061483-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 281; DB 2; Length 559;
Best Local Similarity 23.0%; Pred. No. 3.2e-07;
RESULT 1332
ID AAP80691 standard; protein; 1087 AA.
DE Hybrid plasminogen/t-PA compound 1.
PN EP292326-A.
PD 23-NOV-1988.
PA (BEEC) BEECAM GROUP PLC.
Query Match 7.1%; Score 281; DB 1; Length 1087;
Best Local Similarity 22.3%; Pred. No. 6e-07;
RESULT 1333
ID AAM81778 standard; protein; 264 AA.
DE Tumour-associated antigenic target (TAR) polypeptide PRO2719, SEQ:4580.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280.5; DB 8; Length 264;
Best Local Similarity 27.2%; Pred. No. 1.7e-07;
RESULT 1334

ID ABM94054 standard; protein; 279 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4303.
PN WO2004023873-A2.
PD 25-MAR-2004.
PA (INCY) INCYTE CORP.
Query Match 7.1%; Score 280.5; DB 8; Length 279;
Best Local Similarity 27.2%; Pred. No. 1.8e-07;
RESULT 1335
ID AAO30575 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316H/L305V/V158T/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1336
ID AAO30604 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316H/L305V/V158T/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1337
ID AAO30577 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/V158T/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1338
ID AAO30594 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316H/L305V/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1339
ID AAO30569 standard; protein; 406 AA.
DE Human coagulation factor VII variant (S314E/L305V/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1340
ID AAO30606 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316H/L305V/V158D/K337A/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1341
ID AAO30613 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1342
ID AAO30621 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316Q/L305V/V158T/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1343
ID AAO30619 standard; protein; 406 AA.

DE Human coagulation factor VII variant (K316Q/L305V/V158D/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1344
ID ADJ55876 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant / M298Q/ L305V/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1345
ID ADJ55937 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant M298Q/ L305V/ K316H/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1346
ID ADJ56047 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ V158D/ M298Q/ L305V/ S314E.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1347
ID ADJ55949 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ K316H/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1348
ID ADJ55965 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ K316Q.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1349
ID ADJ55948 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ K316H/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1350
ID ADJ56057 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y V158T M298Q L305V S314E.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1351
ID ADJ55885 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1352
ID ADJ55921 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ S314E.

PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1353
ID ADJ55958 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant M298Q/ L305V/ K316Q.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1354
ID ADJ55963 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ K316Q.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1355
ID ADJ56016 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ L305V/ M298Q/ S314E.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1356
ID ADJ56046 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ V158D/ M298Q/ L305V/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1357
ID ADJ55919 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ S314E.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1358
ID ADJ56056 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ V158T/ M298Q/ L305V/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1359
ID ADJ55887 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ K337A.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1360
ID ADJ55914 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant M298Q/ L305V/ S314E.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1361
ID ADJ56004 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/ L305V/K337A/ M298Q.
PN WO2004000366-A1.

PD 31-DEC-2003.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1362
ID AD010616 standard; protein; 406 AA.
DE Human factor VII/VIIa protein mutant #52.
PN WO2004029091-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.6%; Pred. No. 2.6e-07;
RESULT 1363
ID AD010607 standard; protein; 406 AA.
DE Human factor VII/VIIa protein mutant #43.
PN WO2004029091-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280.5; DB 8; Length 406;
Best Local Similarity 22.6%; Pred. No. 2.6e-07;
RESULT 1364
ID ADV44553 standard; protein; 406 AA.
DE Human factor VII mutant S314E/L305V/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1365
ID ADV44514 standard; protein; 406 AA.
DE Human factor VII mutant L305V/K337A/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1366
ID ADV44526 standard; protein; 406 AA.
DE Human factor VII mutant L305V/M298Q/K337A/V158D.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1367
ID ADV44588 standard; protein; 406 AA.
DE Human factor VII mutant K316H/L305V/V158T/K337A/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1368
ID ADV44597 standard; protein; 406 AA.
DE Human factor VII mutant K316Q/L305V/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1369
ID ADV44605 standard; protein; 406 AA.
DE Human factor VII mutant K316Q/L305V/V158T/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1370
ID ADV44655 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/L305V/M298Q/S314E.

PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1371
ID ADV44645 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/L305V/K337A/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1372
ID ADV44686 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/L305V/V158D/S314E/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1373
ID ADV44524 standard; protein; 406 AA.
DE Human factor VII mutant L305V/M298Q/K337A/V158T.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1374
ID ADV44559 standard; protein; 406 AA.
DE Human factor VII mutant S314E/L305V/V158D/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1375
ID ADV44694 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/V158T/L305V/K337A/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1376
ID ADV44684 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/L305V/V158D/K337A/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1377
ID ADV44561 standard; protein; 406 AA.
DE Human factor VII mutant S314E/L305V/V158T/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1378
ID ADV44696 standard; protein; 406 AA.
DE Human factor VII mutant F374Y/V158T/L305V/S314E/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1379
ID ADV44578 standard; protein; 406 AA.
DE Human factor VII mutant K316H/L305V/K337A/M298Q.
PN WO2004110469-A2.

PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1380
ID ADV44590 standard; protein; 406 AA.
DE Human factor VII mutant K316H/L305V/V158D/K337A/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1381
ID ADV44603 standard; protein; 406 AA.
DE Human factor VII mutant K316Q/L305V/V158D/M298Q.
PN WO2004110469-A2.
PD 23-DEC-2004.
PA (NOVO) NOVO NORDISK AS.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1382
ID ADM20180 standard; protein; 406 AA.
DE Human factor VII (FVII) protein variant sequence #18.
PN WO2004111242-A1.
PD 23-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.6%; Pred. No. 2.6e-07;
RESULT 1383
ID ADM20183 standard; protein; 406 AA.
DE Human factor VII (FVII) protein variant sequence #21.
PN WO2004111242-A1.
PD 23-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.6%; Pred. No. 2.6e-07;
RESULT 1384
ID ADY74113 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #56.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1385
ID ADY74285 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #228.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1386
ID ADY74142 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #85.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1387
ID ADY74150 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #93.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1388
ID ADY74177 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #120.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1389
ID ADY74073 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #16.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.6%; Pred. No. 2.6e-07;
RESULT 1390
ID ADY74148 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #91.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1391
ID ADY74179 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #122.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1392
ID ADY74275 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #218.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1393
ID ADY74283 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #226.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1394
ID ADY74103 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #46.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1395
ID ADY74273 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #216.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1396
ID ADY74194 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #137.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1397
ID ADY74186 standard; protein; 406 AA.
DE Human factor VII variant polypeptide #129.
PN WO2005024006-A2.

PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1398
ID ADY74192 standard; protein; 406 AA.
DE Human Factor VII variant polypeptide #135.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1399
ID ADY74234 standard; protein; 406 AA.
DE Human Factor VII variant polypeptide #177.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1400
ID ADY74115 standard; protein; 406 AA.
DE Human Factor VII variant polypeptide #58.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1401
ID ADY74244 standard; protein; 406 AA.
DE Human Factor VII variant polypeptide #187.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1402
ID ADY74167 standard; protein; 406 AA.
DE Human Factor VII variant polypeptide #110.
PN WO2005024006-A2.
PD 17-MAR-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 9; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1403
ID AEF15119 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #88.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1404
ID AEF15089 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #58.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1405
ID AEF15073 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #42.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1406
ID AEF15099 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #68.
PN WO2005123916-A2.
PD 29-DEC-2005.

PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1407
ID AEF15146 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #115.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1408
ID AEF15136 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #105.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1409
ID AEF15134 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #103.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1410
ID AEF15077 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #46.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1411
ID AEF15086 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #55.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1412
ID AEF15144 standard; protein; 406 AA.
DE Variant human coagulation Factor VII protein #113.
PN WO2005123916-A2.
PD 29-DEC-2005.
PA (NOVO) NOVO NORDISK HEALTH CARE AG.
Query Match 7.1%; Score 280.5; DB 10; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.6e-07;
RESULT 1413
ID ADW20193 standard; protein; 407 AA.
DE Human factor VII (FVII) protein variant sequence #31.
PN WO2004111242-A1.
PD 23-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280.5; DB 9; Length 407;
Best Local Similarity 22.6%; Pred. No. 2.6e-07;
RESULT 1414
ID ADW20196 standard; protein; 407 AA.
DE Human factor VII (FVII) protein variant sequence #34.
PN WO2004111242-A1.
PD 23-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280.5; DB 9; Length 407;
Best Local Similarity 22.6%; Pred. No. 2.6e-07;
RESULT 1415
ID AAR09221 standard; protein; 526 AA.
DE c-PA deletion variant d297.
PN WO9002798-A.

PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280.5; DB 2; Length 526;
Best Local Similarity 23.1%; Pred. No. 3.3e-07;
RESULT 1416
ID AAF70020 standard; protein; 561 AA.
DE Sequence of ribose plasmidogen activator (tPA).
PN EP242836-A.
PD 28-OCT-1987.
PA (BOEP) BOEHRINGER MANNHEIM GMBH.
Query Match 7.1%; Score 280.5; DB 1; Length 561;
Best Local Similarity 21.7%; Pred. No. 3.5e-07;
RESULT 1417
ID ABR62449 standard; protein; 583 AA.
DE Bovine recombinant prothrombin, expressed in Escherichia coli.
PN WO2003052059-A2.
PD 26-JUN-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 7.1%; Score 280.5; DB 7; Length 583;
Best Local Similarity 21.9%; Pred. No. 3.6e-07;
RESULT 1418
ID ABR62451 standard; protein; 635 AA.
DE Bovine recombinant prothrombin, expressed in CHO cells.
PN WO2003052059-A2.
PD 26-JUN-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 7.1%; Score 280.5; DB 7; Length 635;
Best Local Similarity 21.9%; Pred. No. 3.9e-07;
RESULT 1419
ID ADW20176 standard; protein; 406 AA.
DE Human factor VII (FVII) protein variant sequence #14.
PN WO2004111242-A1.
PD 23-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280; DB 9; Length 406;
Best Local Similarity 22.1%; Pred. No. 2.7e-07;
RESULT 1420
ID ADW20188 standard; protein; 407 AA.
DE Human factor VII (FVII) protein variant sequence #26.
PN WO2004111242-A1.
PD 23-DEC-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280; DB 9; Length 407;
Best Local Similarity 22.2%; Pred. No. 2.7e-07;
RESULT 1421
ID AAR37402 standard; protein; 448 AA.
DE Factor X.
PN WO9309803-A1.
PD 27-MAY-1993.
PA (SCHA/) SCHAFER S C.
Query Match 7.1%; Score 280; DB 2; Length 448;
Best Local Similarity 24.0%; Pred. No. 3e-07;
RESULT 1422
ID AAW66092 standard; peptide; 448 AA.
DE Human factor X variant.
PN WO9839456-A1.
PD 11-SEP-1998.
PA (UNIW) UNIV WASHINGTON.
Query Match 7.1%; Score 280; DB 2; Length 448;
Best Local Similarity 24.0%; Pred. No. 3e-07;
RESULT 1423
ID AEC01740 standard; protein; 490 AA.
DE Modified FVII-UAA-GPI cassette.
PN WO2005073375-A1.
PD 11-AUG-2005.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match 7.1%; Score 280; DB 9; Length 490;
Best Local Similarity 22.1%; Pred. No. 3.3e-07;
RESULT 1424

ID AAR09245 standard; protein; 525 AA.
DE t-PA deletion variant d297, d305.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 525;
Best Local Similarity 23.1%; Pred. No. 3.5e-07;
RESULT 1425
ID AAR05488 standard; protein; 527 AA.
DE tPA024 precursor protein.
PN EP373896-A.
PD 20-JUN-1990.
PA (YAMA) YAMANOUCHI PHARM CO LTD.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1426
ID AAR09267 standard; protein; 527 AA.
DE t-PA variant D283A, H287A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1427
ID AAR09282 standard; protein; 527 AA.
DE t-PA variant D460A, R462A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1428
ID AAR13911 standard; protein; 527 AA.
DE T-PA deriv. (II).
PN EP45464-A.
PD 11-SEP-1991.
PA (KANF) KANEGAFUCHI KAGAKU KOGYO KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1429
ID AAR13914 standard; protein; 527 AA.
DE T-PA deriv. (V).
PN EP45464-A.
PD 11-SEP-1991.
PA (KANF) KANEGAFUCHI KAGAKU KOGYO KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1430
ID AAR13912 standard; protein; 527 AA.
DE T-PA deriv. (III).
PN EP45464-A.
PD 11-SEP-1991.
PA (KANF) KANEGAFUCHI KAGAKU KOGYO KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1431
ID AAR13910 standard; protein; 527 AA.
DE T-PA deriv. (I).
PN EP45464-A.
PD 11-SEP-1991.
PA (KANF) KANEGAFUCHI KAGAKU KOGYO KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1432
ID AAR1594 standard; protein; 527 AA.
DE tPA variant - D95A.
PN WO9202612-A.
PD 20-FEB-1992.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1433

ID AAR21593 standard; protein; 527 AA.
DE tPA variant - B94A.
PN WO9202612-A.
PD 20-FEB-1992.
PA (GENTECH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.4%; Pred. No. 3.5e-07;
RESULT 1434
ID AAR20221 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-013.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1435
ID AAR20215 standard; protein; 527 AA.
DE R462E t-PA analogue.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1436
ID AAR20216 standard; protein; 527 AA.
DE R462G t-PA analogue.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1437
ID AAR20222 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-014.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1438
ID AAR20223 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-018.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1439
ID AAR44811 standard; protein; 527 AA.
DE Human tPA variant N67.
PN US5270198-A.
PD 14-DEC-1993.
PA (GENTECH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1440
ID AAR70865 standard; protein; 527 AA.
DE Human t-PA variant (N67,A410).
PN US5385732-A.
PD 31-JAN-1995.
PA (GENTECH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 22.9%; Pred. No. 3.5e-07;
RESULT 1441
ID AAM57778 standard; protein; 527 AA.
DE R275E,H417D human tissue plasminogen activator protein mutant.
PN WO9821320-A2.
PD 22-MAY-1998.
PA (SCRI) SCRIPPS RES INST.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1442
ID AAM45907 standard; peptide; 527 AA.

DE Single chain form of the intact t-PA molecule.
PN WO9802454-A2.
PD 22-JAN-1998.
PA (ADPR-) ADPROTECH PLC.
Query Match 7.1%; Score 280; DB 2; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1443
ID AAR24190 standard; protein; 527 AA.
DE Human tissue plasminogen activator (tPA) protein.
PN WO200240696-A2.
PD 23-MAY-2002.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Query Match 7.1%; Score 280; DB 5; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1444
ID AAG79362 standard; protein; 527 AA.
DE Human tissue plasminogen activator.
PN WO200243747-A2.
PD 06-JUN-2002.
PA (ISIS-) ISIS INNOVATION LTD.
Query Match 7.1%; Score 280; DB 5; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1445
ID AAB25044 standard; protein; 527 AA.
DE Human tissue plasminogen activator (tPA) protein.
PN WO200240650-A2.
PD 23-MAY-2002.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Query Match 7.1%; Score 280; DB 5; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1446
ID ADL92126 standard; protein; 527 AA.
DE Alteplase protein sequence.
PN WO200309862-A1.
PD 04-DEC-2003.
PA (NANO-) APPLIED NANOSYSTEMS BV.
Query Match 7.1%; Score 280; DB 8; Length 527;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1447
ID AED66381 standard; protein; 528 AA.
DE Recombinant human tissue type plasminogen activator (tPA) protein.
PN KR2005018231-A.
PD 23-FEB-2005.
PA (BIOB-) BIOBUD CO LTD.
Query Match 7.1%; Score 280; DB 9; Length 528;
Best Local Similarity 23.0%; Pred. No. 3.5e-07;
RESULT 1448
ID AEM82630 standard; protein; 534 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:2879.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.1%; Score 280; DB 8; Length 534;
Best Local Similarity 22.7%; Pred. No. 3.5e-07;
RESULT 1449
ID ABM82821 standard; protein; 534 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3070.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.1%; Score 280; DB 8; Length 534;
Best Local Similarity 22.7%; Pred. No. 3.5e-07;
RESULT 1450
ID AAR13020 standard; protein; 557 AA.
DE T-PA variant contg. fibrinectin for thrombosis lysis (4).
PN JP03061482-A.
PD 18-MAR-1991.
PA (FUJII) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 280; DB 2; Length 557;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1451
ID AAR13149 standard; protein; 557 AA.
DE T-PA variant contg. fibrinectin for thrombosis lysis (4).

PN JP03061482-A.
PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 280; DB 2; Length 557;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1452
ID AAP50219 standard; protein; 561 AA.
DE Tissue plasminogen activator encoded by cDNA clone.
PN EP143081-A.
PD 29-MAY-1985.
PA (CTBA) CTBA GEIGY AG.
Query Match 7.1%; Score 280; DB 1; Length 561;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1453
ID AAP60790 standard; protein; 562 AA.
DE Sequence of human pre-tissue plasminogen activator (pre-t-PA).
PN GB2173804-A.
PD 22-OCT-1986.
PA (GENTECH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1454
ID AAP60810 standard; protein; 562 AA.
DE Sequence of modified human tissue plasminogen activator (t-PA).
PN FR2581652-A.
PD 14-NOV-1986.
PA (GENE) GENENTECH INC.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1455
ID AAP60214 standard; protein; 562 AA.
DE Sequence of active human uterine tissue plasminogen activator (UTPA).
PN EP18105-A.
PD 16-APR-1986.
PA (INTE-) INTEG GENETICS INC.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1456
ID AAP81913 standard; protein; 562 AA.
DE Tissue plasminogen activator encoded by pEM1-CPA.
PN WO8800242-A.
PD 14-JAN-1988.
PA (DAMO-) DAMON BIOTECH INC.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1457
ID AAP80655 standard; protein; 562 AA.
DE Tissue plasminogen activator analogue.
PN EP293934-A.
PD 07-DEC-1988.
PA (ZYMO) ZYMOGENETICS INC.
PA (NOVO) NOVO IND AS.
PA (EYSA) EYSA CO LTD.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1458
ID AAP94406 standard; protein; 562 AA.
DE Sequence encoded by native tPA of plasmid pST112.
PN EP302456-A.
PD 08-FEB-1989.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1459
ID AAP93716 standard; protein; 562 AA.
DE Human melanoma t-PA encoded by plasmid pKG12.
PN EP297066-A.
PD 28-DEC-1988.
PA (KABI) KABIGEN AB.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1460
ID AAP90916 standard; protein; 562 AA.

DE Human tissue plasminogen activator.
PN JP01174388-A.
PD 10-JUL-1989.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 280; DB 1; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1461
ID AAR09288 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator analogue BBW11 (Ser 67, Leu 68).
PN WO8912681-A.
PD 28-DEC-1989.
PA (BBRI-) BBRI BIO-TECHN LTD.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1462
ID AAR06237 standard; protein; 562 AA.
DE Novel tissue plasminogen activator (tPA) encoded by plasmid pST112.
PN EP379890-A.
PD 01-AUG-1990.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1463
ID AAR04700 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator (t-PA) analogue t-PA C87S, H420S with altered residues 419 and 420.
PN EP351246-A.
PD 17-JAN-1990.
PA (NOVO) NOVO-NORDISK AS.
PA (NOVO) NOVO-NORDISK AS.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1464
ID AAR04701 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator (t-PA) analogue t-PA K419S with altered residue 419.
PN EP351246-A.
PD 17-JAN-1990.
PA (NOVO) NOVO-NORDISK AS.
PA (NOVO) NOVO-NORDISK AS.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1465
ID AAR04699 standard; protein; 562 AA.
DE Native tissue plasminogen activator (t-PA).
PN EP351246-A.
PD 17-JAN-1990.
PA (NOVO) NOVO-NORDISK AS.
PA (NOVO) NOVO-NORDISK AS.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1466
ID AAR13727 standard; protein; 562 AA.
DE T-PA674 mutant with supernumerary N-linked oligosaccharide side chain.
PN US5041376-A.
PD 20-AUG-1991.
PA (TEXA) UNIV TEXAS SYSTEM.
PA (COLD-) COLD SPRING HARBOR LAB.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1467
ID AAR12847 standard; protein; 562 AA.
DE T-PA Kringle 1 domain substitution mutant.
PN JP03127987-A.
PD 31-MAY-1991.
PA (KANF) KANEKAFOCHI CHEM KK.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1468
ID AAR23811 standard; protein; 562 AA.
DE t-PA (Glu 296, Glu 298, Glu 299) triple mutant.
PN WO9206203-A.

PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.5%; Pred. No. 3.7e-07;
RESULT 1469
ID AAR3806 standard; protein; 562 AA.
DE c-PA (Glu 296) mutant.
PN WO206203-A.
PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1470
ID AAR3804 standard; protein; 562 AA.
DE c-PA (Glu 304) mutant.
PN WO206203-A.
PD 16-APR-1992.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1471
ID AAR34426 standard; protein; 562 AA.
DE Sequence of human pre-pro tissue plasminogen activator (c-PA).
PN US200340-A.
PD 06-APR-1993.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1472
ID AAR6220 standard; protein; 562 AA.
DE Full-length tissue plasminogen activator.
PN US5504001-A.
PD 02-APR-1996.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 7.1%; Score 280; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1473
ID AAY50868 standard; protein; 562 AA.
DE Human tissue plasminogen activator protein fragment.
PN WO9957251-A2.
PD 11-NOV-1999.
PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
Query Match 7.1%; Score 280; DB 3; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1474
ID AAY43397 standard; protein; 562 AA.
DE Human tissue plasminogen activator protein sequence.
PN US5985607-A.
PD 16-NOV-1999.
PA (CANG-) CANGENE CORP.
Query Match 7.1%; Score 280; DB 3; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1475
ID AAY9590 standard; protein; 562 AA.
DE Human tissue-type plasminogen activator c-PA.
PN WO200032759-A1.
PD 08-JUN-2000.
PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
Query Match 7.1%; Score 280; DB 3; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1476
ID AAU97700 standard; protein; 562 AA.
DE Human tissue plasminogen activator (c-PA) protein sequence.
PN WO200232446-A2.
PD 23-APR-2002.
PA (PFIZ) PFIZER LTD.
PA (PFIZ) PFIZER INC.
Query Match 7.1%; Score 280; DB 5; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1477
ID AAB37130 standard; protein; 562 AA.
DE Human tissue-type plasminogen activator (tPA) protein.
PN WO2003033009-A2.

PD 24-APR-2003.
PA (OMNI-) OMNIO AB.
Query Match 7.1%; Score 280; DB 6; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1478
ID ABR55851 standard; protein; 562 AA.
DE Human tissue-type plasminogen activator (TPA).
PN WO2003031464-A2.
PD 17-APR-2003.
PA (NEOS-) NEOSE TECHNOLOGIES INC.
Query Match 7.1%; Score 280; DB 6; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1479
ID ABUS7646 standard; protein; 562 AA.
DE Differentially expressed breast cancer associated protein #33.
PN US2002156263-A1.
PD 24-OCT-2002.
PA (CHEN/) CHEN H.
Query Match 7.1%; Score 280; DB 6; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1480
ID ADN95624 standard; protein; 562 AA.
DE Human BEC/LBC-related protein sequence SegID547.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDM-) LUDWIG INST CANCER RES.
PA (LYCN) LYCENTIA LTD.
Query Match 7.1%; Score 280; DB 7; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1481
ID ADN49698 standard; protein; 562 AA.
DE Human tissue type plasminogen activator TPA protein SegID 26.
PN WO2004033651-A2.
PD 22-APR-2004.
PA (NEOS-) NEOSE TECHNOLOGIES INC.
Query Match 7.1%; Score 280; DB 8; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1482
ID ADO28679 standard; protein; 562 AA.
DE Human tPA protein SEQ ID NO:108.
PN WO2004044178-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 8; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1483
ID AEM80983 standard; protein; 562 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO4, SEQ:2535.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 280; DB 8; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1484
ID ADO39248 standard; protein; 562 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 911.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.1%; Score 280; DB 8; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1485
ID ADU06344 standard; protein; 562 AA.
DE Novel bronchial cancer-associated human protein SegID568.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
Query Match 7.1%; Score 280; DB 8; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1486
ID ADU74374 standard; protein; 562 AA.

DE Human plasminogen activator.
PN WO200409231-A2.
PD 18-NOV-2004.
PA (NEOS-) NEOSE TECHNOLOGIES INC.
Query Match 7.1%; Score 280; DB 8; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1487
ID ADY91675 standard; protein; 562 AA.
DE Human tissue plasminogen activator (tPA) isoform 1 protein.
PN WO2005026341-A2.
PD 24-MAR-2005.
PA (PALO-) PALON GMBH.
Query Match 7.1%; Score 280; DB 9; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1488
ID AEB9702 standard; protein; 562 AA.
DE Human tissue plasminogen activator protein.
PN WO2005059142-A1.
PD 30-JUN-2005.
PA (SEEG/) SEEGGER W.
Query Match 7.1%; Score 280; DB 9; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1489
ID AEB6378 standard; protein; 562 AA.
DE Tissue type plasminogen activator (tPA) protein.
PN KR2005018231-A.
PD 23-FEB-2005.
PA (BIOB-) BIOBUD CO LTD.
Query Match 7.1%; Score 280; DB 9; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1490
ID AEB6467 standard; protein; 562 AA.
DE Human tissue plasminogen activator, t-PA, SEQ ID 3.
PN JP2005278550-A.
PD 13-OCT-2005.
PA (HOKK-) HOKKAIDO TLO KK.
Query Match 7.1%; Score 280; DB 9; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1491
ID AEB67990 standard; protein; 562 AA.
DE Amino acid sequence of full length tissue plasminogen activator (t-PA).
PN WO2005103264-A1.
PD 03-NOV-2005.
PA (MEVA-) MENARINI BIOTEC SRL.
Query Match 7.1%; Score 280; DB 9; Length 562;
Best Local Similarity 23.0%; Pred. No. 3.7e-07;
RESULT 1492
ID AAO30591 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316H/L305V/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO-) NOVO NORDISK AS.
Query Match 7.1%; Score 279.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.9e-07;
RESULT 1493
ID AAO30599 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316H/L305V/V158T/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO-) NOVO NORDISK AS.
Query Match 7.1%; Score 279.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.9e-07;
RESULT 1494
ID AAO30597 standard; protein; 406 AA.
DE Human coagulation factor VII variant (K316H/L305V/V158D/M298Q).
PN WO2003037932-A2.
PD 08-MAY-2003.
PA (NOVO-) NOVO NORDISK AS.
Query Match 7.1%; Score 279.5; DB 6; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.9e-07;
RESULT 1495
ID ADU55873 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant M298Q/L305V.

PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO-) NOVO NORDISK AS.
Query Match 7.1%; Score 279.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.9e-07;
RESULT 1496
ID ADJ55985 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/L305V/M298Q.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO-) NOVO NORDISK AS.
Query Match 7.1%; Score 279.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.9e-07;
RESULT 1497
ID ADJ55941 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/M298Q/L305V/K316H.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO-) NOVO NORDISK AS.
Query Match 7.1%; Score 279.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.9e-07;
RESULT 1498
ID ADJ55943 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158T/M298Q/L305V/K316H.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO-) NOVO NORDISK AS.
Query Match 7.1%; Score 279.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.9e-07;
RESULT 1499
ID ADJ56009 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant F374Y/L305V/V158D/M298Q.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO-) NOVO NORDISK AS.
Query Match 7.1%; Score 279.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.9e-07;
RESULT 1500
ID ADJ55879 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant V158D/M298Q/L305V.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO-) NOVO NORDISK AS.
Query Match 7.1%; Score 279.5; DB 8; Length 406;
Best Local Similarity 22.5%; Pred. No. 2.9e-07;

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OM protein - protein search, using sw model

Run on: July 15, 2006, 06:48:16 / Search time 53 Seconds
(without alignments)
1189.095 Million cell updates/sec

Title: US-10-063-546-38
Perfect score: 3945
Sequence: 1 MELGQWQLGTLFLQLLIS.....LSTAFKVLPEKWIERNMK 720

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Issued Patents_AA.*
1: /EMC_Celerra_SID33/ptodata/2/iaa/5.COMB.pep.*
2: /EMC_Celerra_SID33/ptodata/2/iaa/6.COMB.pep.*
3: /EMC_Celerra_SID33/ptodata/2/iaa/7.COMB.pep.*
4: /EMC_Celerra_SID33/ptodata/2/iaa/H.COMB.pep.*
5: /EMC_Celerra_SID33/ptodata/2/iaa/PCTUS.COMB.pep.*
6: /EMC_Celerra_SID33/ptodata/2/iaa/RE.COMB.pep.*
7: /EMC_Celerra_SID33/ptodata/2/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3945	100.0	720	2	US-09-991-181-231 Sequence 231, App
2	3945	100.0	720	2	US-09-990-444-231 Sequence 231, App
3	3945	100.0	720	2	US-09-997-333-231 Sequence 231, App
4	3945	100.0	720	2	US-09-987-598-231 Sequence 231, App
5	3945	100.0	720	2	US-09-988-735-231 Sequence 231, App
6	3945	100.0	720	3	US-09-989-726-231 Sequence 231, App
7	3945	100.0	720	3	US-09-997-514-231 Sequence 231, App
8	3945	100.0	720	3	US-09-989-728-231 Sequence 231, App
9	3945	100.0	720	3	US-09-997-349-231 Sequence 231, App
10	3945	100.0	720	3	US-09-987-653-231 Sequence 231, App
11	3945	100.0	720	3	US-09-989-233A-231 Sequence 231, App
12	2946.5	74.7	570	2	US-10-067-422-9 Sequence 9, Appl
13	672	17.0	1019	1	US-10-183-992-4 Sequence 4, Appl
14	665	16.9	1019	1	US-08-296-014A-4 Sequence 4, Appl
15	665	16.9	1019	1	US-08-596-405-4 Sequence 4, Appl
16	665	16.9	1019	1	US-08-596-405-4 Sequence 4, Appl
17	665	16.9	1019	1	US-08-287-620-4 Sequence 4, Appl
18	665	16.9	1019	1	US-08-287-368-4 Sequence 4, Appl
19	665	16.9	1019	2	US-09-626-795-4 Sequence 4, Appl
20	665	16.9	1083	1	US-10-183-992-8 Sequence 8, Appl
21	665	16.9	1083	1	US-08-596-014A-2 Sequence 2, Appl
22	665	16.9	1083	1	US-08-877-620-2 Sequence 2, Appl
23	665	16.9	1083	2	US-09-287-368-2 Sequence 2, Appl
24	665	16.9	1083	2	US-09-626-795-2 Sequence 2, Appl
25	665	16.9	1083	2	US-10-183-992-6 Sequence 6, Appl
26	482	12.2	699	2	US-09-949-016-6138 Sequence 6138, Ap

27	475	12.0	717	2	US-09-949-016-11182 Sequence 11182, A
28	469.5	11.9	679	2	US-09-874-198-6 Sequence 6, Appl
29	403.5	10.2	688	2	US-09-874-198-7 Sequence 7, Appl
30	403.5	10.2	705	2	US-09-949-002-326 Sequence 326, App
31	401.5	10.2	686	2	US-09-874-198-2 Sequence 2, Appl
32	399.5	10.1	691	2	US-09-949-016-7775 Sequence 7775, Ap
33	334	8.5	673	2	US-09-874-198-8 Sequence 8, Appl
34	332	8.4	855	2	US-10-037-417-132 Sequence 132, App
35	328	8.3	855	3	US-09-410-352F-2 Sequence 2, Appl
36	327	8.3	855	1	US-09-027-337-2 Sequence 2, Appl
37	327	8.3	855	2	US-09-644-600-2 Sequence 2, Appl
38	327	8.3	855	3	US-09-654-600A-2 Sequence 2, Appl
39	327	8.3	855	2	US-09-421-213-2 Sequence 2, Appl
40	321	8.1	460	7	5270178-16 Patent No. 5270178
41	317.5	8.0	798	1	US-08-200-900A-2 Sequence 2, Appl
42	317.5	8.0	798	2	US-08-794-042-2 Sequence 2, Appl
43	317.5	8.0	798	5	PCT-US94-00616-2 Sequence 2, Appl
44	312	7.9	419	2	US-10-168-407-5 Sequence 5, Appl
45	311.5	7.9	461	7	5460953-3 Patent No. 5460953
46	311	7.9	419	2	US-10-168-407-3 Sequence 3, Appl
47	311	7.9	419	2	US-10-168-407-6 Sequence 6, Appl
48	310.5	7.9	409	2	US-09-065-872-2 Sequence 2, Appl
49	310.5	7.9	409	2	US-09-667-570A-2 Sequence 2, Appl
50	310.5	7.9	410	2	US-09-065-872-1 Sequence 1, Appl
51	310.5	7.9	410	2	US-09-667-570A-1 Sequence 1, Appl
52	310.5	7.9	419	1	US-08-295-411-1 Sequence 1, Appl
53	310.5	7.9	419	1	US-08-955-471-1 Sequence 1, Appl
54	310.5	7.9	419	2	US-09-667-570A-3 Sequence 3, Appl
55	310.5	7.9	419	2	US-10-168-263-1 Sequence 1, Appl
56	310.5	7.9	419	2	US-10-168-407-1 Sequence 1, Appl
57	310.5	7.9	419	2	US-09-997-623-4 Sequence 4, Appl
58	310.5	7.9	419	2	US-09-719-911-1 Sequence 1, Appl
59	310.5	7.9	419	2	US-09-719-911-3 Sequence 3, Appl
60	310.5	7.9	419	5	PCT-US92-10242-1 Sequence 1, Appl
61	310.5	7.9	460	1	US-08-756-506-2 Sequence 2, Appl
62	310.5	7.9	460	1	US-08-756-506-4 Sequence 4, Appl
63	310.5	7.9	461	2	US-10-182-263-2 Sequence 2, Appl
64	310.5	7.9	461	2	US-09-054-272-32 Sequence 32, Appl
65	310.5	7.9	461	2	US-09-949-016-5921 Sequence 5921, Ap
66	310.5	7.9	461	2	US-10-168-407-2 Sequence 2, Appl
67	310.5	7.9	461	2	US-09-997-623-2 Sequence 2, Appl
68	310.5	7.9	461	2	US-09-719-911-2 Sequence 2, Appl
69	310.5	7.9	461	7	5225537-2 Patent No. 5225537
70	310.5	7.9	485	2	US-09-949-016-10882 Sequence 10882, A
71	310	7.9	419	2	US-10-182-263-6 Sequence 6, Appl
72	310	7.9	419	2	US-10-168-407-4 Sequence 4, Appl
73	309.5	7.8	419	2	US-09-719-911-4 Sequence 4, Appl
74	309.5	7.8	419	2	US-09-719-911-5 Sequence 5, Appl
75	309	7.8	419	2	US-10-182-263-1 Sequence 1, Appl
76	309	7.8	419	2	US-10-182-263-5 Sequence 5, Appl
77	309	7.8	461	7	5270178-2 Patent No. 5270178
78	308	7.8	419	2	US-10-182-263-4 Sequence 4, Appl
79	307	7.8	460	7	5270178-15 Patent No. 5270178
80	305	7.7	460	7	5270178-13 Patent No. 5270178
81	305	7.7	460	7	5270178-14 Patent No. 5270178
82	302.5	7.7	461	7	5270178-17 Patent No. 5270178
83	302.5	7.7	461	7	5270178-18 Patent No. 5270178
84	298	7.6	397	2	US-10-104-047-3904 Sequence 3904, Ap
85	296	7.5	230	2	US-10-037-417-135 Sequence 135, App
86	288.5	7.3	802	2	US-09-999-833A-169 Sequence 169, App
87	288.5	7.3	802	2	US-10-020-445A-169 Sequence 169, App
88	288.5	7.3	802	2	US-09-978-189-169 Sequence 169, App
89	288.5	7.3	802	3	US-10-017-085A-169 Sequence 169, App
90	288.5	7.3	802	3	US-10-145-129A-169 Sequence 169, App
91	288.5	7.3	802	3	US-10-013-929A-169 Sequence 169, App
92	288.5	7.3	802	3	US-10-013-917A-169 Sequence 169, App
93	288.5	7.3	902	2	US-09-644-600A-10 Sequence 10, Appl
94	288.5	7.3	902	2	US-09-654-600A-10 Sequence 10, Appl
95	288.5	7.3	902	3	US-09-421-213-10 Sequence 10, Appl
96	287.5	7.3	356	2	US-09-054-272-18 Sequence 2, Appl
97	284.5	7.2	587	2	US-09-856-3198-2 Sequence 2, Appl
98	283.5	7.2	587	2	US-09-949-016-11501 Sequence 11501, A
99	282	7.1	527	7	5520913-1 Patent No. 5520913

100	281	7.1	487	1	US-08-469-486-53	Sequence 53, Appl	173	271.5	6.9	244	3	US-09-936-271C-84	Sequence 84, Appl
101	281	7.1	487	1	US-08-469-658-53	Sequence 53, Appl	174	271.5	6.9	325	2	US-09-949-016-7713	Sequence 7713, Ap
102	281	7.1	488	2	US-09-367-777-44	Sequence 44, Appl	175	270.5	6.9	415	1	US-08-295-411-2	Sequence 2, Appl
103	281	7.1	488	2	US-09-367-791A-27	Sequence 27, Appl	176	270.5	6.9	415	1	US-08-955-471-2	Sequence 2, Appl
104	281	7.1	488	2	US-10-348-504-44	Sequence 44, Appl	177	270.5	6.9	415	5	PCT-US92-10242-2	Sequence 2, Appl
105	281	7.1	488	2	US-09-632-722-2	Sequence 2, Appl	178	269.5	6.8	415	3	US-09-936-271C-71	Sequence 71, Appl
106	281	7.1	492	1	US-08-469-486-2	Sequence 2, Appl	179	269	6.8	643	2	US-10-099-322-113	Sequence 113, App
107	281	7.1	492	1	US-08-469-658-2	Sequence 2, Appl	180	269	6.8	643	2	US-10-044-564-113	Sequence 113, App
108	280.5	7.1	267	2	US-09-949-016-9575	Sequence 9575, Ap	181	268.5	6.8	406	1	US-08-293-778-24	Sequence 24, Appl
109	280	7.1	527	1	US-07-609-510B-16	Sequence 16, Appl	182	264.5	6.7	415	1	US-08-073-531B-1	Sequence 1, Appl
110	280	7.1	527	1	US-08-811-949-39	Sequence 39, Appl	183	264.5	6.7	415	1	US-08-766-288-1	Sequence 1, Appl
111	280	7.1	527	2	US-09-600-985-1	Sequence 1, Appl	184	263	6.7	431	2	US-09-101-272G-1	Sequence 1, Appl
112	280	7.1	527	2	US-09-612-314A-51	Sequence 51, Appl	185	263	6.7	431	2	US-09-949-002-245	Sequence 345, App
113	280	7.1	527	2	US-10-360-101-203	Sequence 203, App	186	263	6.7	431	7	5188829-1	Patent No. 5188829
114	280	7.1	527	2	US-10-765-633-1	Sequence 1, Appl	187	263	6.7	437	2	US-09-949-002-115	Sequence 415, App
115	280	7.1	527	2	US-09-987-455A-19	Sequence 19, Appl	188	262.5	6.7	461	2	US-08-742-877-2	Sequence 2, Appl
116	280	7.1	527	2	PCT-US91-01025A-2	Sequence 2, Appl	189	262.5	6.7	461	2	US-09-053-871A-21	Sequence 21, Appl
117	280	7.1	527	7	5185259-8	Patent No. 5185259	190	262.5	6.7	461	2	US-10-133-907-5	Sequence 5, Appl
118	280	7.1	562	1	US-08-811-949-43	Sequence 43, Appl	191	262.5	6.7	461	7	5521070-2	Patent No. 5521070
119	280	7.1	562	1	US-08-560-098A-50	Sequence 50, Appl	192	262.5	6.7	480	2	US-09-949-016-1123	Sequence 1123, A
120	280	7.1	562	1	US-08-883-795A-38	Sequence 38, Appl	193	262.5	6.7	1042	2	US-09-959-392-2	Sequence 2, Appl
121	280	7.1	562	2	US-09-703-695A-4	Sequence 4, Appl	194	261.5	6.6	415	2	US-09-118-748-2	Sequence 2, Appl
122	280	7.1	562	2	US-10-443-701-4	Sequence 4, Appl	195	260.5	6.6	437	1	US-08-487-037-2	Sequence 2, Appl
123	280	7.1	562	7	5185259-3	Patent No. 5185259	196	260	6.6	477	1	US-08-560-098A-51	Sequence 51, Appl
124	280	7.1	562	7	5200340-2	Patent No. 5200340	197	258.5	6.6	411	1	US-08-087-163-1	Sequence 1, Appl
125	280	7.1	562	7	5344773-2	Patent No. 5344773	198	258.5	6.6	411	1	US-08-286-748B-18	Sequence 18, Appl
126	279	7.1	527	2	US-09-600-985-2	Sequence 2, Appl	199	258.5	6.6	411	1	US-08-153-799-18	Sequence 1, Appl
127	279	7.1	527	2	US-10-765-633-2	Sequence 2, Appl	200	258.5	6.6	411	2	US-09-181-816-1	Sequence 1, Appl
128	279	7.1	932	2	US-10-363-937-6	Sequence 6, Appl	201	258.5	6.6	411	2	US-09-880-503-3	Sequence 3, Appl
129	278.5	7.1	932	2	US-07-882-202A-4	Sequence 4, Appl	202	257.5	6.5	430	7	5219569-2	Patent No. 5219569
130	278.5	7.1	466	1	US-08-021-615A-4	Sequence 4, Appl	203	257	6.5	217	2	US-10-037-417-136	Sequence 16, App
131	278.5	7.1	466	1	US-08-321-777-4	Sequence 4, Appl	204	256.5	6.5	264	2	US-09-856-319B-4	Sequence 4, Appl
132	278.5	7.1	466	2	US-09-009-217-14	Sequence 14, Appl	205	256.5	6.5	411	2	US-09-403-736-2	Sequence 2, Appl
133	278.5	7.1	466	2	US-09-009-656-14	Sequence 14, Appl	206	256.5	6.5	430	1	US-07-942-157A-3	Sequence 3, Appl
134	278.5	7.1	466	5	PCT-US93-04493-4	Sequence 4, Appl	207	255.5	6.5	244	2	US-09-618-259-11	Sequence 11, Appl
135	278.5	7.1	483	5	US-09-949-016-9523	Sequence 9523, Ap	208	254.5	6.5	437	1	US-08-467-037-3	Sequence 3, Appl
136	278	7.0	483	5	PCT-US92-10068-1	Sequence 1, Appl	209	254	6.4	261	7	5270178-21	Patent No. 5270178
137	278	7.0	496	2	US-09-949-016-9524	Sequence 9524, Ap	210	251	6.4	261	7	5270178-5	Patent No. 5270178
138	276.5	7.0	655	1	US-08-148-910-12	Sequence 12, Appl	211	250.5	6.3	229	1	US-08-557-146-13	Sequence 13, Appl
139	276.5	7.0	655	1	US-08-448-937A-12	Sequence 12, Appl	212	250.5	6.3	229	1	US-09-154-344-13	Sequence 13, Appl
140	276	7.0	448	1	US-08-295-411-3	Sequence 3, Appl	213	250.5	6.3	411	2	US-08-560-098A-48	Sequence 48, Appl
141	276	7.0	448	1	US-08-955-471-3	Sequence 3, Appl	214	249.5	6.3	403	1	US-09-860-503-6	Sequence 6, Appl
142	276	7.0	527	5	PCT-US92-10242-3	Sequence 3, Appl	215	249.5	6.3	986	2	US-09-285-385C-19	Sequence 19, Appl
143	276	7.0	527	2	US-09-600-985-3	Sequence 3, Appl	216	249	6.3	251	2	US-08-944-483-17	Sequence 47, Appl
144	276	7.0	527	2	US-10-705-633-3	Sequence 3, Appl	217	248.5	6.3	250	2	US-08-944-483-51	Sequence 51, Appl
145	275.5	7.0	405	2	US-10-360-101-225	Sequence 225, App	218	248.5	6.3	261	7	5270178-19	Patent No. 5270178
146	275.5	7.0	406	1	US-08-295-411-5	Sequence 5, Appl	219	248.5	6.3	261	7	5270178-20	Patent No. 5270178
147	275.5	7.0	406	1	US-08-955-471-5	Sequence 5, Appl	220	248.5	6.3	262	1	US-07-720-189-1	Sequence 1, Appl
148	275.5	7.0	406	2	US-09-782-587B-1	Sequence 1, Appl	221	248	6.3	230	2	US-08-944-483-52	Sequence 62, Appl
149	275.5	7.0	406	2	US-09-782-587B-3	Sequence 3, Appl	222	248	6.3	230	3	US-09-410-362F-8	Sequence 8, Appl
150	275.5	7.0	406	2	US-09-969-357B-3	Sequence 3, Appl	223	248	6.3	230	3	US-09-410-362F-40	Sequence 40, Appl
151	275.5	7.0	406	2	US-09-848-107A-1	Sequence 1, Appl	224	248	6.3	231	1	US-09-027-337-6	Sequence 6, Appl
152	275.5	7.0	406	2	US-10-669-537-1	Sequence 1, Appl	225	248	6.3	231	2	US-09-644-600-6	Sequence 6, Appl
153	275.5	7.0	406	2	US-10-281-727-1	Sequence 1, Appl	226	248	6.3	231	2	US-09-654-600A-6	Sequence 6, Appl
154	275.5	7.0	406	5	PCT-US92-10242-5	Sequence 5, Appl	227	248	6.3	231	3	US-09-421-213-6	Sequence 6, Appl
155	275.5	7.0	444	1	US-08-475-845-2	Sequence 2, Appl	228	248	6.3	638	2	US-10-099-322-111	Sequence 111, App
156	275.5	7.0	444	1	US-08-327-690-2	Sequence 2, Appl	229	247	6.3	638	2	US-10-044-564-111	Sequence 111, App
157	275.5	7.0	444	1	US-08-660-289-2	Sequence 2, Appl	230	247	6.3	638	2	US-10-099-322-10	Sequence 30, Appl
158	275.5	7.0	444	1	US-08-537-807-2	Sequence 2, Appl	231	247	6.3	638	2	US-10-044-564-30	Sequence 30, Appl
159	275.5	7.0	444	1	US-08-871-003-2	Sequence 2, Appl	232	247	6.3	764	1	US-08-177-109A-2	Sequence 2, Appl
160	275.5	7.0	444	2	US-08-464-233-2	Sequence 2, Appl	233	247	6.3	764	1	US-08-687-706-2	Sequence 2, Appl
161	275.5	7.0	444	2	US-09-189-607-2	Sequence 2, Appl	234	247	6.3	764	2	US-09-949-002-325	Sequence 325, App
162	275.5	7.0	444	2	US-09-378-907-2	Sequence 2, Appl	235	247	6.3	798	2	US-09-949-016-11021	Sequence 11021, A
163	275.5	7.0	444	5	PCT-US94-05779-2	Sequence 2, Appl	236	247	6.3	798	2	US-09-949-002-546	Sequence 544, App
164	275.5	7.0	461	7	US-09-949-016-8839	Sequence 8839, Ap	237	247	6.3	986	2	US-09-949-016-6690	Sequence 6690, App
165	275	7.0	562	7	5244676-5	Patent No. 5244676	238	246.5	6.2	259	2	US-08-944-483-52	Sequence 52, Appl
166	275	7.0	562	2	US-09-959-392-4	Sequence 4, Appl	239	246.5	6.2	295	2	US-08-338-368-2	Sequence 2, Appl
167	273	6.9	560	2	US-09-949-016-6458	Sequence 6458, Ap	240	246.5	6.2	326	2	US-08-558-269-10	Sequence 10, Appl
168	273	6.9	560	2	US-09-912-559-3	Sequence 3, Appl	241	246.5	6.2	376	2	US-09-410-882-10	Sequence 4, Appl
169	273	6.9	560	2	US-09-912-559-4	Sequence 4, Appl	242	246.5	6.2	579	1	US-08-295-411-4	Sequence 4, Appl
170	272	6.9	488	1	US-08-487-037-1	Sequence 1, Appl	243	246.5	6.2	579	1	US-08-955-471-4	Sequence 4, Appl
171	271.5	6.9	223	3	US-09-856-050-15	Sequence 15, Appl	244	246.5	6.2	579	2	US-09-117-708-14	Sequence 14, Appl
172	271.5	6.9	244	1	US-08-361-395-1	Sequence 1, Appl	245	246.5	6.2	579	5	PCT-US92-10242-4	Sequence 4, Appl

246	246.5	6.2	615	1	US-07-998-972A-3	Sequence 3, Appl1	319	236.5	6.0	416	2	US-10-099-322-138	Sequence 138, App
247	246.5	6.2	615	1	US-08-463-953-3	Sequence 3, Appl1	320	236.5	6.0	416	2	US-10-044-564-138	Sequence 138, App
248	246.5	6.2	615	1	US-08-462-261-3	Sequence 3, Appl1	321	236.5	6.0	472	1	US-08-811-949-53	Sequence 63, Appl
249	246.5	6.2	615	5	PCT-US92-11357-3	Sequence 3, Appl1	322	236.5	6.0	871	2	US-09-246-041-19	Sequence 19, Appl
250	246.5	6.2	622	2	US-08-952-967-8	Sequence 8, Appl1	323	236.5	6.0	871	2	US-09-358-055B-19	Sequence 19, Appl
251	246.5	6.2	622	2	US-09-054-272-42	Sequence 42, Appl1	324	236.5	6.0	871	2	US-09-893-238-19	Sequence 19, Appl
252	246.5	6.2	612	2	US-08-991-761A-7	Sequence 7, Appl1	325	236.5	6.0	1013	1	US-08-866-650-3	Sequence 3, Appl1
253	245.5	6.2	638	2	US-10-099-322-112	Sequence 112, App	326	236.5	6.0	1013	1	US-09-021-287-3	Sequence 3, Appl1
254	245.5	6.2	638	2	US-10-044-564-112	Sequence 112, App	327	236.5	6.0	1013	2	US-09-240-473-3	Sequence 3, Appl1
255	245	6.2	628	1	US-08-278-091-10	Sequence 10, Appl	328	236.5	6.0	1350	2	US-09-246-041-17	Sequence 17, Appl
256	245	6.2	628	1	US-08-483-853-10	Sequence 10, Appl	329	236.5	6.0	1350	2	US-09-358-055B-17	Sequence 17, Appl
257	245	6.2	628	1	US-08-472-173-10	Sequence 10, Appl	330	236.5	6.0	1350	2	US-09-893-238-17	Sequence 17, Appl
258	245	6.2	628	1	US-08-487-167-10	Sequence 10, Appl	331	236.5	6.0	355	1	US-08-811-949-53	Sequence 53, Appl
259	245	6.2	628	1	US-08-482-816-10	Sequence 10, Appl	332	236.5	6.0	270	1	US-08-978-404B-8	Sequence 59, Appl
260	245	6.2	628	1	US-08-296-149-10	Sequence 10, Appl	333	236.5	6.0	270	1	US-08-978-404B-8	Sequence 59, Appl
261	245	6.2	628	1	US-08-801-499-10	Sequence 10, Appl	334	236.5	5.9	252	2	US-08-944-483-72	Sequence 72, Appl
262	245	6.2	628	1	US-08-615-271-10	Sequence 10, Appl	335	236.5	5.9	253	1	US-09-021-337-8	Sequence 8, Appl1
263	245	6.2	628	2	US-09-074-660-10	Sequence 10, Appl	336	236.5	5.9	253	1	US-09-644-600-8	Sequence 8, Appl1
264	245	6.2	628	2	US-09-074-659-10	Sequence 10, Appl	337	236.5	5.9	253	2	US-09-654-600A-8	Sequence 8, Appl1
265	245	6.2	628	2	US-09-106-468-10	Sequence 10, Appl	338	236.5	5.9	253	3	US-09-421-213-8	Sequence 8, Appl1
266	245	6.2	628	2	US-09-106-466A-10	Sequence 10, Appl	339	236.5	5.9	268	2	US-09-987-455A-18	Sequence 18, Appl
267	245	6.2	628	2	US-09-106-467-10	Sequence 10, Appl	340	236.5	5.9	383	1	US-08-558-289-6	Sequence 6, Appl1
268	245	6.2	628	2	US-10-360-101-266	Sequence 266, App	341	236.5	5.9	383	1	US-09-410-882-6	Sequence 6, Appl1
269	244.5	6.2	638	2	US-09-715-994-2	Sequence 2, Appl1	342	236.5	5.9	546	7	5200340-6	Patent No. 5200340
270	244	6.2	638	2	US-10-099-322-114	Sequence 114, App	343	236.5	5.9	259	2	US-10-165-442-2	Sequence 2, Appl1
271	244	6.2	638	2	US-10-044-564-114	Sequence 114, App	344	236.5	5.9	295	2	US-10-165-442-1	Sequence 1, Appl1
272	242.5	6.1	416	1	US-09-000-846-2	Sequence 2, Appl1	345	236.5	5.9	1013	1	US-08-866-650-5	Sequence 5, Appl1
273	242	6.1	322	3	US-10-114-270-134	Sequence 134, App	346	236.5	5.9	1013	1	US-09-021-287-5	Sequence 5, Appl1
274	242	6.1	730	2	US-08-872-757-2	Sequence 2, Appl1	347	236.5	5.9	1013	2	US-08-991-408-2	Sequence 2, Appl1
275	242	6.1	730	2	US-09-850-048A-2	Sequence 2, Appl1	348	236.5	5.9	1013	2	US-09-240-473-5	Sequence 5, Appl1
276	241.5	6.1	347	1	US-08-811-949-1	Sequence 1, Appl1	349	236.5	5.9	1013	2	US-09-432-473-2	Sequence 2, Appl1
277	241.5	6.1	788	1	US-08-572-225-1	Sequence 1, Appl1	350	236.5	5.9	1013	2	US-09-285-385C-20	Sequence 20, Appl1
278	241	6.1	354	1	US-08-811-949-61	Sequence 61, Appl	351	236.5	5.9	416	2	US-10-099-322-137	Sequence 137, App
279	241	6.1	986	2	US-08-872-757-4	Sequence 4, Appl1	352	236.5	5.9	416	2	US-10-044-564-137	Sequence 137, App
280	240.5	6.1	986	2	US-09-850-048A-4	Sequence 4, Appl1	353	236.5	5.9	638	1	US-08-681-151-3	Sequence 3, Appl1
281	240.5	6.1	356	1	US-08-427-640-8	Sequence 8, Appl1	354	236.5	5.9	638	2	US-10-099-322-115	Sequence 115, App
282	240.5	6.1	3571	2	US-09-911-842A-4	Sequence 2, Appl1	355	236.5	5.9	638	2	US-10-044-564-115	Sequence 115, App
283	240	6.1	422	2	US-09-959-392-34	Sequence 34, Appl1	356	231.5	5.9	389	1	US-08-811-949-65	Sequence 65, Appl
284	240	6.1	432	1	US-08-560-098A-47	Sequence 47, Appl	357	231.5	5.9	417	2	US-09-820-002-4	Sequence 4, Appl1
285	239.5	6.1	1015	2	US-09-285-385C-2	Sequence 2, Appl1	358	231	5.9	365	1	US-08-093-741-83	Sequence 83, Appl
286	239.5	6.1	3594	2	US-09-911-842A-4	Sequence 4, Appl1	359	231	5.9	365	1	US-08-720-012-83	Sequence 83, Appl
287	239	6.1	230	2	US-09-601-318-3	Sequence 3, Appl1	360	231	5.9	393	1	US-08-560-098A-44	Sequence 44, Appl
288	239	6.1	356	1	US-08-681-151-1	Sequence 1, Appl1	361	231	5.9	393	2	US-08-967-024C-25	Sequence 25, Appl
289	239	6.1	389	1	US-08-811-949-67	Sequence 67, Appl	362	231	5.9	393	2	US-08-967-024C-25	Sequence 25, Appl
290	238.5	6.0	437	1	US-08-811-949-49	Sequence 49, Appl	363	231	5.9	1012	2	US-09-285-385C-4	Sequence 4, Appl1
291	238.5	6.0	437	1	US-08-811-949-51	Sequence 51, Appl	364	230.5	5.8	259	2	US-10-165-442-6	Sequence 6, Appl1
292	238.5	6.0	437	1	US-08-811-949-55	Sequence 55, Appl	365	230.5	5.8	295	2	US-10-165-442-3	Sequence 3, Appl1
293	238.5	6.0	437	1	US-08-811-949-57	Sequence 57, Appl	366	230.5	5.8	302	2	US-09-220-731-26	Sequence 26, Appl
294	238	6.0	237	2	US-08-163-919A-3	Sequence 3, Appl1	367	230.5	5.8	302	2	US-09-242-999-22	Sequence 22, Appl
295	238	6.0	237	2	US-08-462-515-3	Sequence 3, Appl1	368	230	5.8	232	2	US-09-959-392-11	Sequence 31, Appl
296	238	6.0	237	5	PCT-US94-14073-3	Sequence 3, Appl1	369	230	5.8	248	2	US-08-944-483-63	Sequence 63, Appl
297	238	6.0	335	2	US-09-987-455A-14	Sequence 14, Appl	370	230	5.8	387	2	US-09-032-215-8	Sequence 8, Appl1
298	238	6.0	343	2	US-09-987-455A-16	Sequence 16, Appl	371	230	5.8	387	2	US-09-032-215-13	Sequence 13, Appl
299	236.5	6.0	274	1	US-08-978-404B-5	Sequence 5, Appl	372	229	5.8	242	2	US-09-004-731-16	Sequence 16, Appl
300	236.5	6.0	308	2	US-09-987-455A-17	Sequence 17, Appl	373	229	5.8	242	2	US-08-749-699-37	Sequence 36, Appl
301	236.5	6.0	331	2	US-09-987-455A-12	Sequence 12, Appl	374	229	5.8	242	2	US-09-004-729-16	Sequence 36, Appl
302	236.5	6.0	339	2	US-09-987-455A-13	Sequence 13, Appl	375	229	5.8	400	2	US-09-004-731-30	Sequence 30, Appl
303	236.5	6.0	343	2	US-09-987-455A-15	Sequence 15, Appl	376	229	5.8	400	2	US-09-004-731-33	Sequence 33, Appl
304	236.5	6.0	354	2	US-09-987-455A-11	Sequence 11, Appl	377	229	5.8	400	2	US-08-749-699-37	Sequence 30, Appl
305	236.5	6.0	355	1	US-08-137-116-1	Sequence 1, Appl1	378	229	5.8	400	2	US-08-749-699-33	Sequence 30, Appl
306	236.5	6.0	355	1	US-08-217-618-1	Sequence 1, Appl1	379	229	5.8	400	2	US-09-004-729-13	Sequence 33, Appl
307	236.5	6.0	355	1	US-08-427-640-2	Sequence 2, Appl1	380	229	5.8	235	2	US-08-897-151-3	Sequence 3, Appl1
308	236.5	6.0	355	1	US-08-427-640-6	Sequence 6, Appl1	381	228.5	5.8	235	2	US-08-897-151-3	Sequence 3, Appl1
309	236.5	6.0	355	1	US-08-217-617A-1	Sequence 1, Appl1	382	228.5	5.8	235	2	US-09-478-957-8	Sequence 8, Appl
310	236.5	6.0	355	1	US-08-217-616-1	Sequence 1, Appl1	383	228.5	5.8	343	3	US-10-162-335-86	Sequence 86, Appl
311	236.5	6.0	355	1	US-08-811-949-45	Sequence 45, Appl1	384	228	5.8	287	3	US-10-114-270-130	Sequence 130, App
312	236.5	6.0	355	1	US-08-811-949-47	Sequence 47, Appl1	385	228	5.8	591	2	US-08-991-408-4	Sequence 4, Appl1
313	236.5	6.0	355	1	US-08-794-528-1	Sequence 1, Appl1	386	228	5.8	591	2	US-09-432-473-4	Sequence 4, Appl1
314	236.5	6.0	355	7	5232356-1	Patent No. 5232356	387	228	5.8	809	2	US-08-991-761A-9	Sequence 9, Appl1
315	236.5	6.0	356	1	US-08-427-640-4	Sequence 4, Appl1	388	228	5.8	812	1	US-08-458-629A-1	Sequence 1, Appl1
316	236.5	6.0	377	2	US-09-987-455A-8	Sequence 8, Appl1	389	228	5.8	812	1	US-08-451-932-1	Sequence 1, Appl1
317	236.5	6.0	378	2	US-09-553-498-10	Sequence 10, Appl	390	228	5.8	812	1	US-08-452-260-1	Sequence 1, Appl1
318	236.5	6.0	378	2	US-09-618-869-10	Sequence 10, Appl	391	228	5.8	812	1	US-08-326-785-1	Sequence 1, Appl1

392	228	5.8	812	1	US-08-612-788-1	Sequence 1, Appl1	465	223	5.7	521	2	US-09-949-016-11081	Sequence 11081, A
393	228	5.8	812	1	US-08-605-598B-1	Sequence 1, Appl1	466	223	5.7	521	2	US-09-949-016-11082	Sequence 11082, A
394	228	5.8	812	1	US-08-429-743-1	Sequence 1, Appl1	467	223	5.7	521	2	US-09-949-016-11083	Sequence 11083, A
395	228	5.8	812	1	US-08-866-735-1	Sequence 1, Appl1	468	223.5	5.6	304	2	US-10-099-332-139	Sequence 139, App
396	228	5.8	812	2	US-09-066-028-1	Sequence 1, Appl1	469	222.5	5.6	304	2	US-10-044-564-139	Sequence 2, Appl1
397	228	5.8	812	2	US-09-192-012-3	Sequence 3, Appl1	470	222.5	5.6	380	2	US-10-235-789C-2	Sequence 2, Appl1
398	228	5.8	812	2	US-09-335-325-1	Sequence 1, Appl1	471	222.5	5.6	417	2	US-10-099-332-10	Sequence 40, Appl1
399	228	5.8	812	2	US-08-991-761A-12	Sequence 12, Appl1	472	222.5	5.6	417	2	US-10-099-332-10	Sequence 136, App
400	228	5.8	812	2	US-09-335-614-1	Sequence 1, Appl1	473	222.5	5.6	417	2	US-10-044-564-10	Sequence 40, Appl1
401	228	5.8	812	5	PCR-US95-05107-1	Sequence 1, Appl1	474	222.5	5.6	417	2	US-10-044-564-136	Sequence 136, App
402	227.5	5.8	251	3	US-09-936-271C-66	Sequence 66, Appl	475	222.5	5.6	445	2	US-09-856-371A-8	Sequence 8, Appl1
403	227.5	5.8	251	3	US-09-936-271C-67	Sequence 67, Appl	476	222.5	5.6	452	2	US-09-949-016-1182	Sequence 7162, Ap
404	227	5.8	241	2	US-09-657-986B-2	Sequence 2, Appl1	477	222.5	5.6	790	2	US-08-991-761A-13	Sequence 13, Appl
405	227	5.8	241	3	US-09-410-362F-3	Sequence 3, Appl1	478	222	5.6	274	1	US-09-016-366A-21	Sequence 21, Appl
406	227	5.8	241	3	US-09-410-362F-35	Sequence 35, Appl	479	222	5.6	274	1	US-08-978-404B-16	Sequence 16, Appl
407	227	5.8	285	2	US-09-023-9442A-26	Sequence 26, Appl	480	222	5.6	407	2	US-09-734-675-4	Sequence 4, Appl1
408	227	5.8	308	2	US-08-705-875A-10	Sequence 10, Appl	481	222	5.6	407	2	US-10-060-333-4	Sequence 4, Appl1
409	227	5.8	308	2	US-09-242-999-10	Sequence 10, Appl	482	222	5.6	423	2	US-10-012-231A-269	Sequence 269, App
410	226.5	5.7	454	2	US-09-518-046-2	Sequence 2, Appl1	483	222	5.6	423	2	US-10-015-389A-269	Sequence 269, App
411	226.5	5.7	454	2	US-09-650-371-2	Sequence 2, Appl1	484	222	5.6	423	2	US-10-006-768A-269	Sequence 269, App
412	226.5	5.7	2787	2	US-09-348-055B-15	Sequence 15, Appl	485	222	5.6	423	2	US-10-015-671A-269	Sequence 269, App
413	226.5	5.7	2787	2	US-09-358-055B-15	Sequence 15, Appl	486	222	5.6	423	2	US-10-015-393A-269	Sequence 269, App
414	226.5	5.7	2787	2	US-09-893-238-15	Sequence 15, Appl	487	222	5.6	423	2	US-10-011-833A-269	Sequence 269, App
415	226	5.7	406	2	US-09-851-388-6	Sequence 6, Appl1	488	222	5.6	423	2	US-10-006-041A-269	Sequence 269, App
416	226	5.7	423	2	US-09-656-002-2	Sequence 2, Appl1	489	222	5.6	423	2	US-10-012-064A-269	Sequence 269, App
417	226	5.7	432	2	US-10-012-231A-775	Sequence 275, App	490	222	5.6	423	2	US-10-015-392A-269	Sequence 269, App
418	226	5.7	432	2	US-10-015-389A-775	Sequence 275, App	491	222	5.6	423	3	US-10-011-795B-269	Sequence 269, App
419	226	5.7	432	2	US-10-006-768A-775	Sequence 275, App	492	222	5.6	423	3	US-10-015-386A-269	Sequence 269, App
420	226	5.7	432	2	US-10-015-671A-775	Sequence 275, App	493	222	5.6	423	3	US-10-012-121A-269	Sequence 269, App
421	226	5.7	432	2	US-10-015-393A-775	Sequence 275, App	494	222	5.6	423	3	US-10-006-485A-269	Sequence 269, App
422	226	5.7	432	2	US-10-011-833A-775	Sequence 275, App	495	222	5.6	423	3	US-10-006-746A-269	Sequence 269, App
423	226	5.7	432	2	US-10-006-041A-775	Sequence 275, App	496	222	5.6	423	3	US-10-012-752A-269	Sequence 269, App
424	226	5.7	432	2	US-10-012-064A-775	Sequence 275, App	497	222	5.6	423	3	US-10-017-253A-269	Sequence 269, App
425	226	5.7	432	2	US-10-015-392A-775	Sequence 275, App	498	222	5.6	423	3	US-10-015-519A-269	Sequence 269, App
426	226	5.7	432	3	US-10-011-795B-775	Sequence 275, App	499	222	5.6	423	3	US-10-007-236A-269	Sequence 269, App
427	226	5.7	432	3	US-10-015-386A-775	Sequence 275, App	500	222	5.6	423	3	US-09-999-833A-69	Sequence 69, Appl
428	226	5.7	432	3	US-10-012-121A-775	Sequence 275, App	501	221.5	5.6	453	2	US-10-020-445A-69	Sequence 69, Appl
429	226	5.7	432	3	US-10-006-485A-775	Sequence 275, App	502	221.5	5.6	453	2	US-09-978-189-69	Sequence 69, Appl
430	226	5.7	432	3	US-10-006-746A-775	Sequence 275, App	503	221.5	5.6	453	2	US-09-978-189-69	Sequence 69, Appl
431	226	5.7	432	3	US-10-012-752A-775	Sequence 275, App	504	221.5	5.6	453	2	US-10-017-085A-69	Sequence 69, Appl
432	226	5.7	432	3	US-10-017-253A-775	Sequence 275, App	505	221.5	5.6	453	3	US-10-145-129A-69	Sequence 69, Appl
433	226	5.7	432	3	US-10-015-519A-775	Sequence 275, App	506	221.5	5.6	453	3	US-10-013-929A-69	Sequence 69, Appl
434	226	5.7	432	3	US-10-015-715A-775	Sequence 275, App	507	221.5	5.6	253	3	US-10-013-917A-69	Sequence 69, Appl
435	226	5.7	432	3	US-10-007-236A-775	Sequence 275, App	508	221	5.6	273	1	US-08-944-483-73	Sequence 73, Appl
436	226	5.7	435	2	US-09-008-271A-6	Sequence 6, Appl1	509	221	5.6	300	2	US-08-978-404B-6	Sequence 6, Appl1
437	226	5.7	435	2	US-09-607-745-2	Sequence 2, Appl1	510	221	5.6	300	2	US-08-705-875A-6	Sequence 6, Appl1
438	226	5.7	435	2	US-09-968-415-6	Sequence 6, Appl1	511	221	5.6	1393	2	US-09-242-999-6	Sequence 6, Appl1
439	226	5.7	435	3	US-10-030-688-2	Sequence 2, Appl1	512	221	5.6	1193	2	US-09-949-016-10498	Sequence 10498, A
440	226	5.7	437	3	US-09-851-588-8	Sequence 8, Appl1	513	221	5.6	1355	2	US-09-787-097-10	Sequence 10, Appl
441	226	5.7	481	2	US-09-949-016-9238	Sequence 9238, Ap	514	220.5	5.6	376	2	US-09-820-002-2	Sequence 2, Appl1
442	226	5.7	481	2	US-09-949-016-9239	Sequence 9239, Ap	515	220	5.6	273	1	US-09-016-366A-19	Sequence 19, Appl
443	226	5.7	492	3	US-10-030-688-4	Sequence 4, Appl1	516	220	5.6	273	1	US-08-978-404B-14	Sequence 14, Appl
444	226	5.7	637	2	US-09-949-016-11538	Sequence 11538, A	517	219.5	5.6	245	3	US-09-410-362F-36	Sequence 36, Appl
445	226	5.7	637	2	US-09-948-016-11539	Sequence 11539, A	518	219.5	5.6	254	2	US-08-944-483-50	Sequence 50, Appl
446	225.5	5.7	348	2	US-09-949-016-6979	Sequence 6979, Ap	519	219.5	5.6	255	1	US-09-027-337-7	Sequence 7, Appl1
447	225.5	5.7	457	2	US-09-856-371A-10	Sequence 10, Appl	520	219.5	5.6	255	1	US-09-644-600-7	Sequence 7, Appl1
448	225.5	5.7	1272	2	US-09-787-097-18	Sequence 18, Appl	521	219.5	5.6	255	2	US-09-654-600A-7	Sequence 7, Appl1
449	225.5	5.7	1429	2	US-09-787-097-12	Sequence 12, Appl	522	219.5	5.6	255	3	US-09-421-213-7	Sequence 7, Appl1
450	225	5.7	615	2	US-09-949-002-301	Sequence 301, App	523	219	5.6	343	2	US-09-948-094-2	Sequence 2, Appl1
451	224.5	5.7	232	2	US-09-959-392-32	Sequence 32, Appl	524	219	5.6	343	2	US-10-037-417-130	Sequence 130, App
452	224.5	5.7	235	2	US-08-944-483-65	Sequence 65, Appl	525	218.5	5.5	244	2	US-09-601-318-4	Sequence 4, Appl
453	224.5	5.7	235	3	US-09-410-362F-5	Sequence 5, Appl1	526	218.5	5.5	244	2	US-09-601-318-5	Sequence 5, Appl1
454	224.5	5.7	235	3	US-09-410-362F-37	Sequence 37, Appl	527	218.5	5.5	244	2	US-09-601-318-6	Sequence 6, Appl1
455	224	5.7	275	1	US-09-016-366A-17	Sequence 17, Appl	528	218.5	5.5	244	2	US-09-601-318-7	Sequence 7, Appl1
456	224	5.7	275	1	US-08-978-404B-12	Sequence 12, Appl	529	218.5	5.5	245	2	US-09-079-970A-6	Sequence 6, Appl1
457	224	5.7	275	1	US-09-598-982C-52	Sequence 52, Appl	530	218.5	5.5	245	2	US-09-601-318-1	Sequence 1, Appl1
458	224	5.7	276	2	US-09-880-503-5	Sequence 5, Appl1	531	218.5	5.5	245	2	US-09-598-982C-11	Sequence 11, Appl
459	224	5.7	306	1	US-08-560-098A-45	Sequence 45, Appl	532	218.5	5.5	249	2	US-09-079-970A-5	Sequence 5, Appl1
460	224	5.7	331	1	US-09-880-503-7	Sequence 7, Appl1	533	218.5	5.5	249	2	US-09-598-982C-33	Sequence 33, Appl1
461	224	5.7	331	2	US-08-560-098A-46	Sequence 46, Appl	534	217.5	5.5	245	2	US-09-598-982C-35	Sequence 35, Appl
462	223.5	5.7	346	2	US-09-949-016-9000	Sequence 9000, Ap	535	217.5	5.5	249	2	US-09-598-982C-25	Sequence 25, Appl
463	223.5	5.7	346	2	US-09-944-483-64	Sequence 64, Appl	536	217.5	5.5	249	2	US-09-598-982C-27	Sequence 27, Appl
464	223	5.7	238	2	US-08-944-483-64	Sequence 64, Appl	537	217.5	5.5	249	2	US-09-598-982C-27	Sequence 27, Appl

538	217.5	5.5	1198	2	US-09-245-041-131	Sequence 131, App	611	214	5.4	254	1	US-08-560-098A-49	Sequence 49, Appl
539	217.5	5.5	1198	2	US-09-794-236-3	Sequence 3, Appl	612	214	5.4	292	2	US-09-607-745-9	Sequence 9, Appl
540	217.5	5.5	1198	2	US-09-358-055B-132	Sequence 132, App	613	214	5.4	342	2	US-10-037-417-133	Sequence 133, App
541	217.5	5.5	1198	2	US-09-964-956-35	Sequence 35, Appl	614	214	5.4	342	2	US-10-037-417-134	Sequence 134, App
542	217.5	5.5	1198	2	US-09-787-097-2	Sequence 2, Appl	615	213.5	5.4	114	2	US-09-964-956-68	Sequence 68, Appl
543	217.5	5.5	1429	2	US-09-245-041-130	Sequence 130, App	616	213.5	5.4	255	2	US-08-944-483-67	Sequence 67, Appl
544	217.5	5.5	1429	2	US-09-358-055B-131	Sequence 131, App	617	213.5	5.4	255	3	US-09-410-362F-6	Sequence 6, Appl
545	217	5.5	239	2	US-09-944-483-61	Sequence 61, App	618	213.5	5.4	255	3	US-09-410-362F-8	Sequence 38, Appl
546	217	5.5	268	2	US-09-613-823B-2	Sequence 2, Appl	619	213.5	5.4	256	1	US-09-027-337-3	Sequence 3, Appl
547	217	5.5	273	1	US-08-978-404B-3	Sequence 3, Appl	620	213.5	5.4	256	2	US-09-644-600-3	Sequence 3, Appl
548	217	5.5	344	2	US-10-037-417-44	Sequence 44, Appl	621	213.5	5.4	256	2	US-09-654-600A-3	Sequence 3, Appl
549	217	5.5	357	2	US-10-037-417-46	Sequence 46, Appl	622	213.5	5.4	256	3	US-09-421-213-3	Sequence 3, Appl
550	217	5.5	791	1	US-08-643-219-1	Sequence 1, Appl	623	212.5	5.4	250	2	US-09-205-258-477	Sequence 427, App
551	217	5.5	791	1	US-08-851-350-1	Sequence 1, Appl	624	212.5	5.4	250	2	US-10-004-860-477	Sequence 427, App
552	217	5.5	2703	1	US-08-185-432-19	Sequence 19, Appl	625	212.5	5.4	250	2	US-10-012-231A-170	Sequence 170, App
553	217	5.5	2703	2	US-08-899-223-4	Sequence 4, Appl	626	212.5	5.4	250	2	US-10-015-389A-170	Sequence 170, App
554	217	5.5	2703	2	US-09-121-457-4	Sequence 4, Appl	627	212.5	5.4	250	2	US-10-008-768A-170	Sequence 170, App
555	216.5	5.5	245	2	US-09-598-982C-2	Sequence 2, Appl	628	212.5	5.4	250	2	US-10-015-671A-170	Sequence 170, App
556	216.5	5.5	249	2	US-09-598-982C-6	Sequence 6, Appl	629	212.5	5.4	250	2	US-10-015-393A-170	Sequence 170, App
557	216.5	5.5	498	2	US-10-183-992-2	Sequence 2, Appl	630	212.5	5.4	250	2	US-10-015-833A-170	Sequence 170, App
558	216	5.5	267	1	US-09-016-366A-23	Sequence 23, Appl	631	212.5	5.4	250	2	US-10-006-041A-170	Sequence 170, App
559	216	5.5	267	1	US-08-978-404B-18	Sequence 18, Appl	632	212.5	5.4	250	2	US-10-012-064A-170	Sequence 170, App
560	216	5.5	267	2	US-09-917-234-101	Sequence 101, App	633	212.5	5.4	250	2	US-10-015-392A-170	Sequence 170, App
561	216	5.5	268	1	US-08-568-031-2	Sequence 1, Appl	634	212.5	5.4	250	3	US-10-011-795B-170	Sequence 86, Appl
562	216	5.5	268	1	US-08-966-319-2	Sequence 2, Appl	635	212.5	5.4	250	3	US-09-936-271C-86	Sequence 86, Appl
563	216	5.5	269	2	US-09-153-304-2	Sequence 2, Appl	636	212.5	5.4	250	3	US-10-012-386A-170	Sequence 170, App
564	216	5.5	299	2	US-08-944-483-66	Sequence 6, Appl	637	212.5	5.4	250	3	US-10-006-485A-170	Sequence 170, App
565	216	5.5	319	2	US-09-386-642-12	Sequence 12, Appl	638	212.5	5.4	250	3	US-10-006-485A-170	Sequence 170, App
566	216	5.5	328	2	US-09-386-642-11	Sequence 11, Appl	639	212.5	5.4	250	3	US-10-006-746A-170	Sequence 170, App
567	216	5.5	790	1	US-08-469-486-54	Sequence 54, Appl	640	212.5	5.4	250	3	US-10-012-752A-170	Sequence 170, App
568	216	5.5	790	1	US-08-469-658-54	Sequence 54, Appl	641	212.5	5.4	250	3	US-10-017-253A-170	Sequence 170, App
569	216	5.5	810	7	5200340-8	Patent No. 5200340	642	212.5	5.4	250	3	US-10-015-519A-170	Sequence 170, App
570	215.5	5.5	245	2	US-09-598-982C-49	Sequence 49, Appl	643	212.5	5.4	250	3	US-10-015-715A-170	Sequence 170, App
571	215.5	5.5	245	2	US-09-598-982C-51	Sequence 51, Appl	644	212.5	5.4	250	3	US-10-007-236A-170	Sequence 170, App
572	215.5	5.5	249	2	US-09-598-982C-41	Sequence 41, Appl	645	212.5	5.4	282	2	US-09-025-059-1	Sequence 1, Appl
573	215.5	5.5	249	2	US-09-598-982C-43	Sequence 43, Appl	646	212.5	5.4	282	2	US-09-856-320A-2	Sequence 2, Appl
574	215.5	5.5	317	2	US-09-386-629-7	Sequence 7, Appl	647	212.5	5.4	289	2	US-09-386-642-14	Sequence 14, Appl
575	215.5	5.5	317	2	US-09-907-794A-263	Sequence 263, App	648	212.5	5.4	289	3	US-10-162-335-4	Sequence 4, Appl
576	215.5	5.5	317	2	US-09-905-125A-263	Sequence 263, App	649	212.5	5.4	289	3	US-10-162-335-8	Sequence 8, Appl
577	215.5	5.5	317	2	US-09-902-775A-263	Sequence 263, App	650	212	5.4	260	2	US-09-025-059-3	Sequence 3, Appl
578	215.5	5.5	317	2	US-09-906-700-263	Sequence 263, App	651	212	5.4	260	2	US-09-618-259-8	Sequence 8, Appl
579	215.5	5.5	317	2	US-09-903-603A-263	Sequence 263, App	652	212	5.4	260	2	US-08-915-659A-10	Sequence 10, Appl
580	215.5	5.5	317	2	US-09-904-920A-263	Sequence 263, App	653	212	5.4	814	1	US-08-750-711-1	Sequence 1, Appl
581	215.5	5.5	317	2	US-09-909-064-263	Sequence 263, App	654	211.5	5.4	232	1	US-08-508-448C-19	Sequence 19, Appl
582	215.5	5.5	317	2	US-09-905-381A-263	Sequence 263, App	655	211.5	5.4	235	3	US-09-410-362F-4	Sequence 4, Appl
583	215.5	5.5	317	2	US-09-906-618-263	Sequence 263, App	656	211.5	5.4	266	3	US-10-162-335-6	Sequence 6, Appl
584	215.5	5.5	317	2	US-10-040-803-7	Sequence 7, Appl	657	211.5	5.4	266	3	US-10-162-335-10	Sequence 10, Appl
585	215.5	5.5	317	2	US-09-906-646-263	Sequence 263, App	658	211.5	5.4	418	1	US-08-508-448C-25	Sequence 25, Appl
586	215.5	5.5	317	2	US-09-904-462-263	Sequence 263, App	659	211.5	5.4	418	2	US-09-370-838-82	Sequence 82, Appl
587	215.5	5.5	317	2	US-09-902-736A-263	Sequence 263, App	660	211.5	5.4	418	2	US-09-370-838-83	Sequence 83, Appl
588	215.5	5.5	317	2	US-09-906-722A-263	Sequence 263, App	661	211.5	5.4	418	2	US-09-854-133-82	Sequence 82, Appl
589	215.5	5.5	317	2	US-09-905-449-263	Sequence 263, App	662	211.5	5.4	418	2	US-09-854-133-83	Sequence 83, Appl
590	215.5	5.5	317	2	US-09-903-562B-263	Sequence 263, App	663	211	5.3	276	1	US-09-016-366A-15	Sequence 15, Appl
591	215.5	5.5	317	2	US-09-906-679A-263	Sequence 263, App	664	211	5.3	276	1	US-08-978-404B-21	Sequence 21, Appl
592	215.5	5.5	317	3	US-09-907-841-263	Sequence 263, App	665	211	5.3	300	2	US-08-705-875A-4	Sequence 4, Appl
593	215.5	5.5	1428	2	US-09-964-956-33	Sequence 33, Appl	666	211	5.3	300	2	US-09-220-731-21	Sequence 21, Appl
594	215	5.4	389	2	US-10-037-417-131	Sequence 131, App	667	211	5.3	300	2	US-09-242-999-4	Sequence 4, Appl
595	215	5.4	713	3	US-09-949-016-9983	Sequence 9983, App	668	211	5.3	300	2	US-09-644-022A-1	Sequence 1, Appl
596	215	5.4	790	3	US-09-657-431A-1	Sequence 1, Appl	669	211	5.3	433	2	US-09-949-016-9220	Sequence 8220, App
597	215	5.4	791	1	US-09-131-995-1	Sequence 1, Appl	670	211	5.3	1010	2	US-08-882-046-7	Sequence 7, Appl
598	215	5.4	791	1	US-08-833-087B-1	Sequence 1, Appl	671	211	5.3	1010	2	US-09-566-047-7	Sequence 7, Appl
599	215	5.4	791	2	US-09-133-154-1	Sequence 1, Appl	672	211	5.3	1036	2	US-09-068-740A-6	Sequence 6, Appl
600	215	5.4	791	2	US-08-991-761A-6	Sequence 6, Appl	673	211	5.3	1067	2	US-09-578-536C-18	Sequence 18, Appl
601	215	5.4	791	2	US-08-924-287A-1	Sequence 1, Appl	674	211	5.3	1187	2	US-09-068-740A-7	Sequence 7, Appl
602	215	5.4	791	2	US-10-360-101-257	Sequence 257, App	675	211	5.3	1208	2	US-09-199-865-1	Sequence 1, Appl
603	215	5.4	810	1	US-07-854-603-2	Sequence 2, Appl	676	211	5.3	1208	2	US-10-213-329-1	Sequence 1, Appl
604	215	5.4	810	1	US-08-147-000B-29	Sequence 29, Appl	677	211	5.3	1218	1	US-08-400-159-6	Sequence 6, Appl
605	215	5.4	810	2	US-09-086-514-1	Sequence 1, Appl	678	211	5.3	1218	2	US-08-611-729A-6	Sequence 6, Appl
606	215	5.4	810	2	US-09-192-012-5	Sequence 5, Appl	679	211	5.3	1218	2	US-08-882-046-2	Sequence 2, Appl
607	215	5.4	810	2	US-09-403-736-1	Sequence 1, Appl	680	211	5.3	1218	2	US-09-214-278-7	Sequence 7, Appl
608	215	5.4	810	2	US-09-701-265-1	Sequence 1, Appl	681	211	5.3	1218	2	US-09-068-740A-11	Sequence 11, Appl
609	215	5.4	810	3	US-09-946-893C-2	Sequence 2, Appl	682	211	5.3	1218	2	US-09-855-722-7	Sequence 7, Appl
610	214.5	5.4	1428	2	US-09-964-956-34	Sequence 34, Appl	683	211	5.3	1218	2	US-09-566-047-2	Sequence 2, Appl

664	211	5.3	1218	2	US-09-917-254-85	Sequence 85, Appl	757	204.5	5.2	439	2	US-09-949-016-9260	Sequence 9260, Ap
665	211	5.3	1218	2	US-09-195-524-6	Sequence 6, Appl	758	204	5.2	260	2	US-09-070-524-2	Sequence 2, Appl
666	211	5.3	1218	2	US-09-579-536C-1	Sequence 1, Appl	759	204	5.2	260	2	US-09-618-259-7	Sequence 7, Appl
667	211	5.3	1218	2	US-09-949-016-5902	Sequence 5902, Ap	760	204	5.2	260	2	US-09-999-833A-395	Sequence 395, App
668	211	5.3	1218	2	US-09-310-685-4	Sequence 4, Appl	761	204	5.2	260	2	US-10-020-445A-395	Sequence 395, App
669	211	5.3	1234	2	US-09-949-016-10297	Sequence 10297, A	762	204	5.2	260	2	US-09-978-189-395	Sequence 395, App
690	210.5	5.3	245	2	US-09-598-982C-31	Sequence 31, Appl	763	204	5.2	260	2	US-10-017-085A-395	Sequence 395, App
691	210.5	5.3	249	2	US-09-598-982C-23	Sequence 23, Appl	764	204	5.2	260	3	US-08-915-659A-7	Sequence 7, Appl
692	210.5	5.3	418	2	US-09-370-838-62	Sequence 62, Appl	765	204	5.2	260	3	US-10-145-129A-395	Sequence 395, App
693	210.5	5.3	418	2	US-09-854-133-62	Sequence 62, Appl	766	204	5.2	260	3	US-10-013-929A-395	Sequence 395, App
694	210.5	5.3	1219	2	US-08-882-045-5	Sequence 5, Appl	767	204	5.2	260	3	US-09-936-271C-83	Sequence 83, Appl
695	210.5	5.3	1219	2	US-09-566-047-5	Sequence 5, Appl	768	204	5.2	260	3	US-10-013-917A-395	Sequence 395, App
696	210	5.3	154	2	US-09-261-416-5	Sequence 5, Appl	769	203.5	5.2	224	2	US-08-944-483-74	Sequence 34, Appl
697	210	5.3	446	2	US-08-944-483-24	Sequence 24, Appl	770	203.5	5.2	224	3	US-09-410-362F-7	Sequence 39, Appl
698	210	5.3	446	2	US-10-177-661-4	Sequence 4, Appl	771	203.5	5.2	224	3	US-09-410-362F-39	Sequence 39, Appl
699	209.5	5.3	372	3	US-10-162-335-2	Sequence 2, Appl	772	203.5	5.2	249	2	US-09-949-016-8770	Sequence 8770, Ap
700	209.5	5.3	477	2	US-10-177-661-2	Sequence 2, Appl	773	203.5	5.2	3623	2	US-09-341-461-2	Sequence 2, Appl
701	209.5	5.3	562	2	US-09-879-792-12	Sequence 12, Appl	774	203	5.1	283	2	US-08-807-151-1	Sequence 1, Appl
702	208.5	5.3	245	2	US-09-598-982C-29	Sequence 29, Appl	775	203	5.1	283	2	US-09-478-957-1	Sequence 1, Appl
703	208.5	5.3	245	2	US-09-598-982C-47	Sequence 47, Appl	776	202.5	5.1	288	3	US-09-936-271C-73	Sequence 73, Appl
704	208.5	5.3	249	2	US-09-598-982C-21	Sequence 21, Appl	777	202.5	5.1	701	2	US-10-297-895A-19	Sequence 19, Appl
705	208.5	5.3	249	2	US-09-598-982C-39	Sequence 39, Appl	778	202.5	5.1	766	2	US-10-297-895A-21	Sequence 21, Appl
706	208.5	5.3	492	2	US-09-685-166A-895	Sequence 895, App	779	202.5	5.1	927	2	US-10-297-895A-10	Sequence 10, Appl
707	208.5	5.3	492	2	US-09-879-792-14	Sequence 14, Appl	780	202	5.1	2321	2	US-08-230-652-2	Sequence 2, Appl
708	208.5	5.3	492	2	US-09-679-426-895	Sequence 895, App	781	202	5.1	2321	2	US-08-612-826B-2	Sequence 2, Appl
709	208.5	5.3	492	2	US-09-759-143-895	Sequence 895, App	782	200.5	5.1	226	1	US-08-650-129-4	Sequence 4, Appl
710	208.5	5.3	492	2	US-10-012-896-895	Sequence 895, App	783	200.5	5.1	226	2	US-08-984-417-4	Sequence 4, Appl
711	208.5	5.3	492	2	US-10-144-678A-895	Sequence 895, App	784	200.5	5.1	232	1	US-08-278-091-8	Sequence 8, Appl
712	208	5.3	238	2	US-09-856-371A-2	Sequence 2, Appl	785	200.5	5.1	232	1	US-08-483-859-8	Sequence 8, Appl
713	208	5.3	268	1	US-08-270-584A-2	Sequence 2, Appl	786	200.5	5.1	232	1	US-08-472-173-8	Sequence 8, Appl
714	208	5.3	268	1	US-08-765-192-2	Sequence 2, Appl	787	200.5	5.1	232	1	US-08-467-167-8	Sequence 8, Appl
715	208	5.3	268	1	US-09-199-793-2	Sequence 2, Appl	788	200.5	5.1	232	1	US-08-482-816-8	Sequence 8, Appl
716	208	5.3	271	1	US-08-467-155A-10	Sequence 10, Appl	789	200.5	5.1	232	1	US-08-296-149-8	Sequence 8, Appl
717	208	5.3	271	1	US-08-628-198-10	Sequence 10, Appl	790	200.5	5.1	232	1	US-08-801-499-8	Sequence 8, Appl
718	208	5.3	271	2	US-09-201-038-10	Sequence 10, Appl	791	200.5	5.1	232	1	US-08-615-271-8	Sequence 8, Appl
719	208	5.3	271	5	US-10-021-368-10	Sequence 10, Appl	792	200.5	5.1	232	2	US-08-612-826B-2	Sequence 2, Appl
720	208	5.3	271	5	PCT-US96-07343-10	Sequence 10, Appl	793	200.5	5.1	232	2	US-09-074-650-8	Sequence 8, Appl
721	208	5.3	273	2	US-09-856-371A-4	Sequence 4, Appl	794	200.5	5.1	232	2	US-09-106-468-8	Sequence 8, Appl
722	208	5.3	275	2	US-09-856-320A-6	Sequence 6, Appl	795	200.5	5.1	232	2	US-09-106-468A-8	Sequence 8, Appl
723	208	5.3	311	2	US-09-856-371A-6	Sequence 6, Appl	796	200.5	5.1	232	2	US-09-106-467-8	Sequence 8, Appl
724	207.5	5.3	241	2	US-08-944-483-59	Sequence 59, Appl	797	200.5	5.1	247	1	US-08-956-267A-2	Sequence 2, Appl
725	206.5	5.2	245	2	US-09-598-982C-45	Sequence 45, Appl	798	200.5	5.1	314	2	US-09-636-382A-2	Sequence 2, Appl
726	206.5	5.2	249	2	US-09-598-982C-37	Sequence 37, Appl	799	200.5	5.1	415	2	US-09-907-794A-104	Sequence 104, App
727	206.5	5.2	255	1	US-08-650-129-5	Sequence 5, Appl	800	200.5	5.1	415	2	US-09-905-125A-104	Sequence 104, App
728	206.5	5.2	255	2	US-08-984-417-5	Sequence 5, Appl	801	200.5	5.1	415	2	US-09-902-775A-104	Sequence 104, App
729	206.5	5.2	284	2	US-09-387-375-7	Sequence 7, Appl	802	200.5	5.1	415	2	US-09-906-700-104	Sequence 104, App
730	206.5	5.2	284	2	US-10-041-400A-7	Sequence 7, Appl	803	200.5	5.1	415	2	US-09-903-603A-104	Sequence 104, App
731	206.5	5.2	284	2	US-10-042-091A-7	Sequence 7, Appl	804	200.5	5.1	415	2	US-09-904-920A-104	Sequence 104, App
732	206.5	5.2	284	2	US-10-041-264B-7	Sequence 7, Appl	805	200.5	5.1	415	2	US-09-909-064-104	Sequence 104, App
733	206.5	5.2	316	2	US-09-387-375-9	Sequence 9, Appl	806	200.5	5.1	415	2	US-09-905-381A-104	Sequence 104, App
734	206.5	5.2	316	2	US-10-041-400A-9	Sequence 9, Appl	807	200.5	5.1	415	2	US-09-906-618-104	Sequence 104, App
735	206.5	5.2	316	2	US-10-042-091A-9	Sequence 9, Appl	808	200.5	5.1	415	2	US-09-906-646-104	Sequence 104, App
736	206.5	5.2	316	2	US-10-041-264B-9	Sequence 9, Appl	809	200.5	5.1	415	2	US-09-904-462-104	Sequence 104, App
737	206	5.2	275	3	US-09-936-271C-72	Sequence 72, Appl	810	200.5	5.1	415	2	US-09-902-736A-104	Sequence 104, App
738	206	5.2	1185	2	US-09-964-956-7	Sequence 7, Appl	811	200.5	5.1	415	2	US-09-906-722A-104	Sequence 104, App
739	205.5	5.2	235	2	US-08-944-483-48	Sequence 48, Appl	812	200.5	5.1	415	2	US-09-905-449-104	Sequence 104, App
740	205.5	5.2	269	1	US-08-978-404B-10	Sequence 10, Appl	813	200.5	5.1	415	2	US-09-903-562B-104	Sequence 104, App
741	205.5	5.2	270	2	US-10-360-101-231	Sequence 231, App	814	200.5	5.1	415	2	US-09-906-679A-104	Sequence 104, App
742	205.5	5.2	288	2	US-09-386-642-13	Sequence 13, Appl	815	200.5	5.1	415	3	US-09-907-841-104	Sequence 104, App
743	205.5	5.2	327	2	US-09-386-628-8	Sequence 8, Appl	816	200.5	5.1	769	2	US-09-949-016-11019	Sequence 11019, A
744	205.5	5.2	327	2	US-10-040-803-8	Sequence 8, Appl	817	200.5	5.1	810	2	US-08-991-761A-11	Sequence 11, Appl
745	205.5	5.2	360	3	US-10-162-335-14	Sequence 14, Appl	818	200	5.1	110	2	US-09-964-956-69	Sequence 69, Appl
746	205.5	5.2	360	3	US-10-162-335-18	Sequence 18, Appl	819	200	5.1	385	2	US-09-163-951-16	Sequence 16, Appl
747	205.5	5.2	492	2	US-09-342-749-2	Sequence 2, Appl	820	200	5.1	385	3	US-09-345-881-16	Sequence 16, Appl
748	205.5	5.2	492	2	US-09-691-840-2	Sequence 2, Appl	821	200	5.1	385	2	US-10-000-512-14	Sequence 14, Appl
749	205.5	5.2	492	2	US-09-759-143-932	Sequence 932, App	822	199.5	5.1	1193	1	US-08-400-159-10	Sequence 10, Appl
750	205.5	5.2	492	2	US-10-012-896-932	Sequence 932, App	823	199.5	5.1	1193	2	US-08-611-729A-10	Sequence 10, Appl
751	205.5	5.2	492	3	US-10-144-678A-932	Sequence 932, App	824	199.5	5.1	1193	2	US-09-195-524-10	Sequence 10, Appl
752	205.5	5.2	510	2	US-09-949-016-11074	Sequence 11074, A	825	199.5	5.1	1193	2	US-09-310-685-8	Sequence 8, Appl
753	205	5.2	393	2	US-09-759-143-934	Sequence 934, App	826	199.5	5.1	1275	2	US-09-964-956-16	Sequence 16, Appl
754	205	5.2	393	2	US-10-012-896-934	Sequence 934, App	827	199.5	5.1	2556	1	US-08-185-432-17	Sequence 17, Appl
755	204.5	5.2	393	3	US-10-144-678A-934	Sequence 934, App	828	199.5	5.1	2556	1	US-08-083-590A-20	Sequence 20, Appl
756	204.5	5.2	360	3	US-10-162-335-12	Sequence 12, Appl	829	199.5	5.1	2556	2	US-08-532-384-20	Sequence 20, Appl

830	199.5	5.1	2556	2	US-08-899-232-2	Sequence 2, Appl1	903	195.5	5.0	2471	1	US-08-083-590A-19	Sequence 19, Appl1
831	199.5	5.1	2556	2	US-09-121-457-2	Sequence 2, Appl1	904	195.5	5.0	2471	2	US-08-532-384-19	Sequence 19, Appl1
832	199	5.0	249	2	US-09-949-016-8151	Sequence 8151, Ap	905	195.5	5.0	2471	2	US-08-899-232-1	Sequence 1, Appl1
833	199	5.0	260	2	US-09-008-271A-7	Sequence 7, Appl1	906	195.5	5.0	2471	2	US-09-121-457-1	Sequence 1, Appl1
834	199	5.0	260	2	US-09-968-415-7	Sequence 7, Appl1	907	195	4.9	258	3	US-09-936-271C-85	Sequence 85, Appl1
835	199	5.0	278	1	US-08-392-828C-4	Sequence 4, Appl1	908	194.5	4.9	246	1	US-08-978-404B-44	Sequence 44, Appl1
836	199	5.0	278	1	US-09-330-945-4	Sequence 4, Appl1	909	194.5	4.9	341	3	US-10-162-335-20	Sequence 20, Appl1
837	198.5	5.0	223	1	US-08-278-091-9	Sequence 9, Appl1	910	194.5	4.9	415	2	US-09-032-523-2	Sequence 2, Appl1
838	198.5	5.0	223	1	US-08-483-859-9	Sequence 9, Appl1	911	194.5	4.9	415	2	US-09-802-633-2	Sequence 2, Appl1
839	198.5	5.0	223	1	US-08-472-173-9	Sequence 9, Appl1	912	194	4.9	113	2	US-09-438-046-20	Sequence 20, Appl1
840	198.5	5.0	223	1	US-08-487-167-9	Sequence 9, Appl1	913	194	4.9	113	3	US-09-410-362F-26	Sequence 26, Appl1
841	198.5	5.0	223	1	US-08-482-816-9	Sequence 9, Appl1	914	194	4.9	233	2	US-09-821-255-4	Sequence 4, Appl1
842	198.5	5.0	223	1	US-08-296-149-9	Sequence 9, Appl1	915	193.5	4.9	225	2	US-10-036-371-8	Sequence 8, Appl1
843	198.5	5.0	223	1	US-08-801-499-9	Sequence 9, Appl1	916	193	4.9	228	2	US-08-944-483-44	Sequence 44, Appl1
844	198.5	5.0	223	1	US-08-615-271-9	Sequence 9, Appl1	917	193	4.9	228	2	US-10-202-676-6	Sequence 6, Appl1
845	198.5	5.0	223	2	US-09-074-660-9	Sequence 9, Appl1	918	193	4.9	253	3	US-09-936-271C-69	Sequence 69, Appl1
846	198.5	5.0	223	2	US-09-074-659-9	Sequence 9, Appl1	919	193	4.9	253	7	5223425-8	Patent No. 5223425
847	198.5	5.0	223	2	US-09-106-468-9	Sequence 9, Appl1	920	193	4.9	268	2	US-09-032-215-42	Sequence 42, Appl1
848	198.5	5.0	223	2	US-09-106-466A-9	Sequence 9, Appl1	921	192.5	4.9	225	1	US-08-557-146-12	Sequence 12, Appl1
849	198.5	5.0	223	2	US-09-106-467-9	Sequence 9, Appl1	922	192.5	4.9	225	1	US-09-154-344-12	Sequence 12, Appl1
850	198.5	5.0	223	2	US-09-601-318-2	Sequence 2, Appl1	923	192.5	4.9	276	2	US-09-856-320A-4	Sequence 4, Appl1
851	198.5	5.0	229	2	US-09-120-582-2	Sequence 2, Appl1	924	192.5	4.9	281	1	US-08-467-155A-7	Sequence 7, Appl1
852	198.5	5.0	232	1	US-08-978-404B-45	Sequence 45, Appl1	925	192.5	4.9	281	1	US-08-628-198-7	Sequence 7, Appl1
853	198.5	5.0	849	2	US-09-949-016-10271	Sequence 10271, A	926	192.5	4.9	281	2	US-09-201-038-7	Sequence 7, Appl1
854	198	5.0	242	2	US-08-944-483-57	Sequence 57, Appl1	927	192.5	4.9	281	3	US-10-021-368-7	Sequence 7, Appl1
855	197.5	5.0	221	2	US-08-944-483-54	Sequence 54, Appl1	928	192.5	4.9	281	5	PCT-US96-07343-7	Sequence 7, Appl1
856	197.5	5.0	222	1	US-08-456-840-46	Sequence 46, Appl1	929	192	4.9	149	2	US-09-518-046-20	Sequence 20, Appl1
857	197.5	5.0	222	1	US-08-265-407A-46	Sequence 46, Appl1	930	192	4.9	149	2	US-09-650-371-20	Sequence 20, Appl1
858	197.5	5.0	222	1	US-08-892-544-46	Sequence 46, Appl1	931	191.5	4.9	221	2	US-09-959-382-33	Sequence 33, Appl1
859	197.5	5.0	248	2	US-10-012-231A-194	Sequence 194, App	932	191.5	4.9	224	1	US-08-766-982-13	Sequence 13, Appl1
860	197.5	5.0	248	2	US-10-012-389A-194	Sequence 194, App	933	191.5	4.9	224	2	US-08-944-483-36	Sequence 36, Appl1
861	197.5	5.0	248	2	US-10-006-768A-194	Sequence 194, App	934	191.5	4.9	224	2	US-09-296-219-13	Sequence 13, Appl1
862	197.5	5.0	248	2	US-10-015-671A-194	Sequence 194, App	935	191.5	4.9	225	1	US-09-027-337-5	Sequence 5, Appl1
863	197.5	5.0	248	2	US-10-015-393A-194	Sequence 194, App	936	191.5	4.9	225	2	US-09-644-600-5	Sequence 5, Appl1
864	197.5	5.0	248	2	US-10-011-833A-194	Sequence 194, App	937	191.5	4.9	225	2	US-09-654-600A-5	Sequence 5, Appl1
865	197.5	5.0	248	2	US-10-006-041A-194	Sequence 194, App	938	191.5	4.9	225	3	US-09-421-213-5	Sequence 5, Appl1
866	197.5	5.0	248	2	US-10-012-064A-194	Sequence 194, App	939	191.5	4.9	233	2	US-09-636-382A-24	Sequence 24, Appl1
867	197.5	5.0	248	2	US-10-015-392A-194	Sequence 194, App	940	191.5	4.9	247	3	US-09-936-271C-82	Sequence 82, Appl1
868	197.5	5.0	248	3	US-10-011-795B-194	Sequence 194, App	941	191.5	4.9	579	2	US-10-094-749-1884	Sequence 1884, Ap
869	197.5	5.0	248	3	US-09-936-271C-60	Sequence 60, Appl1	942	191.5	4.9	830	1	US-08-110-158-4	Sequence 4, Appl1
870	197.5	5.0	248	3	US-10-015-386A-194	Sequence 194, App	943	191	4.8	250	7	5223425-4	Patent No. 5223425
871	197.5	5.0	248	3	US-10-012-121A-194	Sequence 194, App	944	191	4.8	254	2	US-09-439-313-525	Sequence 525, App
872	197.5	5.0	248	3	US-10-006-485A-194	Sequence 194, App	945	191	4.8	254	2	US-09-636-215-525	Sequence 525, App
873	197.5	5.0	248	3	US-10-006-746A-194	Sequence 194, App	946	191	4.8	254	2	US-09-685-166A-525	Sequence 525, App
874	197.5	5.0	248	3	US-10-012-752A-194	Sequence 194, App	947	191	4.8	254	2	US-09-679-426-525	Sequence 525, App
875	197.5	5.0	248	3	US-10-017-253A-194	Sequence 194, App	948	191	4.8	254	2	US-09-759-143-525	Sequence 525, App
876	197.5	5.0	248	3	US-10-015-519A-194	Sequence 194, App	949	191	4.8	254	2	US-09-651-236-525	Sequence 525, App
877	197.5	5.0	248	3	US-10-015-715A-194	Sequence 194, App	950	191	4.8	254	2	US-09-657-279-525	Sequence 525, App
878	197.5	5.0	248	3	US-10-007-236A-194	Sequence 194, App	951	191	4.8	254	2	US-10-012-896-525	Sequence 525, App
879	197	5.0	338	2	US-08-991-761A-10	Sequence 10, Appl1	952	191	4.8	254	3	US-09-936-271C-3	Sequence 3, Appl1
880	196.5	5.0	241	2	US-08-944-483-60	Sequence 60, Appl1	953	191	4.8	254	3	US-10-144-678A-525	Sequence 525, App
881	196.5	5.0	248	2	US-08-944-483-71	Sequence 71, Appl1	954	191	4.8	455	2	US-09-261-416-2	Sequence 2, Appl1
882	196.5	5.0	300	1	US-08-148-910-1	Sequence 1, Appl1	955	190.5	4.8	241	3	US-09-936-271C-77	Sequence 77, Appl1
883	196.5	5.0	300	1	US-08-448-937A-1	Sequence 1, Appl1	956	190	4.8	253	2	US-10-202-676-4	Sequence 4, Appl1
884	196.5	5.0	360	3	US-10-162-335-16	Sequence 16, Appl1	957	190	4.8	254	3	US-09-936-271C-81	Sequence 81, Appl1
885	196.5	5.0	2523	1	US-08-185-432-18	Sequence 18, Appl1	958	190	4.8	284	2	US-09-386-642-54	Sequence 54, Appl1
886	196.5	5.0	2523	2	US-08-899-232-3	Sequence 3, Appl1	959	189.5	4.8	234	2	US-10-026-606-1	Sequence 1, Appl1
887	196.5	5.0	2523	2	US-09-121-457-3	Sequence 45, Appl1	960	189.5	4.8	341	3	US-10-114-270-132	Sequence 13, App
888	195.5	5.0	232	2	US-08-944-483-45	Sequence 45, Appl1	961	189	4.8	220	3	US-09-439-313-327	Sequence 327, App
889	195.5	5.0	241	1	US-08-330-978-4	Sequence 4, Appl1	962	189	4.8	220	2	US-09-352-616A-327	Sequence 327, App
890	195.5	5.0	241	1	US-08-474-042-4	Sequence 4, Appl1	963	189	4.8	220	2	US-09-232-149A-327	Sequence 327, App
891	195.5	5.0	241	1	US-08-484-558-4	Sequence 4, Appl1	964	189	4.8	220	2	US-09-651-236-327	Sequence 327, App
892	195.5	5.0	241	1	US-08-774-592-4	Sequence 4, Appl1	965	189	4.8	220	2	US-09-636-215-327	Sequence 327, App
893	195.5	5.0	254	1	US-08-330-978-3	Sequence 3, Appl1	966	189	4.8	220	2	US-09-685-166A-327	Sequence 327, App
894	195.5	5.0	254	1	US-08-474-042-3	Sequence 3, Appl1	967	189	4.8	220	2	US-09-688-489-327	Sequence 327, App
895	195.5	5.0	254	1	US-08-484-558-3	Sequence 3, Appl1	968	189	4.8	220	2	US-09-679-426-327	Sequence 327, App
896	195.5	5.0	254	1	US-08-774-592-3	Sequence 3, Appl1	969	189	4.8	220	2	US-09-759-143-327	Sequence 327, App
897	195.5	5.0	306	1	US-08-330-978-1	Sequence 1, Appl1	970	189	4.8	220	2	US-09-651-236-327	Sequence 327, App
898	195.5	5.0	306	1	US-08-474-042-1	Sequence 1, Appl1	971	189	4.8	220	2	US-09-657-279-327	Sequence 327, App
899	195.5	5.0	306	1	US-08-484-558-1	Sequence 1, Appl1	972	189	4.8	220	2	US-10-012-896-327	Sequence 327, App
900	195.5	5.0	306	1	US-08-774-592-1	Sequence 1, Appl1	973	189	4.8	220	2	US-10-144-678A-327	Sequence 327, App
901	195.5	5.0	309	2	US-10-360-101-233	Sequence 233, App	974	189	4.8	225	2	US-08-944-483-33	Sequence 33, Appl1
902	195.5	5.0	2471	1	US-08-185-432-16	Sequence 16, Appl1	975	189	4.8	225	1	US-09-027-337-4	Sequence 4, Appl1

976	189	4.8	225	2	US-09-654-600A-4	Sequence 4, Appli	1049	185.5	4.7	256	2	US-09-032-215-27	Sequence 27, Appli
977	189	4.8	225	3	US-09-421-213-A	Sequence 4, Appli	1050	185.5	4.7	261	2	US-08-163-919A-2	Sequence 2, Appli
978	189	4.8	237	3	US-09-936-271C-2	Sequence 2, Appli	1051	185.5	4.7	261	2	US-08-462-515-2	Sequence 2, Appli
979	189	4.8	238	7	523425-5	Parent No. 523425	1052	185.5	4.7	261	5	PCT-US94-14073-2	Sequence 2, Appli
980	189	4.8	253	1	US-08-557-146-2	Sequence 2, Appli	1053	185.5	4.7	306	2	US-09-366-642-53	Sequence 53, Appli
981	189	4.8	253	1	US-08-824-874-3	Sequence 3, Appli	1054	185.5	4.7	711	1	US-08-184-012C-8	Sequence 8, Appli
982	189	4.8	253	1	US-09-154-344-2	Sequence 2, Appli	1055	185.5	4.7	711	1	US-08-334-177-2	Sequence 1, Appli
983	189	4.8	253	1	US-08-930-188-2	Sequence 2, Appli	1056	185.5	4.7	711	1	US-08-666-082B-1	Sequence 2, Appli
984	189	4.8	253	2	US-09-210-084-3	Sequence 3, Appli	1057	185.5	4.7	711	5	PCT-US95-13830-2	Sequence 2, Appli
985	189	4.8	253	2	US-09-764-762-3	Sequence 3, Appli	1058	185.5	4.7	713	2	US-08-872-855-5	Sequence 5, Appli
986	189	4.8	253	3	US-10-071-214-2	Sequence 2, Appli	1059	185	4.7	247	2	US-08-944-483-49	Sequence 49, Appli
987	189	4.8	253	3	US-10-071-214-2	Sequence 48, Appli	1060	185	4.7	258	1	US-08-744-026-3	Sequence 3, Appli
988	189	4.8	253	5	PCT-US96-04294-2	Sequence 2, Appli	1061	185	4.7	258	1	US-09-102-732-3	Sequence 3, Appli
989	189	4.8	312	2	US-09-949-016-7716	Sequence 7716, Ap	1062	185	4.7	314	2	US-09-261-767-3	Sequence 3, Appli
990	189	4.8	449	2	US-09-023-942A-4	Sequence 4, Appli	1063	185	4.7	314	2	US-09-023-942A-6	Sequence 6, Appli
991	189	4.8	449	2	US-09-636-215-617	Sequence 617, App	1064	184	4.7	144	2	US-09-618-259-1	Sequence 1, Appli
992	189	4.8	449	2	US-09-685-166A-617	Sequence 617, App	1065	184	4.7	144	3	US-08-915-659A-1	Sequence 1, Appli
993	189	4.8	449	2	US-09-679-426-617	Sequence 617, App	1066	184	4.7	314	2	US-09-008-271A-3	Sequence 1, Appli
994	189	4.8	449	2	US-09-759-143-617	Sequence 617, App	1067	184	4.7	314	2	US-09-907-794A-257	Sequence 257, App
995	189	4.8	449	2	US-09-651-236-617	Sequence 617, App	1068	184	4.7	314	2	US-09-905-125A-257	Sequence 257, App
996	189	4.8	449	2	US-09-657-279-617	Sequence 617, App	1069	184	4.7	314	2	US-09-902-775A-257	Sequence 257, App
997	189	4.8	449	2	US-10-012-896-617	Sequence 617, App	1070	184	4.7	314	2	US-09-906-700-257	Sequence 257, App
998	189	4.8	449	3	US-10-144-678A-617	Sequence 617, App	1071	184	4.7	314	2	US-09-903-603A-257	Sequence 257, App
999	189	4.8	585	3	US-10-144-678A-1020	Sequence 1020, Ap	1072	184	4.7	314	2	US-09-904-920A-257	Sequence 257, App
1000	188.5	4.8	290	2	US-09-386-653A-7	Sequence 7, Appli	1073	184	4.7	314	2	US-09-909-064-257	Sequence 257, App
1001	188.5	4.8	290	2	US-10-040-655-7	Sequence 7, Appli	1074	184	4.7	314	2	US-09-905-381A-257	Sequence 257, App
1002	188.5	4.8	228	2	US-10-041-054-7	Sequence 7, Appli	1075	184	4.7	314	2	US-09-906-618-257	Sequence 257, App
1003	188	4.8	228	2	US-09-821-255-2	Sequence 2, Appli	1076	184	4.7	314	2	US-09-906-646-257	Sequence 257, App
1004	188	4.8	248	1	US-08-744-026-1	Sequence 1, Appli	1077	184	4.7	314	2	US-09-968-415-3	Sequence 3, Appli
1005	188	4.8	248	1	US-09-102-732-1	Sequence 1, Appli	1078	184	4.7	314	2	US-09-904-462-257	Sequence 257, App
1006	188	4.8	248	1	US-09-261-767-1	Sequence 1, Appli	1079	184	4.7	314	2	US-09-906-726A-257	Sequence 257, App
1007	188	4.8	249	3	US-09-936-271C-68	Sequence 68, Appli	1080	184	4.7	314	2	US-09-902-722A-257	Sequence 257, App
1008	188	4.8	253	2	US-10-403-676-2	Sequence 2, Appli	1081	184	4.7	314	2	US-09-905-449-257	Sequence 257, App
1009	188	4.8	254	2	US-09-439-313-523	Sequence 523, App	1082	184	4.7	314	2	US-09-903-562B-257	Sequence 257, App
1010	188	4.8	254	2	US-09-636-215-523	Sequence 523, App	1083	184	4.7	314	2	US-09-906-679A-257	Sequence 257, App
1011	188	4.8	254	2	US-09-685-166A-523	Sequence 523, App	1084	184	4.7	314	3	US-09-907-841-257	Sequence 257, App
1012	188	4.8	254	2	US-09-679-426-523	Sequence 523, App	1085	183.5	4.7	502	2	US-10-099-322-140	Sequence 140, App
1013	188	4.8	254	2	US-09-759-143-523	Sequence 523, App	1086	183.5	4.7	502	2	US-08-766-982-2	Sequence 2, Appli
1014	188	4.8	254	2	US-09-651-236-523	Sequence 523, App	1087	183.5	4.7	711	1	US-08-766-982-2	Sequence 14, Appli
1015	188	4.8	254	2	US-09-657-279-523	Sequence 523, App	1088	183.5	4.7	711	2	US-09-296-219-2	Sequence 2, Appli
1016	188	4.8	254	2	US-10-012-896-523	Sequence 523, App	1089	183.5	4.7	711	2	US-09-600-991-10	Sequence 20, Appli
1017	188	4.8	254	3	US-10-144-678A-523	Sequence 523, App	1090	183.5	4.7	711	2	US-09-601-040A-12	Sequence 12, Appli
1018	188	4.8	263	1	US-08-790-137-4	Sequence 4, Appli	1091	183.5	4.7	711	2	US-09-949-016-5981	Sequence 6981, Ap
1019	188	4.8	263	1	US-08-824-874-5	Sequence 5, Appli	1092	183.5	4.7	722	2	US-08-981-392-12	Sequence 12, Appli
1020	188	4.8	263	2	US-08-807-151-5	Sequence 5, Appli	1093	183.5	4.7	722	2	US-09-908-322-12	Sequence 6, Appli
1021	188	4.8	263	2	US-09-210-084-5	Sequence 5, Appli	1094	183	4.6	418	2	US-10-177-661-6	Sequence 8, Appli
1022	188	4.8	263	2	US-09-478-957-5	Sequence 5, Appli	1095	182.5	4.6	258	2	US-09-023-942A-8	Sequence 8, Appli
1023	188	4.8	263	2	US-09-764-762-5	Sequence 5, Appli	1096	182.5	4.6	484	1	US-08-252-493C-9	Sequence 9, Appli
1024	188	4.8	333	2	US-08-991-761A-8	Sequence 8, Appli	1097	182.5	4.6	484	2	US-09-276-197-9	Sequence 9, Appli
1025	187.5	4.8	224	2	US-08-944-483-35	Sequence 35, Appli	1098	182.5	4.6	720	2	US-08-872-855-4	Sequence 4, Appli
1026	187.5	4.8	242	2	US-08-944-483-29	Sequence 29, Appli	1099	182.5	4.6	722	2	US-09-310-685-14	Sequence 14, Appli
1027	187.5	4.8	255	2	US-08-906-769-83	Sequence 83, Appli	1100	182	4.6	405	2	US-09-734-675-2	Sequence 2, Appli
1028	187.5	4.8	255	2	US-08-906-616-83	Sequence 83, Appli	1101	182	4.6	405	2	US-10-060-333-2	Sequence 2, Appli
1029	187.5	4.8	255	2	US-08-817-795-83	Sequence 83, Appli	1102	182	4.6	721	2	US-08-872-855-7	Sequence 7, Appli
1030	187.5	4.8	255	2	US-08-633-075A-83	Sequence 83, Appli	1103	182	4.6	1055	2	US-09-214-278-2	Sequence 2, Appli
1031	187.5	4.8	255	2	US-09-012-431-83	Sequence 83, Appli	1104	182	4.6	1055	2	US-08-855-722-5	Sequence 5, Appli
1032	187.5	4.8	255	2	US-09-012-692-83	Sequence 83, Appli	1105	182	4.6	1065	1	US-08-400-159-8	Sequence 8, Appli
1033	187.5	4.8	255	2	US-08-906-613-83	Sequence 83, Appli	1106	182	4.6	1212	2	US-09-214-278-3	Sequence 3, Appli
1034	187.5	4.8	255	5	PCT-US95-14442A-83	Sequence 83, Appli	1107	182	4.6	1212	2	US-09-855-722-3	Sequence 3, Appli
1035	187	4.7	296	3	US-09-936-271C-22	Sequence 22, Appli	1108	182	4.6	1238	2	US-09-214-278-5	Sequence 5, Appli
1036	187	4.7	693	3	US-10-297-895A-20	Sequence 20, Appli	1109	182	4.6	1238	2	US-09-855-722-5	Sequence 5, Appli
1037	187	4.7	1004	3	US-10-114-270-32	Sequence 32, Appli	1110	182	4.6	1257	2	US-08-618-198-8	Sequence 8, Appli
1038	186	4.7	110	2	US-09-341-461-28	Sequence 28, Appli	1111	182	4.6	1257	2	US-09-195-524-8	Sequence 8, Appli
1039	186	4.7	230	1	US-08-456-840-47	Sequence 47, Appli	1112	182	4.6	1257	2	US-09-310-685-6	Sequence 6, Appli
1040	186	4.7	230	1	US-08-266-407A-47	Sequence 47, Appli	1113	181.5	4.6	1257	2	US-07-990-301A-2	Sequence 2, Appli
1041	186	4.7	230	1	US-08-892-544-47	Sequence 47, Appli	1114	181.5	4.6	299	1	US-08-467-155A-8	Sequence 8, Appli
1042	186	4.7	230	1	US-08-766-982-12	Sequence 12, Appli	1115	181.5	4.6	299	1	US-08-628-198-8	Sequence 8, Appli
1043	186	4.7	230	2	US-08-944-483-53	Sequence 53, Appli	1116	181.5	4.6	299	2	US-09-201-038-8	Sequence 8, Appli
1044	186	4.7	230	2	US-09-296-219-12	Sequence 12, Appli	1117	181.5	4.6	299	3	PCT-US96-07343-8	Sequence 8, Appli
1045	186	4.7	232	1	US-08-897-340-31	Sequence 31, Appli	1118	181.5	4.6	257	3	US-09-936-271C-87	Sequence 87, Appli
1046	186	4.7	232	2	US-09-252-329-31	Sequence 31, Appli	1119	181	4.6	396	2	US-09-800-729-86	Sequence 86, Appli
1047	186	4.7	326	2	US-09-411-977-3	Sequence 3, Appli	1120	180	4.6	249	3	US-09-071-214-47	Sequence 47, Appli
1048	186	4.7	326	2	US-10-057-951-3	Sequence 3, Appli	1121	180	4.6	249	3	US-10-071-214-47	Sequence 47, Appli

1122	180	4.6	254	2	US-09-949-016-6948	Sequence 6948, App	1195	176.5	4.5	909	2	US-09-439-711C-10	Sequence 10, Appl
1123	180	4.6	254	2	US-09-936-271C-59	Sequence 59, Appl	1196	176.5	4.5	914	2	US-08-936-135-12	Sequence 12, Appl
1124	180	4.6	254	3	5223425-10	Patent No. 5223425	1197	176.5	4.5	914	2	US-09-439-711C-12	Sequence 12, Appl
1125	179.5	4.6	205	2	US-09-020-956-176	Sequence 176, App	1198	176.5	4.5	925	2	US-09-11C-473-2	Sequence 2, Appl
1126	179.5	4.6	205	2	US-09-030-607-176	Sequence 176, App	1199	176.5	4.5	926	2	US-08-936-135-14	Sequence 14, Appl
1127	179.5	4.6	205	2	US-09-439-313-176	Sequence 176, App	1200	176.5	4.5	926	2	US-09-439-711C-14	Sequence 14, Appl
1128	179.5	4.6	205	2	US-09-352-616A-176	Sequence 176, App	1201	176.5	4.5	931	2	US-08-936-135-16	Sequence 16, Appl
1129	179.5	4.6	205	2	US-09-232-149A-176	Sequence 176, App	1202	176.5	4.5	931	2	US-09-439-711C-16	Sequence 16, Appl
1130	179.5	4.6	205	2	US-09-159-812-176	Sequence 176, App	1203	176	4.5	233	2	US-09-004-731-17	Sequence 27, Appl
1131	179.5	4.6	205	2	US-09-636-215-176	Sequence 176, App	1204	176	4.5	233	2	US-08-749-699-27	Sequence 27, Appl
1132	179.5	4.6	205	2	US-09-685-166A-176	Sequence 176, App	1205	176	4.5	233	2	US-09-004-729-27	Sequence 27, Appl
1133	179.5	4.6	205	2	US-09-115-453-176	Sequence 176, App	1206	176	4.5	242	2	US-08-944-483-58	Sequence 58, Appl
1134	179.5	4.6	205	2	US-09-688-489-176	Sequence 176, App	1207	176	4.5	266	2	US-09-004-731-24	Sequence 24, Appl
1135	179.5	4.6	205	2	US-09-679-426-176	Sequence 176, App	1208	176	4.5	266	2	US-08-749-699-24	Sequence 24, Appl
1136	179.5	4.6	205	2	US-09-759-143-176	Sequence 176, App	1209	176	4.5	266	2	US-09-004-729-24	Sequence 24, Appl
1137	179.5	4.6	205	2	US-09-651-236-176	Sequence 176, App	1210	175.5	4.4	243	3	US-10-071-214-46	Sequence 46, Appl
1138	179.5	4.6	205	2	US-09-030-606-176	Sequence 176, App	1211	175.5	4.4	921	2	US-09-439-711C-4	Sequence 4, Appl
1139	179.5	4.6	205	2	US-09-657-279-176	Sequence 176, App	1212	175	4.4	112	2	US-09-438-046-21	Sequence 21, Appl
1140	179.5	4.6	205	2	US-10-012-896-176	Sequence 176, App	1213	175	4.4	909	2	US-08-936-135-18	Sequence 18, Appl
1141	179.5	4.6	205	3	US-09-116-134-176	Sequence 176, App	1214	175	4.4	909	2	US-09-439-711C-18	Sequence 18, Appl
1142	179.5	4.6	205	3	US-10-144-678A-176	Sequence 176, App	1215	175	4.4	926	2	US-08-936-135-20	Sequence 20, Appl
1143	179.5	4.6	250	3	US-09-936-271C-23	Sequence 23, Appl	1216	175	4.4	926	2	US-09-439-711C-20	Sequence 20, Appl
1144	179.5	4.6	259	7	5223425-2	Patent No. 5223425	1217	175	4.4	931	2	US-09-583-638-4	Sequence 4, Appl
1145	179.5	4.6	728	2	US-08-981-392-2	Sequence 2, Appl	1218	174	4.4	265	1	US-08-177-109A-57	Sequence 57, Appl
1146	179.5	4.6	728	2	US-09-908-322-2	Sequence 2, Appl	1219	174	4.4	265	1	US-08-687-706-57	Sequence 57, Appl
1147	179.5	4.6	728	2	US-09-310-685-11	Sequence 11, Appl	1220	174	4.4	286	1	US-08-467-155A-9	Sequence 9, Appl
1148	179.5	4.6	830	5	PCT-US91-05059-2	Sequence 2, Appl	1221	174	4.4	286	1	US-08-628-198-9	Sequence 9, Appl
1149	179.5	4.6	230	1	US-08-1379-621-2	Sequence 2, Appl	1222	174	4.4	286	2	US-09-201-038-9	Sequence 9, Appl
1150	179	4.5	230	1	US-08-147-000B-2	Sequence 2, Appl	1223	174	4.4	286	3	US-10-021-368-9	Sequence 9, Appl
1151	179	4.5	230	1	US-08-889-078-2	Sequence 2, Appl	1224	174	4.4	286	5	PCT-US96-07343-9	Sequence 9, Appl
1152	179	4.5	253	2	US-09-578-303-4	Sequence 4, Appl	1225	173.5	4.4	230	2	US-10-360-101-222	Sequence 22, App
1153	179	4.5	384	2	US-09-032-215-22	Sequence 22, App	1226	173.5	4.4	294	2	US-09-800-729-146	Sequence 146, App
1154	178.5	4.5	250	2	US-08-944-483-68	Sequence 68, App	1227	173.5	4.4	294	2	US-10-067-422-12	Sequence 12, Appl
1155	178.5	4.5	315	2	US-09-386-653A-9	Sequence 9, Appl	1228	173.5	4.4	717	2	US-08-270-767-46426	Sequence 46426, A
1156	178.5	4.5	315	2	US-10-040-655-9	Sequence 9, Appl	1229	173.5	4.4	414	2	US-08-872-855-9	Sequence 9, Appl
1157	178.5	4.5	315	2	US-10-041-054-9	Sequence 9, Appl	1230	173	4.4	211	2	US-09-220-731-25	Sequence 25, Appl
1158	178.5	4.5	401	1	US-08-839-008-5	Sequence 5, Appl	1231	173	4.4	449	1	US-09-242-999-20	Sequence 20, Appl
1159	178.5	4.5	468	1	US-08-839-008-7	Sequence 7, Appl	1232	172.5	4.4	449	1	US-08-839-008-2	Sequence 2, Appl
1160	178.5	4.5	468	2	US-09-033-523-8	Sequence 8, Appl	1233	172.5	4.4	449	2	US-09-919-497-89	Sequence 89, Appl
1161	178.5	4.5	468	2	US-09-802-633-8	Sequence 8, Appl	1234	172.5	4.4	449	2	US-09-949-016-7238	Sequence 7238, App
1162	178.5	4.5	922	2	US-09-116-473-4	Sequence 4, Appl	1235	172.5	4.4	458	2	US-09-999-833A-132	Sequence 132, App
1163	178.5	4.5	923	2	US-08-936-135-6	Sequence 6, Appl	1236	172.5	4.4	571	2	US-10-020-445A-132	Sequence 132, App
1164	178.5	4.5	923	2	US-09-439-711C-6	Sequence 6, Appl	1237	172.5	4.4	571	2	US-09-978-189-132	Sequence 132, App
1165	177.5	4.5	248	1	US-08-851-974-3	Sequence 3, Appl	1238	172.5	4.4	571	2	US-10-017-085A-132	Sequence 132, App
1166	177.5	4.5	248	1	US-09-213-390-3	Sequence 3, Appl	1239	172.5	4.4	571	2	US-10-145-129A-132	Sequence 132, App
1167	177.5	4.5	1964	2	US-09-467-997-1	Sequence 7, Appl	1240	172.5	4.4	571	3	US-10-013-929A-132	Sequence 132, App
1168	177	4.5	102	2	US-09-374-135-7	Sequence 7, Appl	1241	172.5	4.4	571	3	US-10-013-929A-132	Sequence 132, App
1169	177	4.5	110	2	US-09-341-461-29	Sequence 29, Appl	1242	172.5	4.4	571	3	US-10-013-917A-132	Sequence 6, Appl
1170	177	4.5	112	3	US-09-410-362F-27	Sequence 27, Appl	1243	172.5	4.4	1248	2	US-08-882-046-6	Sequence 6, Appl
1171	177	4.5	223	2	US-09-270-767-45768	Sequence 45768, A	1244	172.5	4.4	250	2	US-09-566-047-6	Sequence 3709, A
1172	177	4.5	240	1	US-08-278-091-11	Sequence 11, Appl	1245	172	4.4	357	2	US-09-270-767-33709	Sequence 43564, A
1173	177	4.5	240	1	US-08-483-859-11	Sequence 11, Appl	1246	172	4.4	357	2	US-09-270-767-33564	Sequence 58936, A
1174	177	4.5	240	1	US-08-472-173-11	Sequence 11, Appl	1247	172	4.4	721	2	US-08-981-392-5	Sequence 5, Appl
1175	177	4.5	240	1	US-08-487-167-11	Sequence 11, Appl	1248	172	4.4	721	2	US-09-904-483-19	Sequence 39, Appl
1176	177	4.5	240	1	US-08-482-816-11	Sequence 11, Appl	1249	172	4.4	721	2	US-08-944-483-19	Sequence 190, App
1177	177	4.5	240	1	US-08-296-149-11	Sequence 11, Appl	1250	171.5	4.3	259	2	US-08-906-769-190	Sequence 190, App
1178	177	4.5	240	1	US-08-801-489-11	Sequence 11, Appl	1251	171.5	4.3	259	2	US-08-906-616-190	Sequence 190, App
1179	177	4.5	240	1	US-08-615-271-11	Sequence 11, Appl	1252	171.5	4.3	259	2	US-08-639-075A-190	Sequence 190, App
1180	177	4.5	240	1	US-09-074-660-11	Sequence 11, Appl	1253	171.5	4.3	259	2	US-09-004-731-85	Sequence 85, Appl
1181	177	4.5	240	1	US-09-074-659-11	Sequence 11, Appl	1254	171.5	4.3	259	2	US-09-012-431-190	Sequence 190, App
1182	177	4.5	240	2	US-09-106-468-11	Sequence 11, Appl	1255	171.5	4.3	259	2	US-08-749-699-85	Sequence 85, Appl
1183	177	4.5	240	2	US-09-106-466A-11	Sequence 11, Appl	1256	171.5	4.3	259	2	US-08-692-190	Sequence 190, App
1184	177	4.5	729	2	US-09-106-467-11	Sequence 8, Appl	1257	171.5	4.3	259	2	US-08-906-613-190	Sequence 190, App
1185	177	4.5	830	7	5378464-2	Patent No. 5378464	1258	171.5	4.3	259	2	US-09-004-729-85	Sequence 85, Appl
1186	177	4.5	232	1	US-09-990-301A-4	Sequence 4, Appl	1259	171.5	4.3	262	1	US-08-790-137-1	Sequence 1, Appl
1187	176.5	4.5	901	2	US-08-936-135-22	Sequence 22, Appl	1261	171.5	4.3	262	1	US-08-790-137-1	Sequence 3, Appl
1188	176.5	4.5	901	2	US-09-439-711C-22	Sequence 22, Appl	1262	171.5	4.3	262	1	US-08-601-151-4	Sequence 4, Appl
1189	176.5	4.5	906	2	US-08-936-135-24	Sequence 24, Appl	1263	171.5	4.3	262	1	US-08-824-874-4	Sequence 4, Appl
1190	176.5	4.5	906	2	US-09-439-711C-24	Sequence 24, Appl	1264	171.5	4.3	262	2	US-08-807-151-4	Sequence 4, Appl
1191	176.5	4.5	906	2	US-08-936-135-8	Sequence 8, Appl	1265	171.5	4.3	262	2	US-09-210-084-4	Sequence 4, Appl
1192	176.5	4.5	909	2	US-08-936-135-10	Sequence 10, Appl	1266	171.5	4.3	262	2	US-09-478-957-4	Sequence 4, Appl
1193	176.5	4.5	909	2	US-09-439-711C-8	Sequence 8, Appl	1267	171.5	4.3	262	2	US-09-764-762-4	Sequence 4, Appl

1268	171.5	4.3	262	2	US-09-618-259-9	Sequence 9, Appl1	1341	166	4.2	237	2	US-09-100-264-3	Sequence 3, Appl1
1269	171.5	4.3	666	2	US-09-341-587-1	Sequence 1, Appl1	1342	166	4.2	237	2	US-09-303-339-2	Sequence 2, Appl1
1270	171.5	4.3	1785	2	US-09-341-587-3	Sequence 3, Appl1	1343	166	4.2	237	2	US-08-843-076D-7	Sequence 7, Appl1
1271	171	4.3	256	3	US-09-936-271C-44	Sequence 44, Appl1	1344	166	4.2	237	2	US-09-303-208-1	Sequence 1, Appl1
1272	171	4.3	262	2	US-09-025-059-4	Sequence 4, Appl1	1345	166	4.2	243	2	US-08-944-483-70	Sequence 70, Appl1
1273	171	4.3	262	2	US-09-755-100A-14	Sequence 14, Appl1	1346	166	4.2	241	2	US-09-949-016-10792	Sequence 10792, A
1274	171	4.3	287	3	US-09-936-271C-45	Sequence 45, Appl1	1347	166	4.2	923	2	US-09-439-711C-2	Sequence 2, Appl1
1275	171	4.3	287	3	US-09-270-767-33263	Sequence 33263, A	1348	165.5	4.2	240	1	US-08-472-228A-1	Sequence 1, Appl1
1276	171	4.3	287	2	US-09-270-767-48480	Sequence 48480, A	1349	165.5	4.2	240	2	US-09-146-831-1	Sequence 1, Appl1
1277	171	4.3	290	2	US-09-949-016-8166	Sequence 8166, Ap	1350	165.5	4.2	240	5	PCT-US96-09303-1	Sequence 1, Appl1
1278	171	4.3	717	2	US-09-601-040A-6	Sequence 6, Appl1	1351	165.5	4.2	383	1	US-08-597-545-2	Sequence 2, Appl1
1279	171	4.3	729	2	US-09-601-040A-2	Sequence 2, Appl1	1352	165.5	4.2	383	1	US-08-457-135-2	Sequence 2, Appl1
1280	171	4.3	737	2	US-09-866-028-15	Sequence 15, Appl1	1353	165	4.2	101	2	US-09-374-135-4	Sequence 4, Appl1
1281	171	4.3	737	2	US-09-944-457-15	Sequence 15, Appl1	1354	164	4.2	351	2	US-09-245-041-11	Sequence 11, Appl1
1282	171	4.3	737	2	US-09-945-584-15	Sequence 15, Appl1	1355	164	4.2	351	2	US-09-358-058B-11	Sequence 11, Appl1
1283	171	4.3	737	2	US-09-944-944-15	Sequence 15, Appl1	1356	164	4.2	351	2	US-09-893-238-11	Sequence 11, Appl1
1284	171	4.3	737	2	US-09-945-587-15	Sequence 15, Appl1	1357	164	4.2	812	2	US-09-132-012-9	Sequence 9, Appl1
1285	171	4.3	737	3	US-09-944-884-15	Sequence 15, Appl1	1358	163.5	4.1	267	3	US-10-000-512-4	Sequence 4, Appl1
1286	170	4.3	213	2	US-08-906-769-149	Sequence 149, App	1359	163	4.1	441	2	US-09-949-016-11196	Sequence 11196, A
1287	170	4.3	213	2	US-08-906-616-149	Sequence 149, App	1360	163	4.1	607	2	US-09-907-794A-190	Sequence 190, App
1288	170	4.3	213	2	US-08-639-075A-149	Sequence 149, App	1361	163	4.1	607	2	US-09-905-125A-190	Sequence 190, App
1289	170	4.3	213	2	US-09-012-431-149	Sequence 149, App	1362	163	4.1	607	2	US-09-902-775A-190	Sequence 190, App
1290	170	4.3	213	2	US-09-012-692-149	Sequence 149, App	1363	163	4.1	607	2	US-09-906-700-190	Sequence 190, App
1291	170	4.3	213	2	US-08-906-613-149	Sequence 149, App	1364	163	4.1	607	2	US-09-903-603A-190	Sequence 190, App
1292	170	4.3	717	2	US-09-601-040A-8	Sequence 8, Appl1	1365	163	4.1	607	2	US-09-904-920A-190	Sequence 190, App
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1294	170	4.3	1148	2	US-08-882-046-4	Sequence 4, Appl1	1367	163	4.1	607	2	US-09-905-381A-190	Sequence 190, App
1295	170	4.3	1148	2	US-09-566-047-4	Sequence 4, Appl1	1368	163	4.1	607	2	US-09-906-618-190	Sequence 190, App
1296	169	4.3	95	2	US-09-374-135-8	Sequence 8, Appl1	1369	163	4.1	607	2	US-09-906-646-190	Sequence 190, App
1297	169	4.3	110	2	US-09-341-461-25	Sequence 25, Appl1	1370	163	4.1	607	2	US-09-904-462-190	Sequence 190, App
1298	169	4.3	237	5	US-08-096-946-11	Sequence 11, Appl1	1371	163	4.1	607	2	US-09-902-736A-190	Sequence 190, App
1299	169	4.3	237	5	PCT-US94-07329-11	Sequence 11, Appl1	1372	163	4.1	607	2	US-09-906-722A-190	Sequence 190, App
1300	169	4.3	237	5	PCT-US95-06157-1	Sequence 11, Appl1	1373	163	4.1	607	2	US-09-905-449-190	Sequence 190, App
1301	169	4.3	375	2	US-09-755-100A-11	Sequence 11, Appl1	1374	163	4.1	607	2	US-09-903-562B-190	Sequence 190, App
1302	169	4.3	721	2	US-09-310-685-123	Sequence 12, Appl1	1375	163	4.1	607	2	US-09-906-679A-190	Sequence 190, App
1303	169	4.3	869	2	US-10-104-047-2532	Sequence 2532, Ap	1376	163	4.1	607	3	US-09-907-841-190	Sequence 190, App
1304	168.5	4.3	222	7	5223425-6	Patent No. 5223425	1377	162.5	4.1	1290	1	US-08-470-350B-2	Sequence 2, Appl1
1305	168.5	4.3	383	2	US-09-142-027A-12	Sequence 12, Appl1	1378	161.5	4.1	251	2	US-08-944-483-87	Sequence 28, Appl1
1306	168.5	4.3	470	2	US-10-915-160-4	Sequence 4, Appl1	1379	161.5	4.1	832	2	US-08-981-392-6	Sequence 6, Appl1
1307	168	4.3	245	2	US-08-906-769-121	Sequence 121, App	1380	161.5	4.1	832	2	US-09-908-122-6	Sequence 6, Appl1
1308	168	4.3	245	2	US-08-906-616-121	Sequence 121, App	1381	161.5	4.1	1025	2	US-08-834-309-5	Sequence 5, Appl1
1309	168	4.3	245	2	US-08-639-075A-121	Sequence 121, App	1382	161	4.1	270	2	US-09-949-016-7712	Sequence 7712, Ap
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; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Bacon, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottlieb, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Gurney, Auelin L.
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; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
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; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
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Db 181 YVEVRDGDNDGQIIKKEVCNERPAPIQISGSLHVLPHSDGSKNPFDFHAIYEITACS 240

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Db 241 SSPCFHDGTCVLDKASGYKCAAGYTGRCENILBERNCSDPGGPVNGYOKITGGPGLI 300

Qy 301 NGRHAKIGTVSFCNNNSYVLSGNEKRTCOONGSWSKOPCIACAEKPKISDLVRRRLV 360
Db 301 NGRHAKIGTVSFCNNNSYVLSGNEKRTCOONGSWSKOPCIACAEKPKISDLVRRRLV 360

Qy 361 PMQVQSRETPLHQLYSAFSAFKQKLSAPTKKPALPFGLDPMQYQHLHTOLQYECISPFYR 420
Db 361 PMQVQSRETPLHQLYSAFSAFKQKLSAPTKKPALPFGLDPMQYQHLHTOLQYECISPFYR 420

Qy 421 RLGSSRRRTCLRTGKMSGRADSCIPICGKIENITAPKTQGLRMPWQAAIYRRTSGVHDGSL 480

|||||
Db 421 RLGSRRRLCLRGKMGKSGAPSCIPICGKXENITAPKTOGLFMPQAAIYRRTSGVHDSGL 480
Qy 481 HKGAFLVCSGALVNERIVVAHCVTDLGKVTMKTADLKVLDKFPDRDDRDERTIOS 540
Db 481 HKGAFLVCSGALVNERIVVAHCVTDLGKVTMKTADLKVLDKFPDRDDRDERTIOS 540
Qy 541 LQISAILHPNVPILDLADIALILKLDKARISTVOPICLAASRDLSTSFQESHITVAG 600
Db 541 LQISAILHPNVPILDLADIALILKLDKARISTVOPICLAASRDLSTSFQESHITVAG 600
Qy 601 WNVLDVSPGFKNDTLASGVSVVDSLICFQEHEDHGI PVSVTDNMFCAWSPEPTAPSDI 660
Db 601 WNVLDVSPGFKNDTLASGVSVVDSLICFQEHEDHGI PVSVTDNMFCAWSPEPTAPSDI 660
Qy 661 CTAEFGIAAVSPFRASPEPRMHLGLVSWSYDXTCSHRLSTATKYLFPEDWIERMVK 720
Db 661 CTAEFGIAAVSPFRASPEPRMHLGLVSWSYDXTCSHRLSTATKYLFPEDWIERMVK 720

RESULT 3

US-09-997-333-231
Sequence 231, Application US/09997333
Patent No. 6953836
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrare, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Goddard, Audrey E.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC27
CURRENT APPLICATION NUMBER: US/09/997.333
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982

PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3945; DB 2; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELGWTQGLTPTQLLLISLPREYTYINACGAEWNIMCRECEYDQIECVCPGRE 60
DB 1 MELGWTQGLTPTQLLLISLPREYTYINACGAEWNIMCRECEYDQIECVCPGRE 60

QY 61 VVGTTTPCCRNENBDCSLHPGCTTFENCKSGRNSWGCTLDDFYKGYTCACRAGW 120
DB 61 VVGTTTPCCRNENBDCSLHPGCTTFENCKSGRNSWGCTLDDFYKGYTCACRAGW 120

QY 121 YGDCMRCGOVLRPKQIILLESYPLNAGHGWTHAKRGFVIOIRFWMLSLFPYMCYD 180
DB 121 YGDCMRCGOVLRPKQIILLESYPLNAGHGWTHAKRGFVIOIRFWMLSLFPYMCYD 180

QY 181 YVEVRDGNRDGOIIRKVCNERPAPIQSIGSSLHVLPHSDSKNFDGFHAYEITACS 240
DB 181 YVEVRDGNRDGOIIRKVCNERPAPIQSIGSSLHVLPHSDSKNFDGFHAYEITACS 240

QY 241 SSPCFHDSCTVLDAGSYKCACLAGYQRCENLLEBRNCSDPGPNVNGYOKITGGPGLI 300
DB 241 SSPCFHDSCTVLDAGSYKCACLAGYQRCENLLEBRNCSDPGPNVNGYOKITGGPGLI 300

QY 301 NGRHAKIGTVSPFCNNSYVLSGNEKRTCOONGEMSGKOPICIRACKEPKISDLVRRVL 360
DB 301 NGRHAKIGTVSPFCNNSYVLSGNEKRTCOONGEMSGKOPICIRACKEPKISDLVRRVL 360

QY 361 PMQVOSRETPHQLYSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSA 420
DB 361 PMQVOSRETPHQLYSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSA 420

QY 421 RLSSSRTCLRTGWSGAPSCIPICGKIENITAPKTQGLRWPQAAIYRTSGVHGS 480
DB 421 RLSSSRTCLRTGWSGAPSCIPICGKIENITAPKTQGLRWPQAAIYRTSGVHGS 480

QY 481 HKGAMFLVCSGALVNERTVVAACHVTDLGKVTMIKADLVVAGKYYRDDREKTIQS 540
DB 481 HKGAMFLVCSGALVNERTVVAACHVTDLGKVTMIKADLVVAGKYYRDDREKTIQS 540

QY 541 LQISAILHPNYDILLADADIAIKLADKARISTRVOPICLAARDLSTFSQESHITVAG 600
DB 541 LQISAILHPNYDILLADADIAIKLADKARISTRVOPICLAARDLSTFSQESHITVAG 600

QY 601 WNVLADYRSPGFKNDTIRSGVSVVDSLLCEQHEDHGIPVSVTDNMFCAWSEPTASDI 660
DB 601 WNVLADYRSPGFKNDTIRSGVSVVDSLLCEQHEDHGIPVSVTDNMFCAWSEPTASDI 660

QY 661 CTATGTGIAVSPFGRAPEPRMHLMLGVSYSYKTSRSTAFYVLPKDIERNMK 720
DB 661 CTATGTGIAVSPFGRAPEPRMHLMLGVSYSYKTSRSTAFYVLPKDIERNMK 720

RESULT 4
US-09-992-598-231
Sequence 231, Application US/0992598
Patent No. 6956108
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Bacon, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottlieb, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Klievin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunes, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC20
CURRENT FILING DATE: 2001-11-14
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/049787
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PRIOR APPLICATION NUMBER: 60/065186
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PRIOR FILING DATE: 1998-02-25
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PRIOR FILING DATE: 1998-03-20
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PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-06-24

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;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3945; DB 2; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELGQWTLGLTFLQLLLISSLPREYVINEACPGAEWNIMRECEYDQIECVGPGRE 60
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DB 61 VVGVTYPCCRNENECDSCLHPGCTIFENCKSCNNGSGTLDLPFYVKGFCACRAGW 120
QY 121 YGGDCMRGQYLRAKQIILLESYPLNAHCWETTHAKPGFVQLRFLWLSLEFDYMCQYD 180
DB 121 YGGDCMRGQYLRAKQIILLESYPLNAHCWETTHAKPGFVQLRFLWLSLEFDYMCQYD 180
QY 181 YVEVRDGNRQGOIILKRVCGNERPAPISIGSSLHLVLFHSQSKNPDGFHAIEETIACS 240
DB 181 YVEVRDGNRQGOIILKRVCGNERPAPISIGSSLHLVLFHSQSKNPDGFHAIEETIACS 240
QY 241 SSPCFHDGTCVLDKAGSYKACLAGYTGORCENLLEERNCSDPGAPVANGYQKITGPGILI 300
DB 241 SSPCFHDGTCVLDKAGSYKACLAGYTGORCENLLEERNCSDPGAPVANGYQKITGPGILI 300
QY 301 NGRNAKIGTVVSFCNNNSYVLSGNEKRTCOQNGEMSKQPTICAKCREPKISDLVRRVL 360
DB 301 NGRNAKIGTVVSFCNNNSYVLSGNEKRTCOQNGEMSKQPTICAKCREPKISDLVRRVL 360
QY 361 PMOVOSRETPHOLYSAFSSKXLOAPTKKPALEPGSLPMGYOHLHOLQECISPPYR 420
DB 361 PMOVOSRETPHOLYSAFSSKXLOAPTKKPALEPGSLPMGYOHLHOLQECISPPYR 420
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DB 421 RLGSRRRTCLRTGKMSGAPSCIPICGKIENITAPKTQGLRMPQAAIYRRRTSGVHDSL 480
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DB 481 HKGAMFLVCSGALVNERVTVVAHCVTDLGKVTMIKTADLVKVLGKPYRDDRDREKTIQS 540
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QY 661 CTAETGGIAVSPGGRASPEPRMHLMLVSWSYDKTCSHRLSTAFKTLPRKOWIERNMK 720
DB 661 CTAETGGIAVSPGGRASPEPRMHLMLVSWSYDKTCSHRLSTAFKTLPRKOWIERNMK 720

RESULT 6
US-09-989-726-231
Sequence 231, Application US/09989726
Patent No. 7018811

;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Bocstein, David
;; APPLICANT: Deanoys, Luc
;; APPLICANT: Eacon, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Getlicsen, Mary E.
;; APPLICANT: Goddard, Audrey

;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kijaviri, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Thomas, Daniel
;; APPLICANT: Macanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; TITLE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: P2730P1C60
;; CURRENT APPLICATION NUMBER: US/09/989, 726
;; PRIOR FILING DATE: 2001-11-19
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;; PRIOR FILING DATE: 1998-02-25
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3945; DB 3; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 YGDCMRCGQVLRAPKQOILLESYPLNAHCEWTTHAKGFVITQLRFWMLSLFPDYMCOYD 180
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QY 121 YGDCMRCGQVLRAPKQOILLESYPLNAHCEWTTHAKGFVITQLRFWMLSLFPDYMCOYD 180
DB 121 YGDCMRCGQVLRAPKQOILLESYPLNAHCEWTTHAKGFVITQLRFWMLSLFPDYMCOYD 180
QY 181 YVEVRDGDNRDQOILIKVCGNERBAPIOISIGSSLHVLPHSDGSXNPDGFHAIYEBITACS 240
DB 181 YVEVRDGDNRDQOILIKVCGNERBAPIOISIGSSLHVLPHSDGSXNPDGFHAIYEBITACS 240
QY 181 YVEVRDGDNRDQOILIKVCGNERBAPIOISIGSSLHVLPHSDGSXNPDGFHAIYEBITACS 240
DB 181 YVEVRDGDNRDQOILIKVCGNERBAPIOISIGSSLHVLPHSDGSXNPDGFHAIYEBITACS 240
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DB 241 SSPFHGTCYLDAAAGSYKACCLAGYTGRCENLLEBRNCSDPGAPVNGYOKITGGPELI 300
QY 241 SSPFHGTCYLDAAAGSYKACCLAGYTGRCENLLEBRNCSDPGAPVNGYOKITGGPELI 300
DB 241 SSPFHGTCYLDAAAGSYKACCLAGYTGRCENLLEBRNCSDPGAPVNGYOKITGGPELI 300
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QY 301 NGRHAKIGTVVSPFCNNNSYVLGNEKRTCOONGSEMGKOPICIRACEBPKISDLVRRRYL 360
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QY 361 PMOVOSRETPHLQLYSAAFSKOKLOSAPTKXPALPFDDLPMGYOHLHTQLOYECISPPYR 420
DB 361 PMOVOSRETPHLQLYSAAFSKOKLOSAPTKXPALPFDDLPMGYOHLHTQLOYECISPPYR 420

QY 421 RLSSRRCLRTGKWSGAPSCIPICGKIENITAPKTOGLRMPQAAIYRRTSGVHDSL 480
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QY 661 CTAETGIAAVSPGRASPEPRMHIMGLVSWSYDKTCSHRLSTAFKVLPEKDWIERNMK 720
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RESULT 7
US-09-997-514-231

Sequence 231, Application US/09997514

Patent No. 7019116

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eacon, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kjaavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730FIC46
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DB 181 YVEVRDGNRDGOIIRKVCNBERPAPIQSIGSSLHLVPHSDGXNFDGFHAYEITACS 240

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QY 301 NGRHAKIGTVVSFFCNNSYVLSGNEKRTCOQNGESGKOPICIRACREPKISDLVRRVVL 360
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QY 361 PMOVOSREPLHQYSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAF 420
DB 361 PMOVOSREPLHQYSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAF 420

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DB 421 RLSSSRRTCLRTGMSGABPCIPICGKIENTAPKTOGLMWPQOAIYRRTSGVHDSL 480

QY 481 HKGAMFLVCSGALNBERVVAHCVTDLGVTKMTADLKVYKGFRRDDRDREKTIQS 540
DB 481 HKGAMFLVCSGALNBERVVAHCVTDLGVTKMTADLKVYKGFRRDDRDREKTIQS 540

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RESULT 8
US-09-989-728-231
Sequence 231, Application US/09989728
Patent No. 7029873
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ACIDS
FILE REFERENCE: P2/301C72
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PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3945; DB 3; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELCMTQLGLTFLQLLISSLPREYVINEACPGAENIMCRCECEYDIECVCPGRRE 60
DB 1 MELCMTQLGLTFLQLLISSLPREYVINEACPGAENIMCRCECEYDIECVCPGRRE 60

QY 61 VVGTTIPCCRNENBDCSLHPGCTTFENCKSCRNNGSGTLDFFYKGYCAECRAGW 120
DB 61 VVGTTIPCCRNENBDCSLHPGCTTFENCKSCRNNGSGTLDFFYKGYCAECRAGW 120

QY 121 YGDCMRGQYLRAPKQILLESYPLNHCMTTHAKGFYIQLRFVWLSEFDYMCQYD 180
DB 121 YGDCMRGQYLRAPKQILLESYPLNHCMTTHAKGFYIQLRFVWLSEFDYMCQYD 180

QY 181 YVEVRDGNRDQIIRKVCNERPAPIQSISSSLHVLFHSDSKXNDFGFAHYEBITACS 240
DB 181 YVEVRDGNRDQIIRKVCNERPAPIQSISSSLHVLFHSDSKXNDFGFAHYEBITACS 240

QY 241 SSPFHGTCTLDKAGSKKACLAGYTCORCENLLEBNCGDPGPNVGYOKITGPELI 300
DB 241 SSPFHGTCTLDKAGSKKACLAGYTCORCENLLEBNCGDPGPNVGYOKITGPELI 300

QY 301 NGRRAKIGTVSPFCNNSYVLSGNEKRTCOQNGEMSGKOPICIRACREPKISDLVRRVYL 360
DB 301 NGRRAKIGTVSPFCNNSYVLSGNEKRTCOQNGEMSGKOPICIRACREPKISDLVRRVYL 360

QY 361 PMQVQSEETPLHQLYSAAFSKQKLQSAFTKKPALPFGDLPMGYOHLHTQLQYECISPEYR 420
DB 361 PMQVQSEETPLHQLYSAAFSKQKLQSAFTKKPALPFGDLPMGYOHLHTQLQYECISPEYR 420

QY 421 RLGSRRCTCLRTGMSGRAPSCIPICGKIENTITAPKTQGLWPMQOALYRRTSGVHDSL 480
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QY 481 HKGAMFLVCSGALVNERTVVAACHCTVDLGYVTMKTADLVYLGKFRDDBRDEKTIQS 540
DB 481 HKGAMFLVCSGALVNERTVVAACHCTVDLGYVTMKTADLVYLGKFRDDBRDEKTIQS 540

QY 541 LQISAILLHPYDPIILDADIAIKLIDKARISTRVQPICLAASRDLSFSQESHITVAG 600
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QY 601 WNTLADVRSGFKVDITRSQVSVYDLSLCEBQHEHDCIPVSVTDNMFCAWSWETA9SDI 660
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QY 661 CTAEVTGIAIVSPFGRASPEPRMILMGLVMSYKTCSSHRTAFYKYLPEKMDIERNMK 720
DB 661 CTAEVTGIAIVSPFGRASPEPRMILMGLVMSYKTCSSHRTAFYKYLPEKMDIERNMK 720

RESULT 10
US-09-997-653-231
Sequence 231, Application US/09997653
Patent No. 7034122
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Pong, Sherman
APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Wacnabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C38
CURRENT APPLICATION NUMBER: US/09/997,653
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
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PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3945; DB 3; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MELGCTQLGLTFLQLLISLPLEYTVINACFGAEWNIMRCCEYDQIECVPGKRE 60
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DB 61 VVGTTIPCCRNENEBCSLIHPGCTTFENCKSGRNSWGSTLDDFYKGYACBRAGW 120
QY 121 YGDCMRCGQVLRAPKQIILLESYPLNAHCMTIHAKEGFIQLRFYMLSLFPMQCYD 180
DB 121 YGDCMRCGQVLRAPKQIILLESYPLNAHCMTIHAKEGFIQLRFYMLSLFPMQCYD 180
QY 181 YVEVRDGDNRDQGIKKRYCGNERPAPIQSGSLHVLPHSDGSKNPFQFAHYEITACS 240
DB 181 YVEVRDGDNRDQGIKKRYCGNERPAPIQSGSLHVLPHSDGSKNPFQFAHYEITACS 240
QY 241 SSPCFHGTGVLDAAGSYKACLAGYTGRCENLBERNSDPGCPVNGYOKITGGPGLI 300
DB 241 SSPCFHGTGVLDAAGSYKACLAGYTGRCENLBERNSDPGCPVNGYOKITGGPGLI 300
QY 301 NGRRAKIGTVSFFCNNSYVLSGNEKRTCOQNGEMSKOPICIRACREPKISDLVRRRLV 360
DB 301 NGRRAKIGTVSFFCNNSYVLSGNEKRTCOQNGEMSKOPICIRACREPKISDLVRRRLV 360
QY 361 PMOVOSRETPHLQVLSAASFQKQLQSAPTKKPALPFGDLPMGYOHLHTOLOYECISPYRR 420

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Db 361 PMQVSRFPLQLYSAFSAFKOKQASAPTKPALPFGDLPMQYQHLHTQLQRECIQSPFYR 420
Qy 421 RLGSRRFCLTGKSGRASPSCIPICGKIENITAKTQGLRPMQAAIYRRSSGHDLSL 480
Db 421 RLGSRRFCLTGKSGRASPSCIPICGKIENITAKTQGLRPMQAAIYRRSSGHDLSL 480
Qy 481 HKGAMFLVCSGALVNERVTVAACHVTDLGKVTMTKTDLKVLGKFPYRDDDRDEKTIQS 540
Db 481 HKGAMFLVCSGALVNERVTVAACHVTDLGKVTMTKTDLKVLGKFPYRDDDRDEKTIQS 540
Qy 541 LQISAIILHPNVDPLLDADIAILKLDKARISTVQPICLAASRDLSTSPQESHITVAG 600
Db 541 LQISAIILHPNVDPLLDADIAILKLDKARISTVQPICLAASRDLSTSPQESHITVAG 600
Qy 601 WNVLADVRSFGPKNDTLASGVSVVDSLCEQHDHGI PVSVTNMFCASEPTAPSDI 660
Db 601 WNVLADVRSFGPKNDTLASGVSVVDSLCEQHDHGI PVSVTNMFCASEPTAPSDI 660
Qy 661 CTAEFGIAAVSPGRASPEPRMHLGLVMSYDKTCSHRLSTAFKVL PFKOMIERMUK 720
Db 661 CTAEFGIAAVSPGRASPEPRMHLGLVMSYDKTCSHRLSTAFKVL PFKOMIERMUK 720

RESULT 11
US-09-989-293A-231

Sequence 231. Application US/09989293A

Patent No. 7034136

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnuyers, Luc

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gottlieb, Mary E.

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2730P1C66

CURRENT APPLICATION NUMBER: US/09/989, 293A

PRIOR FILING DATE: 2001-11-20

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

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PRIOR FILING DATE: 1998-03-20

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RESULT 12
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; Sequence 9, Application US/10067422
; Patent No. 6743613
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Bone Morphogenic Protein (BMP) Polynucleotides, Polypeptides, and
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: PT004P1
; CURRENT APPLICATION NUMBER: US/10/067,422
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/685,899

TELEX: 248345
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1019 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-596-405-4

Query Match 16.9%; Score 665; DB 1; Length 1019;

Best Local Similarity 25.4%; Pred. No. 1.9e-46;

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 15, 2006, 06:56:11 ; Search time 180 Seconds
(without alignments)
1852.859 Million cell updates/sec

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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754	3939	99.8	720	4	US-10-098-871-26 Sequence 26, App
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760	3089.5	78.3	567	6	US-11-045-029-2 Sequence 2, App
761	2946.5	74.7	570	4	US-10-067-422-9 Sequence 9, App
762	2413	61.2	455	3	US-09-833-245-1401 Sequence 1401, App
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797	403.5	10.2	705	5	US-10-287-436A-1152	Sequence 1152, App
798	403.5	10.2	705	5	US-10-989-891-144	Sequence 144, App
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868	327	8.3	855	4	US-10-072-012-411	Sequence 411, App	941	296	7.5	799	4	US-10-037-417-135	Sequence 135, App
869	327	8.3	855	4	US-10-072-012-418	Sequence 418, App	942	296	7.5	799	4	US-10-450-763-51801	Sequence 51801, A
870	327	8.3	855	4	US-10-600-187-2	Sequence 2, Appl1	943	293	7.4	799	4	US-10-114-153-50	Sequence 50, Appl
871	327	8.3	855	4	US-10-612-466B-2	Sequence 2, Appl1	944	291.5	7.4	799	4	US-10-741-600-909	Sequence 909, App
872	327	8.3	855	6	US-11-104-110-1	Sequence 1, Appl1	945	291.5	7.4	799	4	US-10-995-561-559	Sequence 559, App
873	327	8.3	855	6	US-11-104-110-1	Sequence 22, Appl1	946	291	7.4	799	4	US-10-406-031-31	Sequence 31, Appl
874	324	8.2	3095	6	US-11-235-733-4	Sequence 4, Appl1	947	289.5	7.3	799	4	US-09-776-191-10	Sequence 10, Appl
875	321	8.1	3130	5	US-10-453-372-42	Sequence 42, Appl1	948	289.5	7.3	799	4	US-10-156-214A-10	Sequence 10, Appl
876	321	8.1	3483	5	US-10-453-372-40	Sequence 40, Appl1	949	289.5	7.3	799	4	US-09-776-191-8	Sequence 8, Appl1
877	321	8.1	3546	5	US-10-453-372-32	Sequence 32, Appl1	950	289.5	7.3	799	4	US-10-156-214A-8	Sequence 8, Appl1
878	319.5	8.1	455	4	US-10-406-031-17	Sequence 17, Appl1	951	288.5	7.3	799	4	US-09-888-615-113	Sequence 113, App
879	318	8.1	2612	5	US-10-453-372-38	Sequence 38, Appl1	966	288.5	7.3	799	4	US-10-167-749A-169	Sequence 169, App
880	318	8.1	2669	4	US-10-016-248-4	Sequence 4, Appl1	1022	288.5	7.3	799	4	US-10-170-481A-169	Sequence 169, App
881	318	8.1	2669	5	US-10-453-372-36	Sequence 36, Appl1	1024	288.5	7.3	799	4	US-10-210-028-169	Sequence 169, App
882	318	8.1	3104	4	US-10-016-248-2	Sequence 2, Appl1	1029	288.5	7.3	799	4	US-10-162-521A-169	Sequence 169, App
883	318	8.1	3104	5	US-10-453-372-34	Sequence 34, Appl1	1041	288.5	7.3	799	4	US-10-918-851-169	Sequence 169, App
884	318	8.1	3104	5	US-10-453-372-62	Sequence 62, Appl1	1042	288.5	7.3	799	4	US-10-805-667-169	Sequence 169, App
885	318	8.1	3104	5	US-10-453-372-64	Sequence 64, Appl1	1043	288.5	7.3	799	4	US-10-897-359-169	Sequence 169, App
886	317.5	8.0	3069	6	US-11-235-733-2	Sequence 2, Appl1	1044	288.5	7.3	799	4	US-10-897-359-169	Sequence 169, App
887	317.5	8.0	3100	6	US-11-235-733-7	Sequence 7, Appl1	1045	288.5	7.3	799	4	US-10-897-359-169	Sequence 169, App
888	314.5	8.0	454	4	US-10-406-031-11	Sequence 11, Appl1	1048	288.5	7.3	799	4	US-11-129-762-169	Sequence 169, App
889	314	8.0	855	3	US-09-900-751-2	Sequence 2, Appl1	1049	288.5	7.3	799	4	US-11-037-243-113	Sequence 113, App
890	314	8.0	855	4	US-10-072-012-355	Sequence 355, App	1050	288.5	7.3	799	4	US-10-333-743-3	Sequence 3, Appl1
891	314	8.0	855	4	US-10-072-012-413	Sequence 413, App	1051	288.5	7.3	799	4	US-10-600-187-101	Sequence 10, Appl1
892	313	7.9	855	4	US-10-072-012-356	Sequence 356, App	1052	288.5	7.3	799	4	US-10-297-9878-11	Sequence 11, Appl1
893	313	7.9	855	4	US-10-072-012-414	Sequence 414, App	1053	287	7.3	799	4	US-10-406-031-5	Sequence 5, Appl1
894	313	7.9	855	4	US-10-072-012-417	Sequence 417, App	1054	283	7.2	799	4	US-10-865-978-35	Sequence 25, Appl1
895	312	7.9	419	4	US-10-168-407-5	Sequence 5, Appl1	1055	281	7.1	799	4	US-10-348-504-44	Sequence 44, Appl1
896	312	7.9	467	4	US-10-406-031-8	Sequence 8, Appl1	1056	281	7.1	799	4	US-10-407-123-27	Sequence 27, Appl1
897	312	7.9	1031	4	US-10-451-168-80	Sequence 80, Appl1	1057	280	7.1	799	4	US-09-987-457-18	Sequence 18, Appl1
898	312	7.9	1031	5	US-10-980-387-80	Sequence 80, Appl1	1058	280	7.1	799	4	US-09-987-455-19	Sequence 19, Appl1
899	311	7.9	419	4	US-10-168-407-3	Sequence 4, Appl1	1059	280	7.1	799	4	US-10-360-101-203	Sequence 203, App
900	311	7.9	419	4	US-10-168-407-6	Sequence 6, Appl1	1060	280	7.1	799	4	US-10-432-842-1	Sequence 1, Appl1
901	310.5	7.9	409	5	US-10-506-301-2	Sequence 2, Appl1	1061	280	7.1	799	4	US-10-705-633-1	Sequence 1, Appl1
902	310.5	7.9	410	5	US-10-506-301-1	Sequence 1, Appl1	1062	280	7.1	799	4	US-10-742-887-51	Sequence 51, Appl1
903	310.5	7.9	415	4	US-10-670-628-2	Sequence 2, Appl1	1063	280	7.1	799	4	US-11-134-385-19	Sequence 19, Appl1
904	310.5	7.9	419	3	US-09-997-623-4	Sequence 4, Appl1	1064	280	7.1	799	4	US-09-969-271-7	Sequence 7, Appl1
905	310.5	7.9	419	3	US-09-978-917A-4	Sequence 4, Appl1	1065	280	7.1	799	4	US-09-974-298-145	Sequence 145, App
906	310.5	7.9	419	4	US-10-182-263-1	Sequence 1, Appl1	1066	280	7.1	799	4	US-10-193-656-8	Sequence 8, Appl1
907	310.5	7.9	419	4	US-10-168-407-1	Sequence 1, Appl1	1067	280	7.1	799	4	US-10-443-701-4	Sequence 4, Appl1
908	310.5	7.9	419	5	US-10-506-301-3	Sequence 3, Appl1	1068	280	7.1	799	4	US-10-411-037-26	Sequence 26, Appl1
909	310.5	7.9	419	5	US-10-492-191-1	Sequence 1, Appl1	1069	280	7.1	799	4	US-10-411-026-26	Sequence 26, Appl1
910	310.5	7.9	419	6	US-11-004-111-4	Sequence 4, Appl1	1070	280	7.1	799	4	US-10-410-962-26	Sequence 26, Appl1
911	310.5	7.9	453	4	US-10-406-031-14	Sequence 14, Appl1	1071	280	7.1	799	4	US-10-410-962-26	Sequence 26, Appl1
912	310.5	7.9	461	3	US-09-997-623-2	Sequence 2, Appl1	1072	280	7.1	799	4	US-10-410-930-26	Sequence 26, Appl1
913	310.5	7.9	461	3	US-09-978-917A-2	Sequence 2, Appl1	1073	280	7.1	799	4	US-10-410-997-26	Sequence 26, Appl1
914	310.5	7.9	461	4	US-10-182-263-2	Sequence 2, Appl1	1074	280	7.1	799	4	US-10-411-012-26	Sequence 26, Appl1
915	310.5	7.9	461	4	US-10-168-407-2	Sequence 2, Appl1	1075	280	7.1	799	4	US-10-287-994-26	Sequence 26, Appl1
916	310.5	7.9	461	4	US-10-756-149-5387	Sequence 5387, Ap	1076	280	7.1	799	4	US-10-410-913-26	Sequence 26, Appl1
917	310.5	7.9	461	6	US-11-004-111-2	Sequence 2, Appl1	1077	280	7.1	799	4	US-10-712-124-108	Sequence 108, App
918	310	7.9	419	4	US-10-182-263-6	Sequence 6, Appl1	1078	280	7.1	799	4	US-10-741-600-911	Sequence 911, App
919	310	7.9	419	4	US-10-168-407-4	Sequence 4, Appl1	1079	280	7.1	799	4	US-10-410-980-26	Sequence 26, Appl1

1080	280	7.1	562	5	US-10-410-897-26	Sequence 26, Appl	1153	275.5	7.0	444	4	US-10-410-997-8	Sequence 8, Appl
1081	280	7.1	562	5	US-10-492-261-26	Sequence 26, Appl	1154	275.5	7.0	444	4	US-10-411-012-8	Sequence 8, Appl
1082	280	7.1	562	5	US-10-999-561-561	Sequence 561, App	1155	275.5	7.0	444	4	US-10-287-994-8	Sequence 8, Appl
1083	280	7.1	562	6	US-11-169-041-153	Sequence 153, App	1156	275.5	7.0	444	4	US-10-410-913-8	Sequence 8, Appl
1084	280	7.1	562	6	US-11-183-205-26	Sequence 26, Appl	1157	275.5	7.0	444	4	US-10-738-777-3	Sequence 3, Appl
1085	279.5	7.1	782	4	US-10-097-340-312	Sequence 312, App	1158	275.5	7.0	444	4	US-10-410-980-8	Sequence 8, Appl
1086	279.5	7.1	782	6	US-11-050-926-312	Sequence 312, App	1159	275.5	7.0	444	5	US-10-410-897-8	Sequence 8, Appl
1087	279	7.1	527	4	US-10-705-633-2	Sequence 2, Appl	1160	275.5	7.0	444	5	US-10-492-261-8	Sequence 8, Appl
1088	279	7.1	932	6	US-10-363-937-6	Sequence 6, Appl	1161	275.5	7.0	444	6	US-11-183-205-8	Sequence 8, Appl
1089	279	7.1	932	4	US-11-167-040-6	Sequence 6, Appl	1162	275.5	7.0	459	4	US-10-741-601-503	Sequence 503, App
1090	279	7.1	970	3	US-09-888-615-101	Sequence 101, App	1163	275.5	7.0	459	4	US-10-741-601-504	Sequence 504, App
1091	279	7.1	970	6	US-11-037-243-101	Sequence 101, App	1164	275.5	7.0	641	4	US-10-617-619-8	Sequence 8, Appl
1092	278.5	7.1	264	3	US-09-978-418-34	Sequence 34, Appl	1165	275.5	7.0	641	6	US-11-227-310-8	Sequence 8, Appl
1093	278.5	7.1	264	5	US-10-485-231-34	Sequence 34, Appl	1166	275.5	7.0	671	6	US-10-841-250-6	Sequence 6, Appl
1094	278.5	7.1	466	4	US-10-017-122-2	Sequence 2, Appl	1167	275.5	7.0	671	6	US-11-029-003-6	Sequence 6, Appl
1095	278.5	7.1	466	4	US-10-375-741-14	Sequence 14, Appl	1168	275.5	7.0	679	4	US-10-617-619-11	Sequence 11, Appl
1096	278.5	7.1	481	4	US-10-741-601-501	Sequence 501, App	1169	275.5	7.0	679	4	US-10-617-619-11	Sequence 11, Appl
1097	278.5	7.1	481	4	US-10-741-601-502	Sequence 502, App	1170	275	7.0	1113	5	US-11-227-340-11	Sequence 11, Appl
1098	278.5	7.1	701	4	US-10-617-619-6	Sequence 6, Appl	1171	273	6.9	560	3	US-09-912-559-3	Sequence 3, Appl
1099	278.5	7.1	701	4	US-11-227-340-6	Sequence 6, Appl	1172	273	6.9	560	3	US-09-912-559-3	Sequence 3, Appl
1100	278	7.0	408	6	US-11-097-143-42048	Sequence 42048, A	1173	273	6.9	560	4	US-10-172-712-32	Sequence 32, Appl
1101	278	7.0	488	4	US-10-406-031-27	Sequence 27, Appl	1174	273	6.9	560	4	US-10-391-215-5	Sequence 5, Appl
1102	278	7.0	488	5	US-10-723-860-261	Sequence 261, App	1175	273	6.9	560	4	US-10-391-215-6	Sequence 6, Appl
1103	278	7.0	488	5	US-10-492-191-23	Sequence 23, Appl	1176	273	6.9	560	4	US-10-391-215-7	Sequence 7, Appl
1104	278	7.0	1113	4	US-10-464-368-78	Sequence 78, Appl	1177	273	6.9	560	4	US-10-391-215-8	Sequence 8, Appl
1105	278	7.0	1113	6	US-11-067-811-4	Sequence 4, Appl	1178	273	6.9	560	5	US-10-719-993-854	Sequence 854, App
1106	277.5	7.0	476	5	US-10-494-004-1	Sequence 4, Appl	1179	273	6.9	560	5	US-10-930-754-3	Sequence 3, Appl
1107	276.5	7.0	426	3	US-09-951-121A-1	Sequence 1, Appl	1180	273	6.9	560	5	US-10-930-754-4	Sequence 4, Appl
1108	276.5	7.0	426	3	US-09-848-107-1	Sequence 1, Appl	1181	273	6.9	560	5	US-10-756-149-5450	Sequence 5450, Ap
1109	276.5	7.0	426	4	US-10-295-682-1	Sequence 1, Appl	1182	272.5	6.9	296	4	US-10-148-671-17	Sequence 17, Appl
1110	276.5	7.0	655	4	US-10-172-712-28	Sequence 28, Appl	1183	272	6.9	488	4	US-10-712-332-1	Sequence 1, Appl
1111	276	7.0	249	3	US-09-961-721-5	Sequence 5, Appl	1184	271.5	6.9	244	4	US-10-097-340-169	Sequence 169, App
1112	276	7.0	249	4	US-10-170-789-46	Sequence 46, Appl	1185	271.5	6.9	244	4	US-10-282-907-2	Sequence 2, Appl
1113	276	7.0	249	6	US-11-151-601-28	Sequence 28, Appl	1186	271.5	6.9	244	4	US-10-301-822-97	Sequence 97, Appl
1114	276	7.0	251	3	US-09-961-721-4	Sequence 4, Appl	1187	271.5	6.9	244	4	US-10-295-027-530	Sequence 530, App
1115	276	7.0	251	4	US-10-170-789-45	Sequence 45, Appl	1188	271.5	6.9	244	4	US-10-173-999-131	Sequence 131, App
1116	276	7.0	251	6	US-11-151-601-27	Sequence 27, Appl	1189	271.5	6.9	244	4	US-10-344-394-35	Sequence 25, Appl
1117	276	7.0	259	4	US-10-107-782-214	Sequence 214, App	1190	271.5	6.9	244	5	US-10-757-262-28	Sequence 28, Appl
1118	276	7.0	259	4	US-10-038-854-100	Sequence 100, App	1191	271.5	6.9	244	5	US-10-868-490A-9	Sequence 9, Appl
1119	276	7.0	396	4	US-10-700-778-1	Sequence 1, Appl	1192	271.5	6.9	244	5	US-10-868-490A-11	Sequence 11, Appl
1120	276	7.0	527	4	US-10-705-633-3	Sequence 3, Appl	1193	271.5	6.9	244	5	US-10-868-490A-13	Sequence 13, Appl
1121	275.5	7.0	405	4	US-10-360-101-225	Sequence 225, App	1194	271.5	6.9	244	5	US-10-868-490A-15	Sequence 15, Appl
1122	275.5	7.0	406	3	US-09-782-587B-1	Sequence 1, Appl	1195	271.5	6.9	244	5	US-10-961-139-14	Sequence 14, Appl
1123	275.5	7.0	406	3	US-09-782-587B-3	Sequence 3, Appl	1196	271.5	6.9	244	5	US-10-756-149-9363	Sequence 143, Ap
1124	275.5	7.0	406	4	US-10-109-498-1	Sequence 1, Appl	1197	271.5	6.9	244	6	US-11-050-926-169	Sequence 169, App
1125	275.5	7.0	406	4	US-10-255-032-1	Sequence 1, Appl	1198	271.5	6.9	244	6	US-11-186-284-57	Sequence 97, Appl
1126	275.5	7.0	406	4	US-10-281-727-1	Sequence 1, Appl	1199	271.5	6.9	244	6	US-11-050-857-570	Sequence 670, App
1127	275.5	7.0	406	4	US-10-386-898-7	Sequence 7, Appl	1200	271.5	6.9	253	6	US-11-050-857-571	Sequence 671, App
1128	275.5	7.0	406	4	US-10-383-898-1	Sequence 1, Appl	1201	271.5	6.9	1006	4	US-10-210-130-52	Sequence 62, Appl
1129	275.5	7.0	406	4	US-10-617-500-1	Sequence 1, Appl	1202	271	6.9	650	4	US-10-401-077-1	Sequence 1, Appl
1130	275.5	7.0	406	4	US-10-263-205B-2	Sequence 2, Appl	1203	269	6.8	462	4	US-10-416-952-2	Sequence 2, Appl
1131	275.5	7.0	406	4	US-10-617-619-1	Sequence 1, Appl	1204	269	6.8	643	3	US-09-808-602-103	Sequence 103, App
1132	275.5	7.0	406	4	US-10-701-294-1	Sequence 1, Appl	1205	269	6.8	643	3	US-09-800-198-86	Sequence 86, Appl
1133	275.5	7.0	406	4	US-10-669-537-1	Sequence 1, Appl	1206	269	6.8	643	3	US-10-099-332-113	Sequence 113, App
1134	275.5	7.0	406	4	US-10-738-777-2	Sequence 2, Appl	1207	269	6.8	643	4	US-10-044-564-113	Sequence 113, App
1135	275.5	7.0	406	5	US-10-900-490-1	Sequence 1, Appl	1208	269	6.8	643	6	US-11-054-281-113	Sequence 113, App
1136	275.5	7.0	406	5	US-10-725-843-3	Sequence 3, Appl	1209	267	6.8	462	4	US-10-411-037-10	Sequence 10, Appl
1137	275.5	7.0	406	5	US-10-609-701A-1	Sequence 1, Appl	1210	267	6.8	462	4	US-10-411-026-10	Sequence 10, Appl
1138	275.5	7.0	406	5	US-10-950-747-1	Sequence 1, Appl	1211	267	6.8	462	4	US-10-410-962-10	Sequence 10, Appl
1139	275.5	7.0	406	5	US-10-950-747-3	Sequence 3, Appl	1212	267	6.8	462	4	US-10-410-930-10	Sequence 10, Appl
1140	275.5	7.0	406	5	US-10-823-943-1	Sequence 1, Appl	1213	267	6.8	462	4	US-10-410-930-10	Sequence 10, Appl
1141	275.5	7.0	406	6	US-11-021-239-1	Sequence 1, Appl	1214	267	6.8	462	4	US-10-410-997-10	Sequence 10, Appl
1142	275.5	7.0	406	6	US-11-111-072-1	Sequence 1, Appl	1215	267	6.8	462	4	US-10-411-012-10	Sequence 10, Appl
1143	275.5	7.0	406	6	US-11-111-079-1	Sequence 1, Appl	1216	267	6.8	462	4	US-10-287-994-10	Sequence 10, Appl
1144	275.5	7.0	406	6	US-11-186-669-1	Sequence 1, Appl	1217	267	6.8	462	4	US-10-410-913-10	Sequence 10, Appl
1145	275.5	7.0	406	6	US-11-227-340-1	Sequence 1, Appl	1218	267	6.8	462	5	US-10-410-980-10	Sequence 10, Appl
1146	275.5	7.0	444	4	US-10-411-037-8	Sequence 8, Appl	1219	267	6.8	462	5	US-10-410-897-10	Sequence 10, Appl
1147	275.5	7.0	444	4	US-10-383-248-34	Sequence 34, Appl	1220	267	6.8	462	5	US-10-492-261-10	Sequence 10, Appl
1148	275.5	7.0	444	4	US-10-411-026-8	Sequence 8, Appl	1221	267	6.8	462	6	US-11-183-205-10	Sequence 10, Appl
1149	275.5	7.0	444	4	US-10-410-962-8	Sequence 8, Appl	1222	265.5	6.7	250	6	US-11-097-143-24561	Sequence 24561, A
1150	275.5	7.0	444	4	US-10-411-049-8	Sequence 8, Appl	1223	265	6.7	419	4	US-10-362-248-36	Sequence 36, Appl
1151	275.5	7.0	444	4	US-10-263-205B-3	Sequence 3, Appl	1224	264.5	6.7	900	5	US-10-865-978-15	Sequence 15, Appl
1152	275.5	7.0	444	4	US-10-410-930-8	Sequence 8, Appl	1225	264	6.7	431	4	US-10-247-671-149	Sequence 149, App

1226	263.5	6.7	411	4	US-10-744-927-1	Sequence 1, Appl1	1299	258.5	6.6	411	4	US-10-407-821-2	Sequence 2, Appl1
1227	263.5	6.7	494	6	US-11-094-519A-35	Sequence 35, Appl1	1300	258.5	6.6	411	5	US-10-828-531B-16	Sequence 16, Appl1
1228	263	6.7	431	4	US-10-076-421-2	Sequence 2, Appl1	1301	258.5	6.6	411	5	US-11-019-448-3	Sequence 3, Appl1
1229	263	6.7	431	4	US-10-171-311-184	Sequence 184, App	1302	258.5	6.6	412	5	US-10-825-911-2	Sequence 2, Appl1
1230	263	6.7	431	4	US-10-301-822-161	Sequence 161, App	1303	258.5	6.6	787	6	US-11-027-143-40698	Sequence 40698, A
1231	263	6.7	431	4	US-10-131-985-21	Sequence 21, Appl	1304	257.5	6.5	591	5	US-10-865-978-11	Sequence 17, Appl
1232	263	6.7	431	4	US-10-295-027-414	Sequence 414, App	1305	257	6.5	215	4	US-10-051-874-102	Sequence 102, App
1233	263	6.7	431	4	US-10-295-027-1275	Sequence 1275, Ap	1306	257	6.5	217	3	US-09-981-151A-88	Sequence 88, Appl
1234	263	6.7	431	4	US-10-411-037-34	Sequence 34, Appl	1307	257	6.5	217	3	US-09-981-151A-97	Sequence 97, Appl
1235	263	6.7	431	4	US-10-411-026-34	Sequence 34, Appl	1308	257	6.5	217	4	US-10-033-189-67	Sequence 67, Appl
1236	263	6.7	431	4	US-10-410-962-34	Sequence 34, Appl	1309	257	6.5	217	4	US-10-074-978A-223	Sequence 223, App
1237	263	6.7	431	4	US-10-410-962-34	Sequence 34, Appl	1310	257	6.5	217	4	US-10-074-978A-223	Sequence 223, App
1238	263	6.7	431	4	US-10-410-930-34	Sequence 34, Appl	1311	257	6.5	217	4	US-10-055-569A-97	Sequence 97, Appl
1239	263	6.7	431	4	US-10-410-997-34	Sequence 34, Appl	1312	257	6.5	217	4	US-10-042-865-156	Sequence 156, App
1240	263	6.7	431	4	US-10-411-012-34	Sequence 34, Appl	1313	257	6.5	217	4	US-10-072-012-805	Sequence 805, App
1241	263	6.7	431	4	US-10-287-994-34	Sequence 34, Appl	1314	257	6.5	217	4	US-10-072-012-813	Sequence 813, App
1242	263	6.7	431	4	US-10-410-913-34	Sequence 34, Appl	1315	257	6.5	217	6	US-11-037-417-136	Sequence 136, App
1243	263	6.7	431	5	US-10-741-600-1265	Sequence 1265, Ap	1316	257	6.5	529	4	US-11-019-711-136	Sequence 136, App
1244	263	6.7	431	5	US-10-741-600-1266	Sequence 1266, Ap	1317	257	6.5	1039	4	US-10-398-037-2	Sequence 2, Appl1
1245	263	6.7	431	5	US-10-901-417-21	Sequence 21, Appl	1318	256	6.5	1039	5	US-10-865-978-30	Sequence 30, Appl
1246	263	6.7	431	5	US-10-410-980-34	Sequence 34, Appl	1319	255.5	6.5	207	4	US-10-004-378A-147	Sequence 147, App
1247	263	6.7	431	5	US-10-645-756-38	Sequence 38, Appl	1320	255.5	6.5	244	3	US-09-796-294-11	Sequence 11, Appl
1248	263	6.7	431	5	US-10-410-897-34	Sequence 34, Appl	1321	255.5	6.5	244	6	US-10-461-787-11	Sequence 11, Appl
1249	263	6.7	431	5	US-10-492-261-34	Sequence 34, Appl	1322	255.5	6.5	244	6	US-11-251-455-13	Sequence 13, Appl
1250	263	6.7	431	5	US-10-995-561-807	Sequence 807, App	1323	255.5	6.5	441	5	US-10-741-600-829	Sequence 825, App
1251	263	6.7	431	5	US-10-995-561-808	Sequence 808, App	1324	254.5	6.5	487	5	US-10-455-772-52	Sequence 52, App
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1265	262.5	6.7	461	4	US-10-038-854-92	Sequence 92, Appl	1338	253	6.4	273	4	US-10-148-671-253	Sequence 25, Appl
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SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
2	3945	100.0	720	7	US-11-101-316-38 Sequence 38, Appl
3	3936	99.8	720	7	US-11-354-653-32 Sequence 32, Appl
4	3828	97.0	699	7	US-11-354-653-86 Sequence 86, Appl
5	3617	91.7	720	7	US-11-354-653-118 Sequence 118, Appl
6	328	8.3	855	7	US-11-254-185-2 Sequence 2, Appl
7	328	8.3	855	7	US-11-253-869-2 Sequence 2, Appl
8	280	7.1	562	6	US-10-505-928-547 Sequence 547, Appl
9	280	7.1	562	7	US-11-183-218-26 Sequence 26, Appl
10	277.5	7.0	476	7	US-11-264-088-1 Sequence 1, Appl
11	277.5	7.0	476	7	US-11-311-475-1 Sequence 1, Appl
12	276.5	7.0	655	7	US-11-242-617-1 Sequence 1, Appl
13	275.5	7.0	406	6	US-10-512-754-2 Sequence 2, Appl
14	275.5	7.0	406	7	US-11-286-211A-1 Sequence 1, Appl
15	275.5	7.0	444	6	US-10-511-937-2962 Sequence 2962, Appl
16	275.5	7.0	444	6	US-10-511-937-3014 Sequence 3014, Appl
17	275.5	7.0	444	6	US-11-183-218-8 Sequence 8, Appl
18	271.5	6.9	244	6	US-10-544-944-6 Sequence 6, Appl
19	271.5	6.9	244	6	US-10-546-435-4 Sequence 4, Appl
20	271.5	6.9	244	6	US-11-319-952-84 Sequence 84, Appl
21	269.5	6.8	239	7	US-11-319-952-71 Sequence 71, Appl
22	267	6.8	462	7	US-11-183-218-10 Sequence 10, Appl
23	264	6.7	653	7	US-11-242-617-2 Sequence 2, Appl
24	263	6.7	431	6	US-10-503-928-465 Sequence 465, Appl
25	263	6.7	431	7	US-11-183-218-34 Sequence 34, Appl
26	248	6.3	230	7	US-11-254-185-8 Sequence 8, Appl
27	248	6.3	230	7	US-11-254-185-40 Sequence 40, Appl

28	248	6.3	230	7	US-11-253-869-8 Sequence 8, Appl
29	248	6.3	230	7	US-11-253-869-40 Sequence 40, Appl
30	246	6.2	812	7	US-11-318-939-7 Sequence 7, Appl
31	244	6.2	477	7	US-11-264-088-2 Sequence 2, Appl
32	244	6.2	477	7	US-11-311-475-2 Sequence 2, Appl
33	236.5	6.0	416	7	US-11-208-257-8 Sequence 8, Appl
34	228.5	5.8	1953	7	US-11-264-243-16 Sequence 16, Appl
35	228	5.8	809	7	US-11-318-939-9 Sequence 9, Appl
36	228	5.8	812	7	US-11-318-939-12 Sequence 12, Appl
37	227.5	5.8	237	7	US-11-319-952-66 Sequence 66, Appl
38	227.5	5.8	231	7	US-11-319-952-67 Sequence 67, Appl
39	227	5.8	241	7	US-11-254-185-3 Sequence 3, Appl
40	227	5.8	241	7	US-11-254-185-35 Sequence 35, Appl
41	227	5.8	241	7	US-11-253-869-3 Sequence 3, Appl
42	227	5.8	241	7	US-11-253-869-35 Sequence 35, Appl
43	226	5.7	432	7	US-11-101-316-112 Sequence 112, Appl
44	224.5	5.7	235	7	US-11-254-185-5 Sequence 5, Appl
45	224.5	5.7	235	7	US-11-254-185-37 Sequence 37, Appl
46	224.5	5.7	235	7	US-11-253-869-5 Sequence 5, Appl
47	224.5	5.7	235	7	US-11-253-869-37 Sequence 37, Appl
48	224.5	5.7	235	7	US-10-511-937-2457 Sequence 2457, Appl
49	224	5.7	275	6	US-10-522-668-2 Sequence 2, Appl
50	223.5	5.7	531	6	US-11-293-697-3002 Sequence 3002, Appl
51	223	5.7	305	7	US-11-318-939-13 Sequence 13, Appl
52	222.5	5.6	790	7	US-11-101-316-106 Sequence 106, Appl
53	222	5.6	423	7	US-11-101-316-106 Sequence 106, Appl
54	222	5.6	245	7	US-11-254-185-36 Sequence 36, Appl
55	219.5	5.6	245	7	US-11-253-869-36 Sequence 36, Appl
56	219.5	5.6	245	7	US-11-253-869-36 Sequence 36, Appl
57	219.5	5.6	245	7	US-11-253-869-36 Sequence 36, Appl
58	215	5.4	790	7	US-11-350-703-1 Sequence 1, Appl
59	215	5.4	791	7	US-11-318-939-6 Sequence 6, Appl
60	213.5	5.4	255	7	US-11-254-185-6 Sequence 6, Appl
61	213.5	5.4	255	7	US-11-254-185-38 Sequence 38, Appl
62	213.5	5.4	255	7	US-11-253-869-38 Sequence 38, Appl
63	213.5	5.4	255	7	US-11-253-869-38 Sequence 38, Appl
64	213.5	5.4	255	7	US-10-544-944-20 Sequence 20, Appl
65	212.5	5.4	250	6	US-10-546-435-12 Sequence 12, Appl
66	212.5	5.4	250	6	US-11-319-952-86 Sequence 86, Appl
67	212.5	5.4	282	6	US-10-544-944-19 Sequence 19, Appl
68	212.5	5.4	282	6	US-10-546-435-11 Sequence 11, Appl
69	211.5	5.4	235	7	US-11-254-185-4 Sequence 4, Appl
70	211.5	5.4	235	7	US-11-253-869-4 Sequence 4, Appl
71	211	5.3	1218	7	US-11-178-724-21 Sequence 21, Appl
72	211	5.3	1218	7	US-11-071-796A-20 Sequence 20, Appl
73	210.5	5.3	505	7	US-11-293-697-3257 Sequence 3257, Appl
74	208	5.3	271	7	US-11-292-215-10 Sequence 10, Appl
75	206	5.2	275	7	US-11-319-952-72 Sequence 72, Appl
76	204	5.2	260	6	US-10-544-944-13 Sequence 13, Appl
77	204	5.2	260	7	US-11-319-952-83 Sequence 83, Appl
78	203.5	5.2	224	7	US-11-254-185-7 Sequence 7, Appl
79	203.5	5.2	224	7	US-11-254-185-39 Sequence 39, Appl
80	203.5	5.2	224	7	US-11-253-869-39 Sequence 39, Appl
81	203.5	5.2	224	7	US-11-253-869-39 Sequence 39, Appl
82	203.5	5.2	2556	7	US-11-264-243-6 Sequence 6, Appl
83	202.5	5.1	228	7	US-11-319-952-73 Sequence 73, Appl
84	200.5	5.1	810	7	US-11-318-939-11 Sequence 11, Appl
85	199.5	5.1	2556	7	US-11-071-796A-22 Sequence 22, Appl
86	198.5	5.0	311	7	US-11-359-858-2 Sequence 2, Appl
87	197.5	5.0	248	7	US-11-319-952-60 Sequence 60, Appl
88	197.5	5.0	269	7	US-11-246-999-127 Sequence 127, Appl
89	197.5	5.0	338	7	US-11-348-939-10 Sequence 10, Appl
90	195.5	5.0	2471	7	US-11-071-796A-23 Sequence 23, Appl
91	195	4.9	258	7	US-11-319-952-85 Sequence 85, Appl
92	194	4.9	113	7	US-11-254-185-26 Sequence 26, Appl
93	194	4.9	113	7	US-11-253-869-26 Sequence 26, Appl
94	193	4.9	253	7	US-11-319-952-69 Sequence 69, Appl
95	192.5	4.9	281	7	US-11-292-215-7 Sequence 7, Appl
96	191.5	4.9	247	7	US-11-319-952-82 Sequence 82, Appl
97	191.5	4.9	830	6	US-10-505-928-469 Sequence 469, Appl
98	191	4.8	254	7	US-11-319-952-3 Sequence 3, Appl
99	190.5	4.8	241	7	US-11-319-952-77 Sequence 77, Appl
100	190	4.8	254	7	US-11-319-952-81 Sequence 81, Appl
101	189	4.8	237	7	US-11-319-952-82 Sequence 82, Appl
102	189	4.8	253	6	US-10-544-944-10 Sequence 10, Appl
103	188	4.8	249	7	US-11-319-952-68 Sequence 68, Appl

104	188	4.8	333	7	US-11-318-939-8	Sequence 8, Appl1	179	150	3.8	276	7	US-11-292-215-1	Sequence 1, Appl1
105	187	4.7	281	7	US-11-293-697-2976	Sequence 2976, Ap	180	150	3.8	276	7	US-11-319-952-88	Sequence 88, Appl1
106	187	4.7	296	7	US-11-319-952-22	Sequence 22, Appl1	181	148.5	3.8	472	7	US-11-217-997-26	Sequence 26, Appl1
107	185.5	4.7	713	7	US-11-175-714-5	Sequence 5, Appl1	182	148.5	3.8	1403	7	US-11-217-997-12	Sequence 12, Appl1
108	182.5	4.6	720	7	US-11-175-714-4	Sequence 4, Appl1	183	148.5	3.8	1404	7	US-11-217-997-22	Sequence 22, Appl1
109	182	4.6	721	6	US-11-175-714-7	Sequence 7, Appl1	184	148.5	3.8	1547	7	US-11-217-997-22	Sequence 22, Appl1
110	182	4.6	1189	6	US-10-540-844-4	Sequence 4, Appl1	185	148.5	3.8	1577	7	US-11-217-997-16	Sequence 16, Appl1
111	182	4.6	1236	6	US-10-540-844-2	Sequence 2, Appl1	186	148.5	3.8	1577	7	US-11-217-997-20	Sequence 20, Appl1
112	182	4.6	1238	7	US-11-178-724-22	Sequence 22, Appl1	187	148.5	3.8	1620	7	US-11-217-997-42	Sequence 42, Appl1
113	182	4.6	1238	7	US-11-071-796A-21	Sequence 21, Appl1	188	148.5	3.8	1653	7	US-11-217-997-40	Sequence 40, Appl1
114	181.5	4.6	299	7	US-11-292-215-8	Sequence 8, Appl1	189	147.5	3.7	4391	7	US-11-183-325-56	Sequence 56, Appl1
115	181	4.6	257	7	US-11-319-952-87	Sequence 87, Appl1	190	147	3.7	244	7	US-11-247-886-3	Sequence 3, Appl1
116	180	4.6	254	7	US-11-319-952-59	Sequence 59, Appl1	191	147	3.7	244	7	US-11-247-886-4	Sequence 4, Appl1
117	179.5	4.6	250	7	US-11-319-952-23	Sequence 23, Appl1	192	146	3.7	244	7	US-11-247-886-5	Sequence 5, Appl1
118	177	4.5	112	7	US-11-254-185-27	Sequence 27, Appl1	193	144	3.7	244	7	US-11-247-886-10	Sequence 10, Appl1
119	177	4.5	112	7	US-11-253-869-27	Sequence 27, Appl1	194	143	3.6	244	7	US-11-247-886-7	Sequence 7, Appl1
120	177	4.5	729	7	US-11-175-714-8	Sequence 8, Appl1	195	141	3.6	244	7	US-11-247-886-9	Sequence 9, Appl1
121	176.5	4.5	2003	7	US-11-264-243-8	Sequence 8, Appl1	196	140	3.5	4590	6	US-10-505-928-569	Sequence 569, App
122	174	4.4	258	6	US-10-449-902-31884	Sequence 31884, A	197	139.5	3.5	207	7	US-11-357-337-4	Sequence 4, Appl1
123	174	4.4	286	7	US-11-292-215-9	Sequence 9, Appl1	198	139	3.5	464	6	US-10-505-928-757	Sequence 757, App
124	173.5	4.4	717	7	US-11-175-714-9	Sequence 9, Appl1	199	138.5	3.5	247	6	US-10-511-937-2422	Sequence 2422, Ap
125	171.5	4.3	2413	6	US-10-511-937-2616	Sequence 2616, Ap	200	138	3.5	291	7	US-11-293-215-11	Sequence 11, Appl1
126	171	4.3	256	7	US-11-319-952-44	Sequence 44, Appl1	201	136.5	3.5	439	7	US-11-293-697-2765	Sequence 2765, Ap
127	171	4.3	277	7	US-11-319-952-45	Sequence 45, Appl1	202	136.5	3.5	618	7	US-11-178-724-19	Sequence 19, Appl1
128	171	4.3	277	7	US-11-296-092-15	Sequence 15, Appl1	203	136.5	3.5	618	7	US-11-178-724-19	Sequence 19, Appl1
129	171	4.3	737	7	US-11-296-155-15	Sequence 15, Appl1	204	136.5	3.5	1198	7	US-11-217-997-14	Sequence 14, Appl1
130	170	4.3	864	7	US-11-178-724-27	Sequence 27, Appl1	205	136	3.4	696	6	US-10-449-902-41608	Sequence 41608, A
131	167.5	4.2	255	7	US-11-319-952-74	Sequence 74, Appl1	206	135	3.4	469	7	US-11-246-999-41	Sequence 41, Appl1
132	167.5	4.2	256	7	US-11-319-952-76	Sequence 76, Appl1	207	135	3.4	469	7	US-11-246-999-30	Sequence 30, Appl1
133	167.5	4.2	256	7	US-11-319-952-78	Sequence 78, Appl1	208	135	3.4	567	7	US-11-246-999-50	Sequence 50, Appl1
134	167.5	4.2	261	7	US-11-319-952-80	Sequence 80, Appl1	209	134	3.4	587	7	US-11-030-653-32	Sequence 32, Appl1
135	167.5	4.2	262	7	US-11-319-952-80	Sequence 80, Appl1	210	134	3.4	1786	6	US-10-519-328-2	Sequence 2, Appl1
136	166.5	4.2	723	7	US-11-178-724-18	Sequence 18, Appl1	211	134	3.4	1821	6	US-10-505-928-451	Sequence 451, App
137	166.5	4.2	723	7	US-11-071-796A-17	Sequence 17, Appl1	212	134	3.4	1821	6	US-10-519-328-1	Sequence 1, Appl1
138	162	4.1	248	6	US-10-449-902-40162	Sequence 40162, A	213	131.5	3.3	810	6	US-10-781-841-34	Sequence 34, Appl1
139	161	4.1	293	6	US-10-544-944-3	Sequence 3, Appl1	214	131	3.3	76	7	US-11-254-185-46	Sequence 46, Appl1
140	161	4.1	293	6	US-10-546-435-1	Sequence 1, Appl1	215	131	3.3	76	7	US-11-253-869-46	Sequence 46, Appl1
141	161	4.1	293	6	US-11-319-952-14	Sequence 14, Appl1	216	130.5	3.3	1398	7	US-11-217-997-4	Sequence 4, Appl1
142	160	4.1	113	7	US-11-254-185-28	Sequence 28, Appl1	217	130.5	3.3	1450	7	US-11-217-997-6	Sequence 6, Appl1
143	160	4.1	113	7	US-11-253-869-28	Sequence 28, Appl1	218	130.5	3.3	1594	7	US-11-217-997-18	Sequence 18, Appl1
144	160	4.1	262	6	US-10-511-937-2431	Sequence 2431, Ap	219	129	3.3	244	7	US-11-247-886-8	Sequence 8, Appl1
145	159	4.0	287	7	US-11-319-952-70	Sequence 70, Appl1	220	129	3.3	490	7	US-11-293-697-3621	Sequence 3621, Ap
147	158.5	4.0	283	7	US-11-357-337-2	Sequence 2, Appl1	221	128	3.2	342	7	US-11-038-753-1	Sequence 1, Appl1
148	158	4.0	465	6	US-10-505-928-549	Sequence 549, App	222	128	3.2	1418	7	US-11-217-997-38	Sequence 38, Appl1
149	157	4.0	686	7	US-11-264-243-4	Sequence 4, Appl1	223	126	3.2	330	6	US-10-505-928-521	Sequence 521, App
150	156	4.0	184	7	US-11-319-952-57	Sequence 57, Appl1	224	126	3.2	708	7	US-11-293-697-4329	Sequence 4329, Ap
151	156	4.0	255	7	US-11-319-952-75	Sequence 75, Appl1	225	124	3.1	911	7	US-11-226-554-89	Sequence 89, Appl1
152	156	4.0	261	7	US-11-319-952-79	Sequence 79, Appl1	226	123.5	3.1	1523	6	US-10-533-365-236	Sequence 236, App
153	155.5	3.9	830	7	US-11-175-714-11	Sequence 11, Appl1	227	123.5	3.1	491	7	US-11-217-997-30	Sequence 30, Appl1
154	154.5	3.9	264	7	US-11-247-886-1	Sequence 1, Appl1	228	121.5	3.1	364	6	US-10-505-928-605	Sequence 605, App
155	154	3.9	246	7	US-11-247-886-2	Sequence 2, Appl1	229	121	3.1	493	7	US-11-267-942-4	Sequence 4, Appl1
156	153.5	3.9	610	6	US-10-505-928-580	Sequence 580, App	230	121	3.1	3396	6	US-10-505-928-449	Sequence 449, App
157	153	3.9	244	7	US-11-247-886-6	Sequence 6, Appl1	231	121	3.1	1431	7	US-11-352-664-2	Sequence 2, Appl1
158	152.5	3.9	264	7	US-11-255-634-1	Sequence 10, Appl1	232	120.5	3.0	493	7	US-11-267-942-3	Sequence 3, Appl1
159	152.5	3.9	642	7	US-11-175-714-10	Sequence 10, Appl1	233	120	3.0	375	7	US-11-289-102-304	Sequence 304, App
160	152	3.9	247	6	US-10-511-937-2472	Sequence 2472, Ap	234	118.5	3.0	332	7	US-11-178-724-1	Sequence 1, Appl1
161	152	3.9	247	6	US-10-511-937-2940	Sequence 2940, Ap	235	117.5	3.0	76	7	US-11-254-185-47	Sequence 47, Appl1
162	152	3.9	686	7	US-11-175-714-25	Sequence 25, Appl1	236	117	3.0	76	7	US-11-253-869-43	Sequence 43, Appl1
163	152	3.9	686	7	US-11-175-714-40	Sequence 40, Appl1	237	117	3.0	76	7	US-11-267-942-5	Sequence 5, Appl1
164	152	3.9	686	7	US-11-175-714-42	Sequence 42, Appl1	238	115.5	2.9	448	7	US-11-267-942-5	Sequence 5, Appl1
165	152	3.9	686	7	US-11-175-714-44	Sequence 44, Appl1	239	115	2.9	775	7	US-11-293-697-4433	Sequence 4433, Ap
166	152	3.9	686	7	US-11-175-714-46	Sequence 46, Appl1	240	114	2.9	575	7	US-11-217-997-32	Sequence 32, Appl1
167	151.5	3.8	277	7	US-11-297-134-17	Sequence 17, Appl1	241	114	2.9	1394	7	US-11-352-664-251	Sequence 251, App
168	150.5	3.8	685	7	US-11-175-714-2	Sequence 2, Appl1	242	112.5	2.9	1247	6	US-10-505-928-171	Sequence 171, App
169	150.5	3.8	685	7	US-11-175-714-28	Sequence 28, Appl1	243	112	2.8	493	6	US-11-505-928-676	Sequence 676, App
170	150.5	3.8	685	7	US-11-175-714-32	Sequence 32, Appl1	244	112	2.8	493	6	US-11-267-942-2	Sequence 2, Appl1
171	150.5	3.8	685	7	US-11-175-714-34	Sequence 34, Appl1	245	112	2.8	2026	6	US-10-505-928-831	Sequence 831, App
172	150.5	3.8	685	7	US-11-175-714-36	Sequence 36, Appl1	246	111.5	2.8	488	7	US-11-274-634-21	Sequence 21, Appl1
173	150.5	3.8	685	7	US-11-175-714-38	Sequence 38, Appl1	247	111.5	2.8	732	7	US-11-274-634-3	Sequence 3, Appl1
174	150.5	3.8	685	7	US-11-178-724-20	Sequence 20, Appl1	248	111.5	2.8	755	7	US-11-274-634-14	Sequence 14, Appl1
175	150.5	3.8	685	7	US-11-264-243-2	Sequence 2, Appl1	249	110.5	2.8	615	6	US-10-953-349-11116	Sequence 11116, A
176	150.5	3.8	685	7	US-11-071-796A-19	Sequence 19, Appl1	250	110	2.8	76	7	US-11-254-185-48	Sequence 48, Appl1
177	150	3.8	276	6	US-10-544-944-16	Sequence 16, Appl1	251	110	2.8	76	7	US-11-253-869-48	Sequence 48, Appl1
178	150	3.8	276	6	US-10-546-435-8	Sequence 8, Appl1	254	108.5	2.8	545	7	US-11-101-316-110	Sequence 110, App

255	108.5	2.8	545	7	US-11-293-697-3725	Sequence 3725, Ap	331	91.5	2.3	1824	7	US-11-174-307B-1444	Sequence 1444, Ap
257	108	2.7	21	7	US-11-354-653-74	Sequence 74, Appl	332	91	2.3	233	7	US-11-321-421-110	Sequence 110, App
258	107	2.7	379	7	US-11-355-441-4	Sequence 4, Appl	333	91	2.3	1732	7	US-11-174-307B-170	Sequence 470, App
259	107	2.7	546	6	US-10-953-349-11117	Sequence 11117, A	334	90.5	2.3	820	6	US-10-982-908-26	Sequence 26, Appl
260	106.5	2.7	113	7	US-11-254-185-23	Sequence 23, Appl	335	90.5	2.3	994	6	US-10-449-902-43721	Sequence 43721, A
261	106.5	2.7	113	7	US-11-253-869-23	Sequence 23, Appl	336	90.5	2.3	1639	7	US-11-174-307B-1134	Sequence 1134, Ap
262	106.5	2.7	5635	6	US-10-766-760-2	Sequence 2, Appl	337	90.5	2.3	1964	7	US-10-541-307B-4458	Sequence 4458, Ap
264	105.5	2.7	374	6	US-10-781-841-25	Sequence 25, Appl	338	90.5	2.3	2804	6	US-11-174-708-48	Sequence 48, Appl
265	105.5	2.7	816	6	US-10-781-841-37	Sequence 37, Appl	339	90	2.3	123	7	US-11-254-185-29	Sequence 29, Appl
266	104.5	2.6	111	7	US-11-254-185-25	Sequence 25, Appl	340	90	2.3	123	7	US-11-253-869-29	Sequence 29, Appl
267	104.5	2.6	111	7	US-11-253-869-25	Sequence 25, Appl	341	90	2.3	246	6	US-10-953-349-18257	Sequence 18257, A
268	104.5	2.6	379	7	US-11-293-697-3405	Sequence 3405, Ap	342	90	2.3	246	6	US-11-056-355B-57360	Sequence 57360, A
269	104.5	2.6	967	6	US-10-449-902-52043	Sequence 52043, A	343	90	2.3	260	6	US-10-953-349-18256	Sequence 18256, A
270	104	2.6	157	7	US-11-175-714-6	Sequence 6, Appl	344	90	2.3	260	6	US-11-056-355B-57359	Sequence 57359, A
271	103.5	2.6	971	6	US-10-505-928-397	Sequence 397, Appl	345	90	2.3	408	6	US-10-953-349-30058	Sequence 30058, A
272	102.5	2.6	112	7	US-11-254-185-30	Sequence 30, Appl	346	90	2.3	411	6	US-10-953-349-10057	Sequence 30057, A
273	102.5	2.6	112	7	US-11-253-869-30	Sequence 30, Appl	347	90	2.3	411	6	US-10-953-349-30056	Sequence 30056, A
274	102	2.6	720	7	US-11-354-079-22	Sequence 22, Appl	348	90	2.3	655	6	US-10-449-902-36872	Sequence 36872, A
275	102	2.6	917	6	US-10-547-530-94	Sequence 94, Appl	349	90	2.3	802	6	US-10-449-902-55592	Sequence 55592, A
276	102	2.6	934	6	US-10-547-530-138	Sequence 138, App	350	89.5	2.3	50	7	US-11-354-079-12	Sequence 12, Appl
277	102	2.6	1013	6	US-10-547-530-106	Sequence 106, App	351	89.5	2.3	53	7	US-11-288-853-21	Sequence 21, Appl
278	102	2.6	289	7	US-10-547-530-122	Sequence 122, App	352	89.5	2.3	53	7	US-11-288-853-21	Sequence 21, Appl
279	101.5	2.6	289	7	US-11-217-997-28	Sequence 28, Appl	353	89.5	2.3	56	6	US-10-547-530-90	Sequence 90, Appl
281	101.5	2.6	685	7	US-11-293-697-3546	Sequence 3546, Ap	354	89.5	2.3	91	7	US-11-226-400-13	Sequence 13, Appl
282	101.5	2.6	726	6	US-10-449-902-54661	Sequence 54661, A	355	89.5	2.3	797	6	US-10-449-902-45223	Sequence 45223, A
283	101	2.6	1822	6	US-10-505-928-700	Sequence 700, App	356	89.5	2.3	996	6	US-10-449-902-45223	Sequence 45223, A
284	100.5	2.5	471	6	US-10-953-349-22152	Sequence 22152, A	357	89.5	2.3	1333	7	US-11-174-307B-1258	Sequence 1258, Ap
285	100.5	2.5	492	6	US-10-953-349-22151	Sequence 22151, A	358	89.5	2.3	1745	7	US-11-174-307B-1220	Sequence 960, App
286	100	2.5	162	7	US-11-357-337-6	Sequence 6, Appl	359	89	2.3	137	7	US-11-113-081A-12	Sequence 12, Appl
287	100	2.5	577	7	US-11-293-697-3485	Sequence 3485, Ap	360	89	2.3	1517	7	US-11-174-307B-616	Sequence 616, App
288	99	2.5	223	7	US-11-293-697-4500	Sequence 4500, Ap	361	89	2.3	1538	7	US-11-174-307B-944	Sequence 944, App
289	99	2.5	259	7	US-11-217-997-34	Sequence 34, Appl	362	89	2.3	1738	7	US-11-174-307B-864	Sequence 864, App
290	99	2.5	502	7	US-11-293-697-4802	Sequence 4802, Ap	363	89	2.3	1768	7	US-11-174-307B-1220	Sequence 1220, Ap
291	98.5	2.5	477	6	US-10-953-349-11118	Sequence 11118, A	364	89	2.3	1919	7	US-11-174-307B-978	Sequence 978, App
292	98	2.5	949	6	US-10-547-530-92	Sequence 92, Appl	365	88.5	2.2	32	7	US-11-244-452-15	Sequence 15, Appl
293	98	2.5	966	6	US-10-547-530-136	Sequence 136, App	366	88.5	2.2	229	7	US-11-293-697-4810	Sequence 4810, Ap
294	98	2.5	993	6	US-10-449-902-45747	Sequence 45747, A	367	88.5	2.2	642	7	US-11-056-355B-53787	Sequence 53787, A
295	98	2.5	1045	6	US-10-547-530-104	Sequence 104, App	368	88.5	2.2	917	7	US-11-293-697-2966	Sequence 2966, Ap
296	98	2.5	1080	6	US-10-547-530-120	Sequence 120, App	369	88.5	2.2	1047	7	US-11-293-697-2852	Sequence 2852, Ap
297	98	2.5	5738	6	US-10-505-928-150	Sequence 150, App	370	88.5	2.2	1252	7	US-11-174-307B-536	Sequence 536, App
298	97	2.5	724	7	US-11-293-697-3363	Sequence 3363, Ap	371	88.5	2.2	1742	7	US-11-174-307B-1238	Sequence 1238, App
299	97	2.5	1193	6	US-10-505-928-537	Sequence 537, App	372	88	2.2	799	6	US-10-505-928-716	Sequence 716, App
300	96.5	2.4	1475	6	US-11-174-307B-988	Sequence 988, App	373	88	2.2	1277	7	US-11-174-307B-634	Sequence 634, App
301	96	2.4	832	6	US-10-505-928-491	Sequence 491, App	374	88	2.2	1607	7	US-11-174-307B-4530	Sequence 4530, Ap
302	95.5	2.4	1611	7	US-11-174-307B-2234	Sequence 2234, App	375	88	2.2	2149	7	US-11-174-307B-3214	Sequence 3214, Ap
303	95.5	2.4	1611	7	US-11-174-307B-2552	Sequence 2552, Ap	376	87.5	2.2	687	7	US-11-289-102-370	Sequence 370, App
304	95	2.4	1220	7	US-11-174-307B-284	Sequence 284, App	378	87.5	2.2	1442	7	US-11-174-307B-1084	Sequence 1084, Ap
305	94	2.4	536	6	US-10-449-902-40167	Sequence 40167, A	379	87.5	2.2	7285	7	US-11-272-521-28	Sequence 28, Appl
306	94	2.4	1721	7	US-10-449-902-968	Sequence 968, App	380	87	2.2	454	7	US-11-283-329-140	Sequence 140, App
307	94	2.4	1768	7	US-11-174-307B-1136	Sequence 1136, Ap	381	87	2.2	476	7	US-11-283-329-138	Sequence 138, App
308	93.5	2.4	433	6	US-10-953-349-1522	Sequence 1522, Ap	382	87	2.2	480	7	US-11-283-329-136	Sequence 136, App
309	93.5	2.4	468	6	US-10-511-937-2595	Sequence 2595, Ap	383	87	2.2	863	6	US-10-449-902-43861	Sequence 43861, A
310	93.5	2.4	486	6	US-10-953-349-1921	Sequence 1921, Ap	384	87	2.2	1248	7	US-11-174-307B-934	Sequence 934, App
311	93.5	2.4	501	6	US-10-953-349-1920	Sequence 1920, Ap	385	87	2.2	1333	7	US-11-174-307B-1404	Sequence 1404, Ap
312	93.5	2.4	687	6	US-10-449-902-53244	Sequence 53244, A	386	87	2.2	1429	7	US-11-174-307B-2274	Sequence 2274, Ap
313	93.5	2.4	880	6	US-10-982-908-28	Sequence 28, Appl	387	86.5	2.2	345	7	US-11-289-102-249	Sequence 249, App
314	93.5	2.4	880	6	US-10-449-902-41499	Sequence 41499, A	388	86.5	2.2	1980	7	US-11-174-307B-1298	Sequence 1298, Ap
315	93.5	2.4	1099	6	US-10-449-902-55236	Sequence 55236, A	389	86	2.2	421	6	US-10-953-349-22153	Sequence 22153, A
316	93.5	2.4	1630	7	US-11-174-307B-2222	Sequence 2222, Ap	390	86	2.2	909	6	US-10-449-902-44686	Sequence 44686, A
317	93	2.4	74	7	US-11-254-185-45	Sequence 45, Appl	391	86	2.2	1019	6	US-10-505-928-94	Sequence 94, Appl
318	93	2.4	74	7	US-11-253-869-45	Sequence 45, Appl	392	86	2.2	969	6	US-10-525-105-27	Sequence 27, Appl
319	93	2.4	483	7	US-11-293-697-3715	Sequence 3715, Ap	393	86	2.2	1023	6	US-10-525-105-25	Sequence 25, Appl
320	93	2.4	801	6	US-10-504-973-38	Sequence 38, Appl	394	86	2.2	1175	6	US-10-449-902-41614	Sequence 41614, A
321	93	2.4	1002	7	US-11-259-133-113	Sequence 113, Appl	395	86	2.2	1316	7	US-11-174-307B-588	Sequence 588, App
322	93	2.4	1418	7	US-11-174-307B-950	Sequence 950, App	396	86	2.2	1373	7	US-11-105-233-187	Sequence 187, App
323	92.5	2.3	569	7	US-11-174-307B-200	Sequence 200, App	397	86	2.2	1516	7	US-11-174-307B-4074	Sequence 4074, Ap
324	92.5	2.3	1042	7	US-11-121-154-176	Sequence 176, App	398	86	2.2	1522	7	US-11-174-307B-1154	Sequence 1154, Ap
325	92.5	2.3	1367	7	US-11-289-102-382	Sequence 382, App	399	86	2.2	1863	7	US-11-174-307B-988	Sequence 988, App
326	92.5	2.3	1544	7	US-11-174-307B-1374	Sequence 1374, Ap	400	86	2.2	1896	7	US-11-174-307B-1376	Sequence 1376, Ap
327	92	2.3	845	6	US-10-449-902-45752	Sequence 45752, A	401	86	2.2	1942	7	US-11-174-307B-1296	Sequence 1296, Ap
328	92	2.3	845	6	US-10-449-902-52863	Sequence 52863, A	402	85.5	2.2	411	6	US-10-953-349-8481	Sequence 8481, Ap
329	91.5	2.3	585	6	US-10-449-902-41383	Sequence 41383, A	403	85.5	2.2	411	6	US-11-056-355B-34823	Sequence 34823, A
330	91.5	2.3	1592	7	US-11-174-307B-1172	Sequence 1172, Ap	404	85.5	2.2	411	7	US-11-056-355B-40040	Sequence 40040, A

405	85.5	2.2	411	7	US-11-056-355B-89035	Sequence 89035, A	479	83.5	2.1	470	7	US-11-056-355B-74178	Sequence 74178, A
406	85.5	2.2	421	7	US-11-056-355B-92791	Sequence 92791, A	480	83.5	2.1	622	7	US-11-056-355B-74177	Sequence 74177, A
407	85.5	2.2	431	7	US-11-056-355B-89034	Sequence 89034, A	481	83.5	2.1	628	7	US-11-056-355B-77083	Sequence 77083, A
408	85.5	2.2	421	7	US-11-056-355B-92790	Sequence 92790, A	482	83.5	2.1	694	7	US-11-056-355B-45870	Sequence 45870, A
409	85.5	2.2	598	7	US-11-296-092-69	Sequence 69, App1	483	83.5	2.1	694	7	US-11-056-355B-77082	Sequence 77082, A
410	85.5	2.2	598	7	US-11-296-153-69	Sequence 69, App1	484	83.5	2.1	697	7	US-11-056-355B-45869	Sequence 45869, A
411	85.5	2.2	673	7	US-11-101-316-16	Sequence 16, App1	485	83.5	2.1	697	7	US-11-056-355B-77081	Sequence 77081, A
412	85.5	2.2	759	6	US-10-449-902-42287	Sequence 42287, A	486	83.5	2.1	748	7	US-11-056-355B-45868	Sequence 45868, A
413	85.5	2.2	1259	7	US-11-174-307B-1126	Sequence 1126, Ap	487	83.5	2.1	838	7	US-11-174-307B-808	Sequence 808, App
414	85.5	2.2	1529	7	US-11-174-307B-1114	Sequence 1114, Ap	488	83.5	2.1	873	7	US-11-174-307B-1072	Sequence 1072, Ap
415	85.5	2.2	1534	7	US-11-174-307B-2156	Sequence 2156, Ap	489	83.5	2.1	1132	7	US-11-174-307B-6648	Sequence 6648, Ap
416	85.5	2.2	1739	7	US-11-174-307B-3342	Sequence 3342, Ap	490	83.5	2.1	1133	7	US-11-174-307B-644	Sequence 644, App
417	85.5	2.2	1881	7	US-11-174-307B-520	Sequence 520, App	491	83.5	2.1	1120	7	US-11-174-307B-1048	Sequence 1048, Ap
418	85.5	2.2	2202	6	US-10-544-731-8	Sequence 8, App1	492	83.5	2.1	1277	7	US-11-174-307B-888	Sequence 888, App
419	85.5	2.2	2227	6	US-10-544-731-7	Sequence 7, App1	493	83.5	2.1	1289	7	US-11-174-307B-2714	Sequence 2714, Ap
420	85.5	2.2	2233	6	US-10-544-731-9	Sequence 9, App1	494	83.5	2.1	1315	7	US-11-174-307B-4248	Sequence 4248, Ap
421	85	2.2	536	6	US-10-449-902-36867	Sequence 36867, A	495	83.5	2.1	1363	7	US-11-174-307B-4900	Sequence 4900, Ap
422	85	2.2	536	6	US-10-449-902-46163	Sequence 46163, A	496	83.5	2.1	1424	7	US-11-174-307B-504	Sequence 504, App
423	85	2.2	594	6	US-10-525-105-7	Sequence 7, App1	497	83.5	2.1	1658	7	US-11-174-307B-2176	Sequence 2176, Ap
424	85	2.2	639	6	US-10-525-105-10	Sequence 10, App1	498	83.5	2.1	1753	7	US-11-174-307B-802	Sequence 802, App
425	85	2.2	732	7	US-11-293-697-3575	Sequence 3575, Ap	499	83	2.1	431	7	US-11-293-697-3749	Sequence 3749, Ap
426	85	2.2	774	6	US-10-525-105-1	Sequence 1, App1	500	83	2.1	673	7	US-11-293-697-4868	Sequence 4868, Ap
427	85	2.2	774	7	US-11-226-554-111	Sequence 11, App	501	83	2.1	1168	7	US-11-174-307B-700	Sequence 700, App
428	85	2.2	1019	6	US-10-525-105-22	Sequence 22, App1	502	83	2.1	1228	7	US-11-174-307B-3388	Sequence 3388, Ap
429	85	2.2	1020	6	US-10-525-105-17	Sequence 17, App1	503	83	2.1	1316	7	US-11-174-307B-704	Sequence 704, App
430	85	2.2	1023	6	US-10-525-105-20	Sequence 20, App1	504	83	2.1	1479	7	US-11-174-307B-758	Sequence 758, App
431	85	2.2	1024	6	US-10-525-105-15	Sequence 15, App1	505	83	2.1	1522	7	US-11-174-307B-1098	Sequence 1098, Ap
432	85	2.2	1302	7	US-11-174-307B-3424	Sequence 2424, Ap	506	83	2.1	1633	7	US-11-174-307B-1088	Sequence 1088, Ap
433	85	2.2	1350	7	US-11-174-307B-1316	Sequence 1316, Ap	507	83	2.1	1637	7	US-11-174-307B-1246	Sequence 1246, Ap
434	85	2.2	1488	7	US-11-174-307B-3986	Sequence 3986, Ap	508	83	2.1	1655	7	US-11-174-307B-3630	Sequence 3630, Ap
435	85	2.2	1518	7	US-11-174-307B-742	Sequence 742, App	509	83	2.1	1702	7	US-11-174-307B-2114	Sequence 2114, Ap
436	85	2.2	1597	7	US-11-174-307B-618	Sequence 618, App	510	83	2.1	1766	7	US-11-174-307B-2554	Sequence 2554, Ap
437	85	2.2	1784	7	US-11-174-307B-2856	Sequence 2856, Ap	511	83	2.1	1806	7	US-11-174-307B-872	Sequence 872, App
438	85	2.2	1796	7	US-11-174-307B-910	Sequence 910, App	512	83	2.1	1848	7	US-11-174-307B-1372	Sequence 1372, Ap
439	85	2.2	1851	7	US-11-174-307B-2240	Sequence 2240, Ap	513	83	2.1	2085	7	US-11-174-307B-954	Sequence 954, App
440	85	2.2	1973	7	US-11-174-307B-1378	Sequence 1378, Ap	514	83	2.1	5179	7	US-11-105-233-185	Sequence 185, App
441	85	2.2	2097	7	US-11-174-307B-1444	Sequence 1444, Ap	515	82.5	2.1	408	7	US-11-175-714-140	Sequence 140, App
442	84.5	2.1	363	7	US-11-354-653-82	Sequence 82, App1	516	82.5	2.1	477	6	US-10-953-349-11023	Sequence 11023, A
443	84.5	2.1	375	7	US-11-246-999-38	Sequence 38, App1	517	82.5	2.1	479	6	US-10-953-349-11022	Sequence 11022, A
444	84.5	2.1	383	6	US-10-505-928-825	Sequence 825, App	518	82.5	2.1	987	7	US-11-174-307B-1224	Sequence 1224, Ap
445	84.5	2.1	383	7	US-11-246-999-45	Sequence 45, App1	519	82.5	2.1	1108	7	US-11-174-307B-1122	Sequence 1122, Ap
446	84.5	2.1	383	7	US-11-246-999-16	Sequence 126, App	520	82.5	2.1	1215	7	US-11-174-307B-2800	Sequence 2800, Ap
447	84.5	2.1	383	7	US-11-354-653-29	Sequence 29, App1	521	82.5	2.1	1300	7	US-11-174-307B-1250	Sequence 1250, Ap
448	84.5	2.1	413	7	US-11-246-999-125	Sequence 125, App	522	82.5	2.1	1375	7	US-11-174-307B-622	Sequence 622, App
449	84.5	2.1	430	7	US-11-175-714-1381	Sequence 138, App	523	82.5	2.1	1481	7	US-11-174-307B-1162	Sequence 1162, Ap
450	84.5	2.1	547	7	US-11-293-697-2751	Sequence 2751, Ap	524	82.5	2.1	1530	7	US-11-174-307B-854	Sequence 854, App
451	84.5	2.1	1367	7	US-11-174-307B-510	Sequence 510, App	525	82.5	2.1	1860	7	US-11-174-307B-4132	Sequence 4132, Ap
452	84.5	2.1	1464	7	US-11-174-307B-1116	Sequence 1116, Ap	526	82.5	2.1	1938	7	US-11-174-307B-996	Sequence 996, App
453	84.5	2.1	1720	7	US-11-174-307B-3676	Sequence 3676, Ap	527	82	2.1	274	7	US-11-254-185-9	Sequence 9, App1
454	84.5	2.1	1859	7	US-11-174-307B-940	Sequence 940, App	528	82	2.1	274	6	US-11-253-869-9	Sequence 9, App1
455	84.5	2.1	2062	7	US-11-174-307B-876	Sequence 876, App	529	82	2.1	758	6	US-10-449-902-65544	Sequence 56544, A
456	84.5	2.1	2740	7	US-11-174-307B-1234	Sequence 1234, Ap	530	82	2.1	863	7	US-11-174-307B-2446	Sequence 2446, Ap
457	84.5	2.1	526	6	US-10-449-902-46218	Sequence 46218, A	531	82	2.1	1005	7	US-11-174-307B-1158	Sequence 1158, Ap
458	84	2.1	526	6	US-10-449-902-51492	Sequence 51492, A	532	82	2.1	1029	7	US-11-174-307B-1900	Sequence 1900, Ap
459	84	2.1	526	6	US-10-449-902-51492	Sequence 51492, A	533	82	2.1	1125	7	US-11-174-307B-1166	Sequence 1166, Ap
460	84	2.1	542	7	US-11-056-355B-53956	Sequence 53956, A	534	82	2.1	1194	7	US-11-174-307B-2338	Sequence 2338, Ap
461	84	2.1	595	7	US-11-293-697-3163	Sequence 3163, A	535	82	2.1	1214	7	US-11-174-307B-986	Sequence 986, App
462	84	2.1	909	6	US-10-525-105-4	Sequence 4, App1	536	82	2.1	1245	7	US-11-174-307B-850	Sequence 850, App
463	84	2.1	1285	7	US-11-174-307B-1124	Sequence 1124, Ap	537	82	2.1	1283	7	US-11-174-307B-678	Sequence 678, App
464	84	2.1	1294	7	US-11-174-307B-314	Sequence 314, App	538	82	2.1	1449	7	US-11-174-307B-1362	Sequence 1362, Ap
465	84	2.1	1294	7	US-11-174-307B-3608	Sequence 2608, Ap	539	82	2.1	1462	7	US-11-174-307B-1412	Sequence 1412, Ap
466	84	2.1	1432	7	US-11-174-307B-946	Sequence 946, App	540	82	2.1	1504	7	US-11-174-307B-932	Sequence 932, App
467	84	2.1	1600	7	US-11-174-307B-636	Sequence 636, App	541	82	2.1	1653	7	US-11-174-307B-626	Sequence 626, App
468	84	2.1	1676	7	US-11-174-307B-628	Sequence 628, App	542	82	2.1	1680	7	US-11-174-307B-712	Sequence 712, App
469	84	2.1	1759	7	US-11-174-307B-942	Sequence 942, App	543	82	2.1	1957	7	US-11-174-307B-2192	Sequence 2192, Ap
470	84	2.1	1764	7	US-11-174-307B-900	Sequence 900, App	544	81.5	2.1	382	7	US-11-354-653-50	Sequence 50, App1
471	84	2.1	1792	7	US-11-174-307B-1192	Sequence 1192, Ap	545	81.5	2.1	407	7	US-11-174-307B-4	Sequence 4, App1
472	84	2.1	1811	7	US-11-174-307B-924	Sequence 924, App	546	81.5	2.1	777	6	US-10-449-902-42956	Sequence 42956, A
473	84	2.1	1818	7	US-11-174-307B-586	Sequence 586, App	547	81.5	2.1	800	7	US-11-056-355B-73161	Sequence 73161, A
474	84	2.1	1847	7	US-11-174-307B-2852	Sequence 2852, Ap	548	81.5	2.1	862	6	US-10-449-902-55157	Sequence 55157, A
475	84	2.1	1860	7	US-11-174-307B-612	Sequence 612, App	549	81.5	2.1	896	7	US-11-056-355B-73160	Sequence 73160, A
476	84	2.1	1917	7	US-11-174-307B-2172	Sequence 2172, Ap	550	81.5	2.1	930	6	US-10-449-902-4161	Sequence 4161, A
477	84	2.1	2195	7	US-11-174-307B-5412	Sequence 5412, Ap	551	81.5	2.1	985	7	US-11-293-697-2874	Sequence 2874, Ap
478	83.5	2.1	426	6	US-10-953-349-33790	Sequence 33790, A							

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553	81.5	2.1	1161	7	US-11-174-307B-1150	Sequence 1150, App	626	80	2.0	335	6	US-10-511-937-7469	Sequence 2469, App
554	81.5	2.1	1370	7	US-11-174-307B-858	Sequence 858, App	627	80	2.0	350	6	US-10-520-783-10	Sequence 10, Appl
555	81.5	2.1	1542	7	US-11-174-307B-1248	Sequence 1248, App	628	80	2.0	442	6	US-10-449-902-46671	Sequence 46671, A
556	81.5	2.1	1610	7	US-11-174-307B-1472	Sequence 1472, App	629	80	2.0	533	6	US-10-449-902-43727	Sequence 43727, A
557	81.5	2.1	1761	7	US-11-174-307B-1306	Sequence 1306, App	630	80	2.0	1017	7	US-11-174-307B-956	Sequence 956, App
558	81.5	2.1	1771	7	US-11-174-307B-928	Sequence 928, App	631	80	2.0	1053	7	US-11-174-307B-1230	Sequence 1230, App
559	81.5	2.1	1786	7	US-11-174-307B-602	Sequence 602, App	632	80	2.0	1217	7	US-11-105-233-186	Sequence 186, App
560	81.5	2.1	2013	7	US-11-174-307B-1226	Sequence 1226, App	633	80	2.0	1283	7	US-11-174-307B-578	Sequence 578, App
561	81	2.1	243	7	US-11-356-373-13	Sequence 13, Appl	634	80	2.0	1336	7	US-11-174-307B-1036	Sequence 1036, App
562	81	2.1	324	6	US-10-449-902-50892	Sequence 50892, A	635	80	2.0	1485	7	US-11-174-307B-1180	Sequence 1180, App
563	81	2.1	325	7	US-11-293-697-3615	Sequence 3615, App	636	80	2.0	1914	7	US-11-174-307B-1256	Sequence 1256, App
564	81	2.1	426	6	US-10-449-902-54143	Sequence 54143, A	637	80	2.0	2124	7	US-11-174-307B-3446	Sequence 3446, App
565	81	2.1	523	6	US-10-953-349-8167	Sequence 8167, App	638	80	2.0	3696	7	US-11-330-363-4	Sequence 4, Appl1
566	81	2.1	662	6	US-10-953-349-8167	Sequence 8167, App	639	79.5	2.0	33	7	US-11-134-871-1040	Sequence 1040, App
567	81	2.1	662	7	US-11-056-355B-38224	Sequence 38224, A	640	79.5	2.0	195	7	US-11-056-355B-73250	Sequence 73250, A
568	81	2.1	662	7	US-11-056-355B-103367	Sequence 103367, A	641	79.5	2.0	217	6	US-10-471-571A-4354	Sequence 4354, App
569	81	2.1	662	7	US-11-056-355B-114606	Sequence 114606, A	642	79.5	2.0	286	6	US-10-449-902-37451	Sequence 37451, A
570	81	2.1	732	6	US-10-953-349-1606	Sequence 1606, App	643	79.5	2.0	407	6	US-10-449-902-36216	Sequence 36216, A
571	81	2.1	732	7	US-11-056-355B-38223	Sequence 38223, A	644	79.5	2.0	801	6	US-10-449-902-47499	Sequence 47499, A
572	81	2.1	732	7	US-11-056-355B-103366	Sequence 103366, A	645	79.5	2.0	868	7	US-11-056-355B-83749	Sequence 83749, A
573	81	2.1	732	7	US-11-056-355B-114605	Sequence 114605, A	646	79.5	2.0	923	7	US-11-174-307B-4314	Sequence 4314, App
574	81	2.1	734	6	US-10-953-349-1505	Sequence 1605, App	647	79.5	2.0	1077	7	US-11-056-355B-79530	Sequence 79530, A
575	81	2.1	754	7	US-11-056-355B-38222	Sequence 38222, A	648	79.5	2.0	1088	7	US-11-056-355B-79529	Sequence 79529, A
576	81	2.1	754	7	US-11-056-355B-103365	Sequence 103365, A	649	79.5	2.0	1097	7	US-11-174-307B-638	Sequence 638, App
577	81	2.1	754	7	US-11-056-355B-114604	Sequence 114604, A	650	79.5	2.0	1254	7	US-11-056-355B-79528	Sequence 79528, A
578	81	2.1	765	7	US-11-165-586-36	Sequence 36, Appl	651	79.5	2.0	1263	7	US-11-174-307B-1290	Sequence 1290, App
579	81	2.1	1135	7	US-11-174-307B-2204	Sequence 2204, App	652	79.5	2.0	1307	7	US-11-174-307B-4164	Sequence 4164, App
580	81	2.1	1133	7	US-11-174-307B-1236	Sequence 1236, App	653	79.5	2.0	1346	7	US-11-174-307B-676	Sequence 676, App
581	81	2.1	1233	7	US-11-174-307B-734	Sequence 734, App	654	79.5	2.0	1376	7	US-11-174-307B-3652	Sequence 3652, App
582	81	2.1	1351	7	US-11-174-307B-994	Sequence 994, App	655	79.5	2.0	1421	7	US-11-174-307B-1108	Sequence 1108, App
583	81	2.1	1395	7	US-11-174-307B-1130	Sequence 1130, App	656	79.5	2.0	1446	7	US-11-174-307B-662	Sequence 662, App
584	81	2.1	1432	7	US-11-174-307B-1100	Sequence 1100, App	657	79.5	2.0	1713	7	US-11-174-307B-2224	Sequence 2224, App
585	81	2.1	1436	7	US-11-174-307B-958	Sequence 958, App	658	79.5	2.0	1744	7	US-11-174-307B-580	Sequence 580, App
586	81	2.1	1443	7	US-11-174-307B-870	Sequence 870, App	659	79.5	2.0	2762	7	US-11-174-307B-2672	Sequence 2672, App
587	81	2.1	1510	7	US-11-174-307B-584	Sequence 584, App	660	79	2.0	493	6	US-10-449-902-35429	Sequence 35429, A
588	81	2.1	1573	7	US-11-174-307B-770	Sequence 770, App	661	79	2.0	487	6	US-11-056-355B-48545	Sequence 48545, A
589	81	2.1	1599	7	US-11-174-307B-1050	Sequence 1050, App	662	79	2.0	579	6	US-10-449-902-56026	Sequence 56026, A
590	81	2.1	1641	7	US-11-174-307B-760	Sequence 760, App	663	79	2.0	762	6	US-10-449-902-45396	Sequence 45396, A
591	81	2.1	1828	7	US-11-056-355B-88825	Sequence 88825, A	664	79	2.0	869	7	US-11-056-355B-83114	Sequence 83114, A
592	81	2.1	1828	7	US-11-056-355B-82581	Sequence 82581, A	665	79	2.0	871	7	US-11-056-355B-83113	Sequence 83113, A
593	81	2.1	1842	7	US-11-056-355B-82005	Sequence 82005, A	666	79	2.0	928	6	US-10-449-902-42253	Sequence 42253, A
594	81	2.1	1850	7	US-11-056-355B-82004	Sequence 82004, A	667	79	2.0	1007	7	US-11-174-307B-4898	Sequence 4898, App
595	81	2.1	1895	7	US-11-056-355B-82003	Sequence 82003, A	668	79	2.0	1181	7	US-11-174-307B-1288	Sequence 1288, App
596	81	2.1	3658	7	US-11-174-307B-1668	Sequence 1668, App	669	79	2.0	1250	7	US-11-174-307B-1204	Sequence 1204, App
597	80.5	2.0	45	7	US-11-217-997-43	Sequence 43, Appl	670	79	2.0	1268	7	US-11-174-307B-744	Sequence 744, App
598	80.5	2.0	220	7	US-11-056-355B-11964	Sequence 11964, A	671	79	2.0	1306	7	US-11-174-307B-1254	Sequence 1254, App
599	80.5	2.0	221	7	US-11-056-355B-11963	Sequence 11963, A	672	79	2.0	1325	6	US-10-449-902-51794	Sequence 51794, A
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601	80.5	2.0	470	7	US-11-056-355B-119000	Sequence 119000, A	674	79	2.0	1449	7	US-11-174-307B-790	Sequence 790, App
602	80.5	2.0	620	7	US-11-056-355B-107760	Sequence 107760, A	675	79	2.0	1493	7	US-11-174-307B-4196	Sequence 4196, App
603	80.5	2.0	620	7	US-11-056-355B-118999	Sequence 118999, A	676	79	2.0	1537	7	US-11-174-307B-716	Sequence 716, App
604	80.5	2.0	626	6	US-10-449-902-55581	Sequence 55581, A	677	79	2.0	1564	7	US-11-174-307B-798	Sequence 798, App
605	80.5	2.0	626	6	US-11-056-355B-107759	Sequence 107759, A	678	79	2.0	1597	7	US-11-174-307B-798	Sequence 798, App
606	80.5	2.0	626	6	US-11-056-355B-118998	Sequence 118998, A	679	79	2.0	1681	7	US-11-174-307B-874	Sequence 874, App
607	80.5	2.0	728	6	US-10-449-902-44535	Sequence 44535, A	680	79	2.0	1711	7	US-11-174-307B-2190	Sequence 2190, App
608	80.5	2.0	742	7	US-11-289-102-241	Sequence 241, App	681	79	2.0	1722	6	US-10-505-8978-780	Sequence 780, App
609	80.5	2.0	798	7	US-11-292-634-6	Sequence 6, Appl1	682	79	2.0	1736	7	US-11-174-307B-664	Sequence 664, App
610	80.5	2.0	823	7	US-11-056-355B-84007	Sequence 84007, A	683	79	2.0	1816	7	US-11-174-307B-590	Sequence 590, App
611	80.5	2.0	943	6	US-10-449-902-55109	Sequence 55109, A	684	79	2.0	1844	7	US-11-174-307B-930	Sequence 930, App
612	80.5	2.0	1055	7	US-11-174-307B-3194	Sequence 3194, App	685	79	2.0	2337	7	US-11-174-307B-1868	Sequence 1868, App
613	80.5	2.0	1086	7	US-11-174-307B-600	Sequence 600, App	686	78.5	2.0	62	7	US-11-324-846-3	Sequence 3, Appl1
614	80.5	2.0	1162	7	US-11-174-307B-2244	Sequence 2244, App	687	78.5	2.0	157	7	US-11-354-079-2	Sequence 2, Appl1
615	80.5	2.0	1234	7	US-11-174-307B-656	Sequence 656, App	688	78.5	2.0	194	7	US-11-056-355B-73251	Sequence 73251, A
616	80.5	2.0	1310	6	US-10-449-902-41328	Sequence 41328, A	689	78.5	2.0	464	6	US-10-449-902-10823	Sequence 10823, A
617	80.5	2.0	1322	7	US-11-174-307B-592	Sequence 592, App	690	78.5	2.0	986	7	US-11-226-554-101	Sequence 101, App
618	80.5	2.0	1407	7	US-11-174-307B-2194	Sequence 648, App	691	78.5	2.0	1017	7	US-11-174-307B-3140	Sequence 3140, App
619	80.5	2.0	1448	7	US-11-174-307B-6198	Sequence 2194, App	692	78.5	2.0	1055	7	US-11-259-133-24	Sequence 24, Appl
620	80.5	2.0	1517	7	US-11-174-307B-1202	Sequence 1202, App	693	78.5	2.0	1174	7	US-11-174-307B-666	Sequence 666, App
621	80.5	2.0	1549	7	US-11-174-307B-552	Sequence 552, App	694	78.5	2.0	1194	7	US-11-174-307B-5030	Sequence 5030, App
622	80.5	2.0	1662	7	US-11-174-307B-1966	Sequence 1966, App	695	78.5	2.0	1221	7	US-11-174-307B-1260	Sequence 1260, App
623	80.5	2.0	1865	7	US-11-174-307B-2174	Sequence 2174, App	696	78.5	2.0	1222	7	US-11-174-307B-2688	Sequence 2688, App
624	80	2.0	197	6	US-10-533-153-1	Sequence 1, Appl1	697	78.5	2.0	1291	7	US-11-174-307B-1080	Sequence 1080, App

658	78.5	2.0	1336	7	US-11-174-307B-532	Sequence 532, App	771	77.5	2.0	1101	7	US-11-056-355B-92745	Sequence 92745, A
659	78.5	2.0	1396	7	US-11-174-307B-2698	Sequence 2698, Ap	772	77.5	2.0	1182	7	US-11-174-307B-1872	Sequence 1872, Ap
700	78.5	2.0	1481	7	US-11-174-307B-878	Sequence 878, App	773	77.5	2.0	1212	7	US-11-174-307B-1696	Sequence 1696, Ap
701	78.5	2.0	1495	7	US-11-174-307B-776	Sequence 776, App	774	77.5	2.0	1228	7	US-11-174-307B-980	Sequence 980, App
702	78.5	2.0	1645	6	US-10-505-928-582	Sequence 582, App	775	77.5	2.0	1259	7	US-11-056-355B-8898	Sequence 8898, A
703	78.5	2.0	1696	7	US-11-174-307B-630	Sequence 630, App	776	77.5	2.0	1259	7	US-11-056-355B-92744	Sequence 92744, A
704	78.5	2.0	1663	7	US-11-174-307B-1830	Sequence 1830, Ap	777	77.5	2.0	1261	7	US-11-174-307B-668	Sequence 668, App
705	78.5	2.0	1918	7	US-11-174-307B-692	Sequence 692, App	778	77.5	2.0	1365	7	US-11-174-307B-2318	Sequence 2318, Ap
706	78.5	2.0	1919	7	US-11-174-307B-2170	Sequence 2170, Ap	779	77.5	2.0	1404	7	US-11-174-307B-1240	Sequence 1240, Ap
707	78.5	2.0	2101	7	US-11-174-307B-778	Sequence 778, App	780	77.5	2.0	1410	7	US-11-174-307B-964	Sequence 964, App
708	78.5	2.0	2327	7	US-11-174-307B-1292	Sequence 1292, Ap	781	77.5	2.0	1471	7	US-11-174-307B-1160	Sequence 1160, Ap
709	78.5	2.0	2366	7	US-11-174-307B-804	Sequence 804, App	782	77.5	2.0	1487	7	US-11-174-307B-696	Sequence 696, App
710	78	2.0	304	6	US-10-449-902-54577	Sequence 54577, A	783	77.5	2.0	1600	7	US-11-174-307B-544	Sequence 544, App
711	78	2.0	353	7	US-10-953-349-2	Sequence 2, App1.1	784	77.5	2.0	1600	7	US-11-174-307B-754	Sequence 754, App
712	78	2.0	382	6	US-10-953-349-2679	Sequence 2679, Ap	785	77.5	2.0	1648	7	US-11-174-307B-670	Sequence 670, App
713	78	2.0	382	7	US-11-056-355B-43481	Sequence 43481, A	786	77.5	2.0	1705	7	US-11-174-307B-1152	Sequence 1152, Ap
714	78	2.0	382	7	US-11-056-355B-84830	Sequence 84830, A	787	77.5	2.0	1713	7	US-11-174-307B-3720	Sequence 3720, Ap
715	78	2.0	401	6	US-10-953-349-2678	Sequence 2678, Ap	788	77.5	2.0	1735	7	US-11-174-307B-2246	Sequence 2246, Ap
716	78	2.0	401	7	US-10-953-349-2678	Sequence 2678, Ap	789	77.5	2.0	1868	7	US-11-174-307B-4320	Sequence 4320, Ap
717	78	2.0	401	7	US-11-056-355B-43480	Sequence 43480, A	790	77.5	2.0	2062	7	US-11-174-307B-1454	Sequence 1454, Ap
718	78	2.0	412	7	US-11-056-355B-84829	Sequence 84829, A	791	77.5	2.0	3460	6	US-10-505-928-104	Sequence 104, App
719	78	2.0	413	6	US-10-953-349-2677	Sequence 2677, Ap	792	77	2.0	162	7	US-11-217-997-10	Sequence 10, App1
720	78	2.0	413	7	US-11-056-355B-43479	Sequence 43479, A	793	77	2.0	167	6	US-10-449-902-29673	Sequence 29673, A
721	78	2.0	479	6	US-10-505-928-835	Sequence 835, App	794	77	2.0	167	6	US-10-449-902-32487	Sequence 32487, A
722	78	2.0	502	6	US-10-449-902-53133	Sequence 53133, A	795	77	2.0	173	6	US-11-217-997-36	Sequence 36, App1
723	78	2.0	694	6	US-10-449-902-53143	Sequence 53143, A	796	77	2.0	286	7	US-11-056-355B-49911	Sequence 49911, A
724	78	2.0	709	7	US-11-337-061-2	Sequence 2, App1.1	797	77	2.0	294	7	US-11-056-355B-49910	Sequence 49910, A
725	78	2.0	765	7	US-11-292-634-2	Sequence 2, App1.1	798	77	2.0	308	7	US-11-056-355B-49909	Sequence 49909, A
726	78	2.0	864	6	US-10-449-902-46975	Sequence 46975, A	799	77	2.0	317	7	US-11-315-825-76	Sequence 25, App1
727	78	2.0	987	7	US-11-259-133-26	Sequence 26, App1	801	77	2.0	452	7	US-11-056-355B-25445	Sequence 25445, A
728	78	2.0	987	7	US-11-226-584-100	Sequence 100, App	802	77	2.0	458	7	US-11-056-355B-25444	Sequence 25444, A
729	78	2.0	1027	7	US-11-174-307B-1296	Sequence 1296, Ap	803	77	2.0	508	6	US-10-449-902-26555	Sequence 26555, A
730	78	2.0	1049	7	US-11-174-307B-624	Sequence 624, App	804	77	2.0	508	6	US-10-449-902-64005	Sequence 64005, A
731	78	2.0	1068	6	US-10-449-902-51003	Sequence 51003, A	805	77	2.0	547	7	US-11-174-307B-3762	Sequence 3762, Ap
732	78	2.0	1144	7	US-11-174-307B-506	Sequence 506, App	806	77	2.0	604	7	US-11-372-770-5	Sequence 5, App1.1
733	78	2.0	1168	7	US-11-174-307B-3226	Sequence 3226, Ap	807	77	2.0	695	7	US-11-056-355B-73410	Sequence 73410, A
734	78	2.0	1379	7	US-11-174-307B-646	Sequence 646, App	808	77	2.0	698	7	US-11-056-355B-73409	Sequence 73409, A
735	78	2.0	1395	7	US-11-056-355B-99118	Sequence 99118, A	809	77	2.0	699	7	US-11-056-355B-46826	Sequence 46826, A
736	78	2.0	1395	7	US-11-056-355B-110417	Sequence 110417, A	810	77	2.0	702	7	US-11-056-355B-46825	Sequence 46825, A
737	78	2.0	1478	7	US-11-174-307B-1102	Sequence 1102, Ap	811	77	2.0	757	7	US-11-292-634-4	Sequence 4, App1.1
738	78	2.0	1478	7	US-11-174-307B-710	Sequence 710, App	812	77	2.0	820	7	US-11-056-355B-73408	Sequence 73408, A
739	78	2.0	1483	7	US-11-174-307B-5082	Sequence 5082, Ap	813	77	2.0	821	7	US-11-326-389-10	Sequence 10, App1
740	78	2.0	1549	7	US-11-174-307B-608	Sequence 608, App	814	77	2.0	824	7	US-11-056-355B-46824	Sequence 46824, A
741	78	2.0	1733	7	US-11-174-307B-814	Sequence 814, App	815	77	2.0	836	6	US-10-449-902-74466	Sequence 74466, A
742	78	2.0	1737	7	US-11-174-307B-674	Sequence 674, App	816	77	2.0	1050	7	US-11-174-307B-2762	Sequence 2762, Ap
743	78	2.0	1753	7	US-11-174-307B-1070	Sequence 1070, Ap	817	77	2.0	1156	7	US-11-174-307B-756	Sequence 756, App
744	78	2.0	1937	7	US-11-174-307B-3074	Sequence 3074, Ap	818	77	2.0	1201	7	US-11-174-307B-2186	Sequence 2186, Ap
745	78	2.0	2016	7	US-11-174-307B-2188	Sequence 2188, Ap	819	77	2.0	1233	7	US-11-174-307B-784	Sequence 784, App
746	78	2.0	2017	7	US-11-174-307B-2682	Sequence 2682, Ap	820	77	2.0	1310	7	US-11-174-307B-1186	Sequence 1186, Ap
747	78	2.0	2030	7	US-11-174-307B-3682	Sequence 3682, Ap	821	77	2.0	1319	7	US-11-174-307B-774	Sequence 774, App
748	77.5	2.0	195	7	US-11-056-355B-89931	Sequence 89931, A	822	77	2.0	1394	7	US-11-174-307B-640	Sequence 640, App
749	77.5	2.0	195	7	US-11-056-355B-93687	Sequence 93687, A	823	77	2.0	1401	7	US-11-174-307B-764	Sequence 764, App
750	77.5	2.0	250	7	US-11-356-373-3	Sequence 3, App1.1	824	77	2.0	1431	7	US-11-174-307B-1112	Sequence 1112, Ap
751	77.5	2.0	255	7	US-11-056-355B-89930	Sequence 89930, A	825	77	2.0	1449	7	US-11-056-355B-86756	Sequence 86756, A
752	77.5	2.0	255	7	US-11-056-355B-93686	Sequence 93686, A	826	77	2.0	1462	7	US-11-174-307B-1174	Sequence 1174, Ap
753	77.5	2.0	299	7	US-11-293-697-3744	Sequence 3744, Ap	827	77	2.0	1482	7	US-11-174-307B-880	Sequence 880, App
754	77.5	2.0	315	7	US-11-140-450-63	Sequence 63, App1	828	77	2.0	1532	7	US-11-056-355B-86755	Sequence 86755, A
755	77.5	2.0	324	6	US-10-449-902-31015	Sequence 31015, A	829	77	2.0	1552	7	US-11-174-307B-1110	Sequence 1110, Ap
756	77.5	2.0	324	6	US-10-449-902-54402	Sequence 54402, A	830	77	2.0	1552	7	US-11-056-355B-86754	Sequence 86754, A
757	77.5	2.0	324	6	US-10-449-902-56347	Sequence 56347, A	831	77	2.0	1663	7	US-11-056-355B-938	Sequence 938, App
758	77.5	2.0	363	7	US-11-293-697-3879	Sequence 3879, Ap	832	77	2.0	2325	7	US-11-174-307B-938	Sequence 938, App
759	77.5	2.0	404	7	US-11-293-697-4601	Sequence 4601, Ap	833	77	2.0	58	7	US-11-324-846-7	Sequence 7, App1.1
760	77.5	2.0	517	7	US-11-056-355B-53957	Sequence 53957, A	834	76.5	1.9	194	7	US-11-056-355B-89932	Sequence 89932, Ap
761	77.5	2.0	531	7	US-11-293-697-2762	Sequence 2762, Ap	835	76.5	1.9	194	7	US-11-056-355B-93688	Sequence 93688, A
762	77.5	2.0	552	7	US-11-174-307B-192	Sequence 192, App	836	76.5	1.9	229	6	US-10-953-349-13475	Sequence 13475, A
763	77.5	2.0	599	7	US-11-313-836-13	Sequence 13, App1	837	76.5	1.9	254	6	US-10-953-349-33474	Sequence 33474, A
764	77.5	2.0	711	7	US-11-174-307B-4400	Sequence 4400, Ap	838	76.5	1.9	274	7	US-11-056-355B-37586	Sequence 37586, A
765	77.5	2.0	888	7	US-11-174-307B-852	Sequence 852, App	839	76.5	1.9	280	6	US-10-953-349-33473	Sequence 33473, A
766	77.5	2.0	931	7	US-11-174-307B-2082	Sequence 2082, Ap	840	76.5	1.9	289	6	US-11-056-355B-37585	Sequence 37585, A
767	77.5	2.0	1035	7	US-11-174-307B-1704	Sequence 1704, Ap	841	76.5	1.9	291	6	US-10-953-349-19822	Sequence 19822, A
768	77.5	2.0	1067	7	US-11-056-355B-88990	Sequence 88990, A	842	76.5	1.9	291	7	US-11-056-355B-92746	Sequence 92746, A
769	77.5	2.0	1067	7	US-11-056-355B-92746	Sequence 92746, A	843	76.5	1.9	291	7	US-11-056-355B-55600	Sequence 55600, A
770	77.5	2.0	1101	7	US-11-056-355B-88989	Sequence 88989, A	844	76.5	1.9	302	6	US-10-953-349-10130	Sequence 10130, A

845	76.5	1.9	303	6	US-10-953-349-19821	Sequence 19821, A	918	75.5	1.9	197	7	US-11-211-917-139	Sequence 139, App
846	76.5	1.9	309	7	US-11-056-355B-55559	Sequence 55559, A	920	75.5	1.9	237	6	US-10-504-973-22	Sequence 22, App1
847	76.5	1.9	309	6	US-10-953-349-19820	Sequence 19820, A	920	75.5	1.9	277	6	US-10-511-937-5518	Sequence 2518, App
848	76.5	1.9	309	7	US-11-056-355B-55558	Sequence 55558, A	921	75.5	1.9	277	7	US-11-170-797-5	Sequence 5, App1
849	76.5	1.9	331	6	US-10-953-349-10129	Sequence 10129, A	922	75.5	1.9	283	6	US-10-449-902-69086	Sequence 49086, A
850	76.5	1.9	419	7	US-11-056-355B-48547	Sequence 48547, A	923	75.5	1.9	315	7	US-11-140-450-62	Sequence 62, App1
851	76.5	1.9	464	6	US-10-488-015-17	Sequence 17, App1	924	75.5	1.9	323	6	US-10-449-902-65777	Sequence 56777, A
852	76.5	1.9	483	7	US-11-056-355B-48546	Sequence 48546, A	925	75.5	1.9	361	6	US-10-449-902-48803	Sequence 48803, A
853	76.5	1.9	804	6	US-10-449-902-53390	Sequence 53390, A	926	75.5	1.9	409	6	US-10-449-902-12429	Sequence 31249, A
854	76.5	1.9	824	6	US-10-449-902-53677	Sequence 53677, A	927	75.5	1.9	409	6	US-10-449-902-49417	Sequence 49417, A
855	76.5	1.9	824	6	US-11-174-307B-1042	Sequence 1042, App	928	75.5	1.9	553	7	US-11-233-089-6	Sequence 6, App1
856	76.5	1.9	924	6	US-10-449-902-41181	Sequence 41181, A	929	75.5	1.9	553	7	US-11-233-089-8	Sequence 8, App1
857	76.5	1.9	1125	7	US-11-174-307B-650	Sequence 650, App	930	75.5	1.9	595	7	US-11-293-697-4475	Sequence 4475, App
858	76.5	1.9	1187	7	US-11-174-307B-11442	Sequence 11442, App	931	75.5	1.9	633	7	US-11-372-770-13	Sequence 13, App1
859	76.5	1.9	1188	7	US-11-174-307B-1544	Sequence 1544, App	932	75.5	1.9	700	7	US-11-246-999-67	Sequence 49, App1
860	76.5	1.9	1252	7	US-11-174-307B-966	Sequence 966, App	933	75.5	1.9	756	6	US-10-449-902-4363	Sequence 44363, A
861	76.5	1.9	1259	7	US-11-223-945-40	Sequence 40, App1	934	75.5	1.9	802	7	US-11-174-307B-5486	Sequence 5486, App
862	76.5	1.9	1275	7	US-11-174-307B-1886	Sequence 1886, App	935	75.5	1.9	860	6	US-10-449-902-35078	Sequence 35078, A
863	76.5	1.9	1337	7	US-11-174-307B-1360	Sequence 1360, App	936	75.5	1.9	989	6	US-10-449-902-41201	Sequence 41201, A
864	76.5	1.9	1378	7	US-11-174-307B-1818	Sequence 1818, App	937	75.5	1.9	1022	7	US-11-174-307B-4710	Sequence 4710, App
865	76.5	1.9	1383	7	US-11-174-307B-1286	Sequence 1286, App	938	75.5	1.9	1049	7	US-11-174-307B-468	Sequence 468, App
866	76.5	1.9	1413	7	US-11-174-307B-1200	Sequence 1200, App	939	75.5	1.9	1103	7	US-11-174-307B-2450	Sequence 2450, App
867	76.5	1.9	1433	7	US-11-174-307B-1804	Sequence 1804, App	940	75.5	1.9	1179	7	US-11-174-307B-508	Sequence 508, App
868	76.5	1.9	1482	7	US-11-174-307B-2236	Sequence 2236, App	941	75.5	1.9	1191	7	US-11-174-307B-2166	Sequence 2166, App
869	76.5	1.9	1486	7	US-11-174-307B-550	Sequence 550, App	942	75.5	1.9	1210	7	US-11-289-102-285	Sequence 285, App
870	76.5	1.9	1512	7	US-11-174-307B-860	Sequence 860, App	943	75.5	1.9	1210	7	US-11-294-621-512	Sequence 621, App1
871	76.5	1.9	1649	7	US-11-174-307B-1178	Sequence 1178, App	944	75.5	1.9	1230	7	US-11-313-104-15	Sequence 1156, App
872	76.5	1.9	1673	7	US-11-174-307B-718	Sequence 718, App	945	75.5	1.9	1336	7	US-11-174-307B-904	Sequence 904, App
873	76.5	1.9	1698	7	US-11-174-307B-1148	Sequence 1148, App	946	75.5	1.9	1336	7	US-11-174-307B-2248	Sequence 2248, App
874	76.5	1.9	1721	7	US-11-174-307B-1148	Sequence 3, App1	947	75.5	1.9	1345	7	US-11-174-307B-1946	Sequence 1946, App
875	76.5	1.9	1776	6	US-10-933-854-3	Sequence 1742, App	948	75.5	1.9	1357	7	US-11-174-307B-2238	Sequence 2238, App
876	76.5	1.9	1934	7	US-11-174-307B-1742	Sequence 1532, App	949	75.5	1.9	1358	7	US-11-174-307B-3364	Sequence 3364, App
877	76.5	1.9	2068	7	US-11-174-307B-1032	Sequence 1532, App	950	75.5	1.9	1439	6	US-10-505-8928-69	Sequence 69, App1
878	76.5	1.9	3060	7	US-11-174-307B-1532	Sequence 25384, App	951	75.5	1.9	1456	6	US-11-174-307B-1094	Sequence 1094, App
879	76.5	1.9	167	6	US-10-953-349-25384	Sequence 41963, A	952	75.5	1.9	1457	7	US-11-174-307B-1056	Sequence 1056, App
880	76.5	1.9	186	7	US-11-056-355B-11965	Sequence 23, App1	953	75.5	1.9	1482	7	US-11-174-307B-4372	Sequence 4372, App
881	76.5	1.9	272	7	US-11-356-373-23	Sequence 25, App1	954	75.5	1.9	1522	7	US-11-174-307B-3906	Sequence 3906, App
882	76.5	1.9	292	7	US-10-953-349-8163	Sequence 52619, A	955	75.5	1.9	1523	7	US-11-174-307B-786	Sequence 786, App
883	76.5	1.9	350	6	US-10-449-902-52619	Sequence 54055, A	956	75.5	1.9	1602	7	US-11-174-307B-688	Sequence 688, App
884	76.5	1.9	473	6	US-10-449-902-54055	Sequence 55943, A	957	75.5	1.9	1659	7	US-11-174-307B-3184	Sequence 3184, App
885	76.5	1.9	642	6	US-10-449-902-55943	Sequence 8, App1	958	75.5	1.9	1721	7	US-11-174-307B-908	Sequence 908, App
886	76.5	1.9	682	6	US-10-480-021-8	Sequence 41300, A	959	75.5	1.9	1723	7	US-11-174-307B-1096	Sequence 1096, App
887	76.5	1.9	740	6	US-10-449-902-41300	Sequence 42322, A	960	75.5	1.9	1982	7	US-11-174-307B-2860	Sequence 2860, App
888	76.5	1.9	764	6	US-11-056-355B-89192	Sequence 89192, A	961	75.5	1.9	2072	7	US-11-174-307B-1184	Sequence 1184, App
889	76.5	1.9	838	7	US-11-056-355B-92948	Sequence 89191, A	962	75.5	1.9	2117	7	US-11-174-307B-2836	Sequence 2836, App
890	76.5	1.9	848	7	US-11-056-355B-89191	Sequence 92347, A	963	75.5	1.9	2773	7	US-11-174-307B-1466	Sequence 1466, App
891	76.5	1.9	873	7	US-11-174-307B-1646	Sequence 1646, App	964	75.5	1.9	2782	7	US-11-174-307B-2825	Sequence 2825, App
892	76.5	1.9	927	7	US-11-056-355B-89190	Sequence 89190, A	965	75.5	1.9	2791	7	US-11-174-307B-1566	Sequence 1566, App
893	76.5	1.9	927	7	US-11-056-355B-92946	Sequence 92946, A	966	75.5	1.9	2973	7	US-11-174-307B-1566	Sequence 1566, App
894	76.5	1.9	1149	7	US-11-174-307B-4390	Sequence 4390, App	967	75.5	1.9	4834	6	US-10-505-928-827	Sequence 827, App1
895	76.5	1.9	1254	7	US-11-174-307B-886	Sequence 3538, App	968	75.5	1.9	718	7	US-11-217-997-84	Sequence 24, App1
896	76.5	1.9	1292	7	US-11-174-307B-910	Sequence 910, App	969	75.5	1.9	192	6	US-11-056-355B-73252	Sequence 73252, A
897	76.5	1.9	1298	7	US-11-174-307B-914	Sequence 914, App	970	75.5	1.9	205	6	US-10-449-902-12167	Sequence 42167, A
898	76.5	1.9	1329	7	US-11-174-307B-882	Sequence 882, App	971	75.5	1.9	285	6	US-10-449-902-10160	Sequence 30160, App
899	76.5	1.9	1348	7	US-11-174-307B-828	Sequence 828, App	972	75.5	1.9	344	6	US-11-056-355B-50453	Sequence 50453, A
900	76.5	1.9	1382	7	US-11-174-307B-4402	Sequence 2402, App	973	75.5	1.9	410	6	US-10-953-349-30835	Sequence 30835, A
901	76.5	1.9	1395	7	US-11-174-307B-3624	Sequence 2624, App	974	75.5	1.9	456	6	US-11-056-355B-38134	Sequence 38134, A
902	76.5	1.9	1396	7	US-11-174-307B-366	Sequence 366, App	975	75.5	1.9	514	6	US-10-449-902-44440	Sequence 44440, A
903	76.5	1.9	1413	7	US-11-174-307B-336	Sequence 936, App	976	75.5	1.9	556	7	US-11-056-355B-53788	Sequence 53788, A
904	76.5	1.9	1435	7	US-11-174-307B-572	Sequence 572, App	977	75.5	1.9	585	7	US-11-056-355B-38133	Sequence 38133, A
905	76.5	1.9	1655	7	US-11-174-307B-962	Sequence 962, App	978	75.5	1.9	600	7	US-11-056-355B-10212	Sequence 10207, A
906	76.5	1.9	1739	7	US-11-174-307B-118	Sequence 318, App	979	75.5	1.9	603	6	US-10-953-349-10207	Sequence 10207, A
907	76.5	1.9	1826	7	US-11-174-307B-1400	Sequence 1400, App	980	75.5	1.9	609	6	US-11-246-999-67	Sequence 67, App1
908	76.5	1.9	1957	7	US-11-174-307B-2230	Sequence 2230, App	981	75.5	1.9	769	7	US-11-246-999-67	Sequence 67, App1
909	76.5	1.9	2052	7	US-11-174-307B-552	Sequence 652, App	982	75.5	1.9	909	7	US-11-226-554-80	Sequence 80, App1
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913	76.5	1.9	151	6	US-10-953-349-10119	Sequence 10119, A	986	75.5	1.9	1146	7	US-11-174-307B-2372	Sequence 2372, App
914	76.5	1.9	151	6	US-10-953-349-10119	Sequence 10119, A	987	75.5	1.9				
915	76.5	1.9	151	6	US-10-953-349-10119	Sequence 10119, A	988	75.5	1.9				
916	76.5	1.9	151	6	US-10-953-349-10119	Sequence 10119, A	989	75.5	1.9				
917	76.5	1.9	151	6	US-10-953-349-10119	Sequence 10119, A	990	75.5	1.9				

991	75	1.9	1167	7	US-11-174-307B-2134	Sequence 2734, Ap	1065	74	1.9	307	7	US-11-056-355B-31027	Sequence 31027, A
992	75	1.9	1195	7	US-11-174-307B-2420	Sequence 2420, Ap	1066	74	1.9	307	7	US-11-056-355B-34617	Sequence 34617, A
993	75	1.9	1199	7	US-11-174-307B-392	Sequence 392, Ap	1067	74	1.9	308	6	US-10-953-349-20717	Sequence 20717, A
994	75	1.9	1205	7	US-11-174-307B-418	Sequence 418, App	1068	74	1.9	311	7	US-11-056-355B-31026	Sequence 31026, A
995	75	1.9	1205	7	US-11-174-307B-2392	Sequence 2392, Ap	1069	74	1.9	311	7	US-11-056-355B-34616	Sequence 34616, A
996	75	1.9	1242	7	US-11-174-307B-1058	Sequence 1058, Ap	1070	74	1.9	312	6	US-10-449-902-28596	Sequence 28596, A
997	75	1.9	1245	7	US-11-174-307B-1904	Sequence 1904, Ap	1071	74	1.9	322	6	US-10-449-902-29063	Sequence 29063, A
998	75	1.9	1254	7	US-11-174-307B-1038	Sequence 1038, Ap	1072	74	1.9	334	6	US-10-449-902-11147	Sequence 11147, A
999	75	1.9	1276	7	US-11-174-307B-768	Sequence 768, App	1073	74	1.9	334	6	US-10-449-902-16942	Sequence 16942, A
1000	75	1.9	1335	7	US-11-174-307B-3964	Sequence 3964, Ap	1074	74	1.9	359	7	US-11-056-355B-171729	Sequence 17129, A
1001	75	1.9	1343	7	US-11-174-307B-1146	Sequence 1146, Ap	1075	74	1.9	367	6	US-10-953-349-27896	Sequence 27896, A
1002	75	1.9	1370	7	US-11-174-307B-2124	Sequence 2124, Ap	1076	74	1.9	367	7	US-11-056-355B-69128	Sequence 69128, A
1003	75	1.9	1452	7	US-11-174-307B-926	Sequence 926, App	1077	74	1.9	403	7	US-11-056-355B-71728	Sequence 71728, A
1004	75	1.9	1479	7	US-11-174-307B-460	Sequence 460, App	1079	74	1.9	423	7	US-11-056-355B-71727	Sequence 71727, A
1005	75	1.9	1535	7	US-11-174-307B-2384	Sequence 2384, Ap	1080	74	1.9	442	6	US-10-953-349-27895	Sequence 27895, A
1006	75	1.9	1596	7	US-11-174-307B-792	Sequence 792, App	1081	74	1.9	442	7	US-11-056-355B-89127	Sequence 69127, A
1007	75	1.9	1692	7	US-11-174-307B-8858	Sequence 8858, Ap	1082	74	1.9	476	6	US-10-953-349-27894	Sequence 27894, A
1008	75	1.9	1709	7	US-11-174-307B-3210	Sequence 3210, Ap	1083	74	1.9	476	7	US-11-056-355B-69126	Sequence 69126, A
1009	75	1.9	1861	7	US-11-174-307B-1744	Sequence 1744, App	1084	74	1.9	543	7	US-11-174-307B-3406	Sequence 3406, Ap
1010	75	1.9	1873	7	US-11-174-307B-846	Sequence 846, App	1085	74	1.9	551	7	US-11-233-089-844	Sequence 44, App1
1011	75	1.9	1873	7	US-11-174-307B-846	Sequence 846, App	1086	74	1.9	626	6	US-10-449-902-50861	Sequence 50861, A
1012	75	1.9	2003	7	US-11-051-725-5	Sequence 5, App1i	1087	74	1.9	631	7	US-11-312-958-60	Sequence 28, App1
1013	75	1.9	2169	7	US-11-140-487A-772	Sequence 772, App	1088	74	1.9	692	7	US-10-370-959-5	Sequence 5, App1i
1014	75	1.9	3020	7	US-11-174-307B-2802	Sequence 2802, Ap	1089	74	1.9	730	6	US-11-056-355B-87776	Sequence 87776, A
1015	75	1.9	3273	7	US-11-056-355B-57541	Sequence 57541, A	1090	74	1.9	778	7	US-11-056-355B-87751	Sequence 87751, A
1016	74.5	1.9	199	7	US-11-056-355B-12144	Sequence 12144, A	1091	74	1.9	778	7	US-11-056-355B-87775	Sequence 87775, A
1017	74.5	1.9	223	7	US-11-056-355B-12143	Sequence 12143, A	1092	74	1.9	780	7	US-11-056-355B-83750	Sequence 83750, A
1018	74.5	1.9	242	7	US-10-511-937-2519	Sequence 2519, Ap	1093	74	1.9	780	7	US-11-056-355B-87774	Sequence 87774, A
1019	74.5	1.9	260	6	US-11-056-355B-12142	Sequence 12142, A	1094	74	1.9	832	7	US-11-174-307B-1324	Sequence 1324, Ap
1020	74.5	1.9	279	7	US-11-254-185-42	Sequence 42, App1	1095	74	1.9	832	7	US-10-449-902-42960	Sequence 42960, A
1021	74.5	1.9	290	7	US-11-253-869-42	Sequence 42, App1	1096	74	1.9	943	6	US-11-370-424-7	Sequence 7, App1i
1022	74.5	1.9	302	6	US-10-449-902-33401	Sequence 33401, A	1098	74	1.9	945	7	US-11-174-307B-782	Sequence 782, App
1023	74.5	1.9	312	6	US-10-449-902-45977	Sequence 45977, A	1099	74	1.9	988	7	US-11-056-355B-79318	Sequence 79318, A
1024	74.5	1.9	312	6	US-10-449-902-33001	Sequence 33001, A	1100	74	1.9	995	7	US-11-056-355B-79317	Sequence 79317, A
1025	74.5	1.9	326	6	US-10-449-902-37235	Sequence 37235, A	1101	74	1.9	1022	6	US-10-449-902-52308	Sequence 52308, A
1026	74.5	1.9	333	6	US-10-953-349-20311	Sequence 20311, A	1102	74	1.9	1055	7	US-11-174-307B-2854	Sequence 2854, A
1027	74.5	1.9	354	6	US-10-953-349-20310	Sequence 20310, A	1103	74	1.9	1079	7	US-11-174-307B-4958	Sequence 4958, Ap
1028	74.5	1.9	364	6	US-10-953-349-20309	Sequence 20309, A	1104	74	1.9	1164	7	US-11-056-355B-79316	Sequence 79316, A
1029	74.5	1.9	370	6	US-10-953-349-3935	Sequence 3935, Ap	1105	74	1.9	1276	7	US-11-174-307B-1764	Sequence 1764, Ap
1030	74.5	1.9	384	7	US-11-293-697-2758	Sequence 2758, A	1106	74	1.9	1276	7	US-11-174-307B-440	Sequence 440, App
1031	74.5	1.9	424	7	US-11-056-355B-54573	Sequence 54573, A	1107	74	1.9	1280	7	US-11-174-307B-2512	Sequence 2512, App
1032	74.5	1.9	425	7	US-11-056-355B-54572	Sequence 54572, A	1108	74	1.9	1280	7	US-11-174-307B-560	Sequence 560, App
1033	74.5	1.9	428	6	US-10-953-349-3934	Sequence 3934, Ap	1109	74	1.9	1298	7	US-11-174-307B-836	Sequence 836, App
1034	74.5	1.9	557	6	US-10-953-349-3933	Sequence 3933, Ap	1110	74	1.9	1376	7	US-11-174-307B-2636	Sequence 2636, Ap
1035	74.5	1.9	636	6	US-10-521-401A-3	Sequence 3, App1i	1111	74	1.9	1403	7	US-11-174-307B-738	Sequence 738, App
1036	74.5	1.9	776	6	US-10-449-902-53465	Sequence 53465, A	1112	74	1.9	1425	7	US-11-174-307B-706	Sequence 706, App
1037	74.5	1.9	799	6	US-10-449-902-51122	Sequence 51122, A	1113	74	1.9	1463	7	US-11-174-307B-1990	Sequence 1920, Ap
1038	74.5	1.9	832	7	US-11-056-355B-75226	Sequence 75226, A	1114	74	1.9	1528	7	US-11-174-307B-4854	Sequence 4854, Ap
1039	74.5	1.9	840	7	US-11-056-355B-75225	Sequence 75225, A	1115	74	1.9	1659	7	US-11-174-307B-984	Sequence 984, App
1040	74.5	1.9	907	7	US-11-174-307B-1040	Sequence 1040, Ap	1116	74	1.9	1765	7	US-11-174-307B-2666	Sequence 2666, Ap
1041	74.5	1.9	929	7	US-11-174-307B-3988	Sequence 3988, Ap	1117	74	1.9	1751	7	US-11-174-307B-4242	Sequence 4242, Ap
1042	74.5	1.9	984	6	US-10-528-029-1	Sequence 1, App1i	1118	74	1.9	1865	7	US-11-174-307B-1108	Sequence 1108, Ap
1043	74.5	1.9	985	7	US-11-174-307B-5470	Sequence 5470, Ap	1119	74	1.9	2192	7	US-11-051-725-147	Sequence 147, App
1044	74.5	1.9	987	7	US-11-259-123-30	Sequence 30, App1	1120	74	1.9	2221	6	US-10-829-000-3	Sequence 3, App1
1045	74.5	1.9	987	7	US-11-226-554-88	Sequence 88, App1	1121	74	1.9	2221	6	US-11-051-725-162	Sequence 162, App
1046	74.5	1.9	989	6	US-10-449-902-48457	Sequence 48457, A	1122	74	1.9	2240	7	US-11-174-307B-1294	Sequence 1294, Ap
1047	74.5	1.9	1138	7	US-11-174-307B-4612	Sequence 4612, Ap	1123	74	1.9	222	7	US-11-356-373-15	Sequence 15, App1
1048	74.5	1.9	1251	7	US-11-174-307B-4014	Sequence 4014, Ap	1124	74	1.9	229	7	US-11-356-373-6	Sequence 6, App1i
1049	74.5	1.9	1496	7	US-11-174-307B-548	Sequence 548, App	1125	73.5	1.9	247	6	US-10-304-973-6	Sequence 18, App1
1050	74.5	1.9	1527	7	US-11-174-307B-2694	Sequence 2694, Ap	1126	73.5	1.9	263	7	US-11-356-973-18	Sequence 18, App1
1051	74.5	1.9	1536	7	US-11-174-307B-1218	Sequence 1218, Ap	1127	73.5	1.9	463	6	US-10-449-902-33444	Sequence 33444, A
1052	74.5	1.9	1577	7	US-11-174-307B-1118	Sequence 1118, Ap	1128	73.5	1.9	562	7	US-11-056-355B-18117	Sequence 18317, A
1053	74.5	1.9	1623	7	US-11-174-307B-1512	Sequence 1512, Ap	1129	73.5	1.9	571	6	US-10-449-902-42882	Sequence 42832, A
1054	74.5	1.9	1681	7	US-11-174-307B-5166	Sequence 5166, Ap	1130	73.5	1.9	594	7	US-11-056-355B-18939	Sequence 18939, A
1055	74.5	1.9	1703	7	US-11-174-307B-1104	Sequence 1104, Ap	1131	73.5	1.9	625	7	US-11-174-307B-5446	Sequence 5446, Ap
1056	74.5	1.9	1723	6	US-10-466-020-6	Sequence 6, App1i	1132	73.5	1.9	639	6	US-10-449-902-53967	Sequence 53967, A
1057	74.5	1.9	1845	7	US-11-174-307B-1310	Sequence 1310, App	1133	73.5	1.9	641	6	US-10-449-902-55962	Sequence 55962, A
1058	74.5	1.9	1883	7	US-11-174-307B-708	Sequence 708, App	1134	73.5	1.9	645	7	US-10-449-902-41230	Sequence 41230, A
1059	74.5	1.9	1972	7	US-11-253-190-1	Sequence 1, App1i	1135	73.5	1.9	645	7	US-11-056-355B-94823	Sequence 94823, A
1060	74.5	1.9	2143	7	US-11-174-307B-1284	Sequence 1284, Ap	1136	73.5	1.9	710	7	US-11-056-355B-94829	Sequence 94829, A
1061	74.5	1.9	2250	7	US-11-174-307B-1394	Sequence 1394, Ap	1137	73.5	1.9	710	7	US-11-174-307B-4112	Sequence 4112, App
1062	74.5	1.9	2762	7	US-11-174-307B-2676	Sequence 2676, A	1138	73.5	1.9	737	6	US-10-449-902-41609	Sequence 41609, A
1063	74.5	1.9	187	6	US-10-953-349-10131	Sequence 10131, A	1139	73.5	1.9				

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1141	73.5	1.9	739	7	US-11-056-355B-94628	Sequence 94628, A	1215	73	1.9	1558	7	US-11-174-307B-856	Sequence 856, App
1142	73.5	1.9	741	6	US-10-449-902-53293	Sequence 53293, A	1216	73	1.9	1565	7	US-11-174-307B-1824	Sequence 1824, Ap
1143	73.5	1.9	777	6	US-10-953-349-35469	Sequence 35469, A	1217	73	1.9	1567	7	US-11-174-307B-2116	Sequence 2116, Ap
1144	73.5	1.9	780	7	US-11-056-355B-90871	Sequence 90871, A	1218	73	1.9	1581	7	US-11-174-307B-906	Sequence 906, App
1145	73.5	1.9	780	7	US-11-056-355B-94627	Sequence 94627, A	1219	73	1.9	1605	7	US-11-056-355B-88407	Sequence 88407, A
1146	73.5	1.9	893	6	US-10-953-349-35468	Sequence 35468, A	1220	73	1.9	1605	7	US-11-056-355B-92163	Sequence 92163, A
1147	73.5	1.9	913	6	US-10-953-349-35467	Sequence 35467, A	1221	73	1.9	1641	7	US-11-174-307B-1340	Sequence 1340, Ap
1148	73.5	1.9	937	6	US-10-449-902-45265	Sequence 45265, A	1222	73	1.9	1646	7	US-11-056-355B-88406	Sequence 88406, A
1149	73.5	1.9	1059	7	US-11-174-307B-1214	Sequence 1214, Ap	1223	73	1.9	1646	7	US-11-056-355B-92162	Sequence 92162, A
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1151	73.5	1.9	1231	7	US-11-174-307B-1168	Sequence 1168, Ap	1225	73	1.9	1689	7	US-11-174-307B-1196	Sequence 1196, Ap
1152	73.5	1.9	1258	7	US-11-174-307B-1612	Sequence 1612, Ap	1226	73	1.9	1703	7	US-11-174-307B-558	Sequence 558, App
1153	73.5	1.9	1289	7	US-11-174-307B-2922	Sequence 2922, Ap	1227	73	1.9	1703	7	US-11-174-307B-2214	Sequence 2214, Ap
1154	73.5	1.9	1291	7	US-11-174-307B-1206	Sequence 1206, Ap	1228	73	1.9	1703	7	US-11-174-307B-2576	Sequence 2576, Ap
1155	73.5	1.9	1300	7	US-11-174-307B-1112	Sequence 1112, App	1229	73	1.9	1714	7	US-11-174-307B-1068	Sequence 1068, Ap
1156	73.5	1.9	1302	7	US-11-174-307B-2152	Sequence 2152, Ap	1230	73	1.9	1757	7	US-11-174-307B-554	Sequence 554, App
1157	73.5	1.9	1324	7	US-11-174-307B-1210	Sequence 1210, Ap	1231	73	1.9	1773	7	US-11-056-355B-88405	Sequence 88405, A
1158	73.5	1.9	1389	7	US-11-174-307B-1304	Sequence 1304, Ap	1232	73	1.9	1773	7	US-11-056-355B-92161	Sequence 92161, A
1159	73.5	1.9	1391	7	US-11-174-307B-4782	Sequence 4782, Ap	1233	73	1.9	2047	7	US-11-174-307B-680	Sequence 680, App
1160	73.5	1.9	1405	7	US-11-174-307B-2296	Sequence 2296, Ap	1234	73	1.9	2133	7	US-11-174-307B-894	Sequence 894, App
1161	73.5	1.9	1428	7	US-11-174-307B-1144	Sequence 1144, Ap	1235	73	1.9	2209	7	US-11-301-554-1903	Sequence 1903, App
1162	73.5	1.9	1437	7	US-11-174-307B-2014	Sequence 2014, Ap	1236	73	1.9	2235	7	US-11-174-307B-2036	Sequence 2036, Ap
1163	73.5	1.9	1438	7	US-11-174-307B-1176	Sequence 1176, Ap	1237	73	1.9	2235	7	US-11-174-307B-2262	Sequence 2262, Ap
1164	73.5	1.9	1481	7	US-11-174-307B-1190	Sequence 1190, Ap	1238	73	1.9	3250	7	US-11-174-307B-2486	Sequence 2486, Ap
1165	73.5	1.9	1506	7	US-11-174-307B-1870	Sequence 1870, Ap	1239	73	1.9	3682	7	US-11-174-307B-2486	Sequence 2486, Ap
1166	73.5	1.9	1657	7	US-11-174-307B-1212	Sequence 1212, Ap	1240	73	1.8	62	7	US-11-324-846-4	Sequence 4, Appl
1167	73.5	1.9	1750	7	US-11-174-307B-570	Sequence 570, App	1241	72.5	1.8	234	6	US-10-449-902-69114	Sequence 49114, A
1168	73.5	1.9	1751	7	US-11-174-307B-4426	Sequence 4426, Ap	1242	72.5	1.8	279	6	US-10-505-928-623	Sequence 623, App
1169	73.5	1.9	1818	7	US-11-174-307B-732	Sequence 732, App	1243	72.5	1.8	321	7	US-11-056-355B-9750	Sequence 9750, App
1170	73.5	1.9	1869	7	US-11-174-307B-746	Sequence 746, App	1244	72.5	1.8	370	6	US-10-449-902-33564	Sequence 33564, A
1171	73.5	1.9	1942	7	US-11-174-307B-2732	Sequence 2732, Ap	1245	72.5	1.8	384	6	US-10-953-349-9071	Sequence 9071, Ap
1172	73.5	1.9	1942	7	US-11-174-307B-4732	Sequence 4732, Ap	1246	72.5	1.8	406	7	US-11-056-355B-9749	Sequence 9749, Ap
1173	73.5	1.9	1959	7	US-11-174-307B-1428	Sequence 1428, Ap	1247	72.5	1.8	428	6	US-10-449-902-44200	Sequence 44200, A
1174	73.5	1.9	2681	7	US-11-174-307B-1714	Sequence 1714, Ap	1248	72.5	1.8	459	6	US-10-953-349-9070	Sequence 9070, Ap
1175	73.5	1.9	2681	7	US-11-174-307B-1692	Sequence 1692, Ap	1249	72.5	1.8	466	6	US-11-174-307B-1342	Sequence 1342, Ap
1176	73.5	1.9	241	7	US-11-547-530-47	Sequence 47, Appl	1250	72.5	1.8	470	6	US-10-953-349-9071	Sequence 9071, Ap
1177	73	1.9	241	7	US-11-315-825-3	Sequence 3, Appl	1251	72.5	1.8	513	7	US-11-056-355B-68863	Sequence 68863, A
1178	73	1.9	245	6	US-10-449-902-38546	Sequence 38546, A	1252	72.5	1.8	513	6	US-10-953-349-92711	Sequence 92711, A
1179	73	1.9	311	7	US-11-351-617-8	Sequence 8, Appl	1253	72.5	1.8	542	7	US-11-056-355B-45215	Sequence 45215, A
1180	73	1.9	319	6	US-10-953-349-3374	Sequence 3374, Ap	1254	72.5	1.8	548	6	US-10-953-349-32710	Sequence 32710, A
1181	73	1.9	329	6	US-10-953-349-13707	Sequence 13707, A	1255	72.5	1.8	548	7	US-11-056-355B-68862	Sequence 68862, A
1182	73	1.9	329	7	US-11-056-355B-44862	Sequence 44862, A	1256	72.5	1.8	557	7	US-11-056-355B-71276	Sequence 71276, A
1183	73	1.9	329	7	US-11-056-355B-55583	Sequence 55583, A	1257	72.5	1.8	591	7	US-11-056-355B-91853	Sequence 91853, A
1184	73	1.9	338	6	US-10-953-349-3273	Sequence 3273, Ap	1258	72.5	1.8	594	7	US-11-056-355B-95609	Sequence 95609, A
1185	73	1.9	353	6	US-10-953-349-13706	Sequence 13706, Ap	1259	72.5	1.8	594	7	US-11-056-355B-71275	Sequence 71275, A
1186	73	1.9	353	6	US-11-056-355B-55582	Sequence 55582, A	1260	72.5	1.8	595	7	US-11-293-697-3046	Sequence 3046, Ap
1187	73	1.9	354	6	US-10-449-902-40808	Sequence 40808, A	1261	72.5	1.8	603	7	US-11-293-697-3185	Sequence 3185, Ap
1188	73	1.9	382	6	US-10-449-902-28753	Sequence 28753, A	1262	72.5	1.8	613	6	US-10-953-349-92709	Sequence 92709, A
1189	73	1.9	457	6	US-10-449-902-31359	Sequence 31359, A	1263	72.5	1.8	613	7	US-11-056-355B-68861	Sequence 68861, A
1190	73	1.9	518	7	US-10-449-902-50709	Sequence 50709, A	1264	72.5	1.8	617	7	US-11-056-355B-45214	Sequence 45214, A
1191	73	1.9	518	7	US-11-174-307B-7402	Sequence 3402, Ap	1265	72.5	1.8	631	6	US-10-449-902-46154	Sequence 46154, A
1192	73	1.9	521	6	US-10-526-905-11	Sequence 11, Appl	1266	72.5	1.8	648	7	US-11-056-355B-71274	Sequence 71274, A
1193	73	1.9	605	6	US-10-449-902-45413	Sequence 45413, A	1267	72.5	1.8	666	7	US-11-289-102-309	Sequence 309, App
1194	73	1.9	631	6	US-10-449-902-53311	Sequence 53311, A	1268	72.5	1.8	720	7	US-11-174-307B-91862	Sequence 91862, Ap
1195	73	1.9	731	6	US-10-480-963-13	Sequence 13, Appl	1269	72.5	1.8	725	7	US-11-056-355B-99666	Sequence 99666, A
1196	73	1.9	731	7	US-11-293-697-4126	Sequence 4126, Ap	1270	72.5	1.8	725	7	US-11-056-355B-95608	Sequence 95608, A
1197	73	1.9	764	6	US-11-191-244-65	Sequence 65, Appl	1271	72.5	1.8	733	7	US-11-056-355B-45213	Sequence 45213, A
1198	73	1.9	814	6	US-10-449-902-54355	Sequence 54355, A	1272	72.5	1.8	733	7	US-11-056-355B-91851	Sequence 91851, A
1199	73	1.9	862	6	US-10-449-902-46465	Sequence 46465, A	1273	72.5	1.8	733	7	US-11-056-355B-95607	Sequence 95607, A
1200	73	1.9	1050	7	US-11-174-307B-720	Sequence 720, App	1274	72.5	1.8	738	7	US-11-174-307B-816	Sequence 816, App
1201	73	1.9	1066	6	US-10-449-902-43289	Sequence 43289, A	1275	72.5	1.8	748	7	US-11-056-355B-1100755	Sequence 1100755, A
1202	73	1.9	1136	7	US-11-174-307B-2504	Sequence 2504, Ap	1276	72.5	1.8	748	7	US-11-056-355B-1119994	Sequence 1119994, A
1203	73	1.9	1299	7	US-11-174-307B-1524	Sequence 1524, Ap	1277	72.5	1.8	947	6	US-10-449-902-41153	Sequence 41153, A
1204	73	1.9	1377	7	US-11-174-307B-518	Sequence 518, App	1278	72.5	1.8	989	7	US-11-283-329-168	Sequence 168, App
1205	73	1.9	1402	7	US-11-174-307B-3462	Sequence 3462, Ap	1279	72.5	1.8	1053	7	US-11-174-307B-596	Sequence 596, App
1206	73	1.9	1434	7	US-11-174-307B-1194	Sequence 1194, Ap	1280	72.5	1.8	1144	7	US-11-174-307B-3420	Sequence 3420, Ap
1207	73	1.9	1462	7	US-11-174-307B-542	Sequence 542, App	1281	72.5	1.8	1154	7	US-11-174-307B-2720	Sequence 2720, Ap
1208	73	1.9	1486	7	US-11-174-307B-684	Sequence 684, App	1282	72.5	1.8	1210	7	US-11-105-233-189	Sequence 189, App
1209	73	1.9	1502	7	US-11-174-307B-632	Sequence 632, App	1283	72.5	1.8	1282	7	US-11-174-307B-1140	Sequence 1140, Ap
1210	73	1.9	1511	7	US-11-174-307B-1120	Sequence 1120, Ap	1284	72.5	1.8	1347	7	US-11-174-307B-1066	Sequence 1066, Ap
1211	73	1.9	1531	7	US-11-174-307B-170	Sequence 170, App	1285	72.5	1.8	1353	7	US-11-174-307B-66	Sequence 66, Appl
1212	73	1.9	1539	7	US-11-174-307B-2180	Sequence 2180, Ap	1286	72.5	1.8	1381	7	US-11-174-307B-3378	Sequence 3378, Ap

1287	72.5	1.8	1410	7	US-11-174-307B-5448	Sequence 5448, Ap	1360	72	1.8	858	7	US-11-174-307B-1934	Sequence 1934, Ap
1288	72.5	1.8	1439	7	US-11-174-307B-604	Sequence 604, App	1361	72	1.8	929	7	US-11-174-307B-1296	Sequence 1296, Ap
1289	72.5	1.8	1523	7	US-11-174-307B-766	Sequence 766, App	1362	72	1.8	945	7	US-11-293-697-2739	Sequence 2739, Ap
1290	72.5	1.8	1660	7	US-11-174-307B-3908	Sequence 2908, Ap	1363	72	1.8	998	7	US-11-174-307B-2338	Sequence 2338, Ap
1291	72.5	1.8	1700	7	US-11-174-307B-1010	Sequence 1010, Ap	1364	72	1.8	1093	6	US-10-449-902-41338	Sequence 41338, A
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1293	72.5	1.8	1730	7	US-11-174-307B-2288	Sequence 2288, Ap	1366	72	1.8	1131	7	US-11-174-307B-5558	Sequence 2558, Ap
1294	72.5	1.8	1783	7	US-11-174-307B-902	Sequence 902, App	1367	72	1.8	1181	7	US-11-174-307B-2684	Sequence 2684, Ap
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1296	72.5	1.8	2309	7	US-11-174-307B-1562	Sequence 1562, Ap	1369	72	1.8	1197	7	US-11-174-307B-140	Sequence 340, App
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1308	72	1.8	181	6	US-10-953-349-1454	Sequence 1454, Ap	1381	72	1.8	1480	7	US-11-174-307B-3308	Sequence 3308, Ap
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1483	71.5	1.8	1355	7	US-11-056-355B-70176	Sequence 70176, A
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1493	71.5	1.8	1560	7	US-11-174-307B-1846	Sequence 1846, Appl
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1495	71.5	1.8	1638	7	US-11-174-307B-660	Sequence 660, Appl
1496	71.5	1.8	1714	7	US-11-174-307B-740	Sequence 740, Appl
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1498	71.5	1.8	1741	7	US-11-174-307B-726	Sequence 726, Appl
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SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	949	24.1	181	2	T08805 hypothetical prote
2	672	17.0	1019	2	A38738 coagulation factor
3	482	12.2	699	1	I54763 Ra-reactive factor
4	403.5	10.2	705	1	C1HURB complement subcomp
5	400.5	10.2	686	1	A59271 Ra-reactive factor
6	378.5	9.6	695	1	S05008 complement subcomp
7	354	9.0	1524	2	T30337 polypeptide - Afri
8	340.5	8.6	694	2	JC6554 complement subcomp
9	334	8.5	688	1	C1HUS complement subcomp
10	331.5	8.4	1019	1	A56318 enteropeptidase (B
11	330.5	8.4	1034	1	A56663 enteropeptidase (B
12	320	8.1	461	1	JX0210 protein C (activat
13	317.5	8.0	1035	1	A43090 enteropeptidase (B
14	314.5	8.0	475	1	EXCH coagulation factor
15	313	7.9	855	2	JC7731 membrane-bound arg
16	310.5	7.9	461	1	KXHU protein C (activat
17	299.5	7.6	443	2	I46932 coagulation factor
18	293.5	7.4	407	1	KPB07 coagulation factor
19	292	7.4	461	1	S18994 protein C (activat
20	285.5	7.2	452	1	A30351 coagulation factor
21	283.5	7.2	482	1	EXRT coagulation factor
22	282	7.1	456	1	KXBO protein C (activat
23	281.5	7.1	558	2	JC5878 plasma hyaluronan-
24	281	7.1	492	1	EXBO coagulation factor
25	280.5	7.1	264	2	I38136 chymotrypsin-like
26	280	7.1	562	1	KFHUT t-plasminogen acti
27	278.5	7.0	466	1	KFHUT coagulation factor
28	278	7.0	488	1	EXHU coagulation factor
29	278	7.0	1113	2	JB0315 low-density lipopr

30	277	7.0	559	1	A29941 t-plasminogen acti
31	277	7.0	559	1	A35029 t-plasminogen acti
32	276.5	7.0	655	1	A46688 hepatocyte growth
33	274.5	7.0	625	1	TBBO thrombin (EC 3.4.2
34	273	6.9	560	1	UC4795 plasma hyaluronan-
35	270	6.8	477	2	J50597 t-plasminogen acti
36	264.5	6.7	431	2	J50599 t-plasminogen acti
37	264.5	6.7	618	2	A35827 thrombin (EC 3.4.2
38	262.5	6.7	461	1	KFHU coagulation factor
39	262	6.6	477	2	J50598 t-plasminogen acti
40	261.5	6.6	442	1	UKPG u-plasminogen acti
41	261	6.6	431	1	UKHU u-plasminogen acti
42	261	6.6	433	1	JN0560 u-plasminogen acti
43	260	6.6	477	1	A34369 t-plasminogen acti
44	259	6.6	244	2	S72219 t-plasminogen acti
45	259	6.6	416	1	KPB0 coagulation factor
46	258.5	6.6	786	1	A47547 serine proteinase
47	258	6.5	251	2	PC1235 29k serine protein
48	258	6.5	433	1	UKBAY u-plasminogen acti
49	257.5	6.5	1004	2	T30338 oviductin (EC 3.4.
50	255.5	6.5	763	2	I50807 complement factor
51	254	6.4	617	2	S10511 thrombin (EC 3.4.2
52	253	6.4	1070	2	T31069 tolloid-BMP-1 like
53	249.5	6.3	400	1	A48050 coagulation factor
54	249.5	6.3	986	1	B58788 procollagen C-endo
55	248.5	6.3	459	2	JQ0419 coagulation factor
56	248	6.3	263	2	A31299 chymotrypsin (EC 3
57	248	6.3	638	1	KQHUP plasma kallikrein
58	247.5	6.3	991	2	I49540 procollagen C-endo
59	247	6.3	275	2	A32410 complement factor
60	247	6.3	764	1	BBHU hapoglobin - blac
61	246.5	6.2	347	2	G00006 procollagen C-endo
62	246.5	6.2	622	1	TBHU thrombin (EC 3.4.2
63	246	6.2	236	2	C42696 thrombin (EC 3.4.2
64	246	6.2	812	1	PLBO plasmin (EC 3.4.21
65	245	6.2	234	2	F42696 thrombin (EC 3.4.2
66	244	6.2	638	1	KQMSPL plasma kallikrein
67	242.5	6.1	730	1	BMHU1 procollagen C-endo
68	241.5	6.1	823	1	A58788 procollagen C-endo
69	240	6.1	242	2	S43489 trypsin (EC 3.4.21
70	239.5	6.1	406	1	HPHUT hapoglobin precu
71	239	6.1	245	1	KYBOA chymotrypsin (EC 3
72	238	6.0	237	1	TRCY1 trypsin (EC 3.4.21
73	238	6.0	263	2	A21195 chymotrypsin (EC 3
74	238	6.0	347	1	HPHUT hapoglobin precu
75	238	6.0	375	1	A23689 limulus clotting e
76	237.5	6.0	810	2	I46260 plasmin (EC 3.4.21
77	237	6.0	263	1	KYRTB chymotrypsin (EC 3
78	236.5	6.0	274	2	JC4171 trypsin (EC 3.4.2
79	236.5	6.0	707	2	JC2218 procollagen C-endo
80	235	6.0	270	2	S56160 maer cell trypsin
81	235	6.0	345	2	I36941 hapoglobin - chlm
82	235	6.0	1420	2	A32869 apolipoprotein(a)
83	233.5	5.9	263	2	S47537 chymotrypsin (EC 3
84	232	5.9	416	1	S31777 hepsin (EC 3.4.21.
85	232	5.9	638	1	KORPL plasma kallikrein
86	229.5	5.8	329	1	HPDG hapoglobin precu
87	228.5	5.8	235	2	B42696 thrombin (EC 3.4.2
88	228.5	5.8	347	1	HPMS Notch homolog Mocc
89	228.5	5.8	861	2	A48825 notch-1 protein -
90	228.5	5.8	2531	2	A46019 plasmin (EC 3.4.21
91	228	5.8	812	1	PLMS plasmin (EC 3.4.21
92	227.5	5.8	242	2	S31775 hapoglobin - chlm
93	227.5	5.8	349	2	I36944 trypsin (EC 3.4.21
94	227	5.8	242	2	S58984 development protei
95	227	5.8	1464	2	S31779 trypsin (EC 3.4.21
96	226.5	5.7	238	2	JC5759 brain-specific ser
97	226.5	5.7	761	2	JC5759 t-plasminogen acti
98	226	5.7	394	2	KF0600 coagulation factor
99	226	5.7	625	1	KFHU1 coagulation factor
100	225	5.7	615	1	KFHU12 pancreatic elastase
101	224.5	5.7	271	1	BLRT2 chymotrypsin (EC 3
102	224	5.7	245	1	KYBOB

103	223.5	5.7	274	2	S35339	trypsin (EC 3.4.21	176	199.5	5.1	2555	2	A40043	notch protein homo
104	223.5	5.7	348	1	HPHUR	haptoglobin-relate	177	198.5	5.0	229	1	TRB0TR	trypsin (EC 3.4.21
105	222.5	5.6	417	1	S00845	hepzin (EC 3.4.21.	178	198.5	5.0	232	1	KORG	tissue kallikrein
106	222.5	5.6	434	1	A35005	u-plasminogen acti	179	198.5	5.0	237	2	S55378	serine proteinase
107	222.5	5.6	790	1	PLRG	plasmin (EC 3.4.21	180	198	5.0	259	2	S68424	allergen Der f III
108	222	5.6	269	2	A26823	pancreatic elastase	181	198	5.0	270	2	B29934	pancreatic elastase
109	222	5.6	275	2	B35863	trypsin (EC 3.4.2	182	198	5.0	760	1	C2MS	classical-compleme
110	221.5	5.6	231	2	S18188	notch protein homo	183	197.5	5.0	250	2	T01779	haptoglobin Hpp -
111	221	5.6	231	2	S31778	trypsin (EC 3.4.21	184	197.5	5.0	258	2	T36947	trypsin (EC 3.4.21
112	220.5	5.6	274	2	A45754	trypsin (EC 3.4.2	185	196.5	5.0	269	2	C26823	pancreatic elastase
113	220.5	5.6	1057	1	A39288	dorsal-ventral pat	186	196.5	5.0	570	2	A48836	fibropellin C prec
114	220	5.6	275	2	A35863	trypsin (EC 3.4.2	187	196.5	5.0	767	2	T30018	hypothetical prote
115	219.5	5.6	235	2	H42696	thrombin (EC 3.4.2	188	196.5	5.0	2524	2	A35844	Xorch protein - Af
116	219.5	5.6	721	1	A25528	pancreatic elastase	189	196	5.0	3623	2	T08618	intricinc factor-B
117	219.5	5.6	761	1	B2MS	complement factor	190	195.5	5.0	271	2	I46580	factor IX - pig (f
118	219	5.6	343	1	A57014	proctasin (EC 3.4.	191	195	4.9	432	1	S18932	u-plasminogen acti
119	218	5.5	271	2	A43308	berine proteinase	192	194.5	4.9	246	1	TRRT1	trypsin (EC 3.4.21
120	217.5	5.5	243	2	A56338	venom proteinase (193	194	4.9	261	2	A25606	tissue kallikrein
121	217	5.5	239	2	A27207	tissue kallikrein	194	194	4.9	267	2	S40006	trypsin (EC 3.4.21
122	217	5.5	268	2	S68825	pancreatic elastase	195	193.5	4.9	249	2	A55634	granzyme M (EC 3.4
123	217	5.5	273	2	A47246	trypsin (EC 3.4.2	196	193.5	4.9	347	1	HPRT	haptoglobin precu
124	217	5.5	603	2	S28941	coagulation factor	197	193.5	4.9	2471	2	A49128	cell-fate determin
125	217	5.5	2703	1	A24420	notch protein - fir	198	193	4.9	240	1	CEB0A3	procarboxypeptidase
126	216.5	5.5	236	2	I42696	chrombin (EC 3.4.2	199	193	4.9	246	1	DBRU	complement factor
127	216.5	5.5	346	2	I36942	haptoglobin - chim	200	191.5	4.9	247	1	A25852	trypsin (EC 3.4.21
128	216.5	5.5	2616	2	A57096	nudel protein prec	201	191.5	4.9	281	2	T13596	P-selectin homolog -
129	216	5.5	810	1	PLHU	trypsin (EC 3.4.21	202	191.5	4.9	830	2	A30359	membrane-type friz
130	215.5	5.5	247	1	TRDG	trypsin (EC 3.4.21	203	190.5	4.8	579	2	JC7629	P-selectin precurs
131	215.5	5.5	248	2	S55066	trypsin (EC 3.4.21	204	190.5	4.8	768	2	A42755	trypsin (EC 3.4.21
132	215	5.4	241	2	S39048	trypsin (EC 3.4.21	205	190.5	4.8	1064	2	A40136	fibropellin Ia - B
133	215	5.4	268	2	S68826	pancreatic elastase	206	189.5	4.8	266	2	S54146	trypsin (EC 3.4.21
134	214.5	5.4	247	2	S13813	trypsin (EC 3.4.21	207	189.5	4.8	1737	2	T00209	MEGF8 protein - hu
135	214.5	5.4	366	2	JEO105	testicular serine	208	189	4.8	246	2	J01472	trypsin (EC 3.4.21
136	214.5	5.4	593	2	S45281	coagulation factor	209	189	4.8	247	2	S05494	trypsin (EC 3.4.21
137	214	5.4	275	2	C35863	trypsin (EC 3.4.2	210	189	4.8	253	2	A53968	serine proteinase
138	213.5	5.4	235	2	D42696	chrombin (EC 3.4.2	211	189	4.8	258	4	S70439	pancreatic elastase
139	213.5	5.4	2352	2	T30201	Notch homolog prot	212	189	4.8	267	4	A56615	probable pancreati
140	212	5.4	460	2	I56559	neupopsin - mouse	213	189	4.8	646	2	JN0473	P-selectin precurs
141	212	5.4	455	2	A61545	plasmin (EC 3.4.21	214	188.5	4.8	282	2	I46621	coagulation factor
142	211	5.3	237	2	S68702	trypsin (EC 3.4.2	215	188	4.8	263	2	S15686	tissue kallikrein
143	211	5.3	276	2	A38654	maet cell proteina	216	187.5	4.8	250	2	S55493	serine proteinase
144	210.5	5.3	1220	2	A56136	jagged protein pre	217	187.5	4.8	259	2	I38363	trypsin (EC 3.4.21
145	210	5.3	2437	2	S42612	transmembrane prot	218	187.5	4.8	304	2	S33496	trypsin (EC 3.4.21
146	209	5.3	433	1	UKMS	u-plasminogen acti	219	187	4.7	246	2	J01471	trypsin (EC 3.4.21
147	208.5	5.3	258	2	I36945	haptoglobin Hp - c	220	187	4.7	261	2	S45303	tissue kallikrein
148	207.5	5.3	239	2	G42696	chrombin (EC 3.4.2	221	187	4.7	271	2	S29239	chymotrypsin (EC 3
149	207.5	5.3	268	2	B26823	pancreatic elastase	222	186	4.7	1594	2	T30549	hensin - rabbit
150	207	5.2	238	1	TRWV5T	trypsin (EC 3.4.21	223	185.5	4.7	721	1	A47136	macrophage-stimula
151	206.5	5.2	246	1	TRRT2	trypsin (EC 3.4.21	224	185.5	4.7	911	1	J00948	AS antigen precurs
152	206.5	5.2	256	2	T10109	trypsin (EC 3.4.21	225	185	4.7	256	1	NGMSA	7S nerve growth fa
153	206	5.2	430	1	A24702	serine proteinase	226	183.5	4.7	1372	2	T25933	hypothetical prote
154	206	5.2	4548	1	S00657	apoptocytoma protei	227	183	4.6	265	1	KORTP	tissue kallikrein
155	205.5	5.2	269	2	B32410	plasmin (EC 3.4.21	228	183	4.6	392	1	A30100	serine proteinase
156	205.5	5.2	460	2	B61545	plasmin (EC 3.4.21	229	182.5	4.6	482	2	JCS092	E-selectin - pig
157	204.5	5.2	367	2	JEO104	testicular serine	230	182.5	4.6	722	2	I48324	DELTA-like 1 - mou
158	204.5	5.2	752	1	C2HU	complement C2 prec	231	182.5	4.6	2531	2	T31070	notch-homolog -
159	204.5	5.2	1203	2	A49175	Morch B protein -	232	182	4.6	261	1	TRMSMS	tissue kallikrein
160	203.5	5.2	247	1	B25852	trypsin (EC 3.4.21	233	181.5	4.6	247	1	PRMSCL	granzyme B (EC 3.4
161	203.5	5.2	263	1	I55608	complement factor	234	181.5	4.6	247	2	S12764	trypsin (EC 3.4.21
162	203.5	5.2	285	2	I48144	coagulation factor	235	181.5	4.6	258	2	A45161	serine proteinase
163	203.5	5.2	309	2	B49878	coagulation factor	236	181.5	4.6	437	2	S18407	acrosin (EC 3.4.21
164	203.5	5.2	3623	2	T09456	intrinsic factor-B	237	181	4.6	261	1	NGMSG	7S nerve growth fa
165	203	5.1	403	2	C82228	probable trypsin-V	238	181	4.6	418	2	A37344	acrosin (EC 3.4.21
166	202	5.1	240	2	S39047	trypsin (EC 3.4.21	239	181	4.6	1291	2	T21694	hypothetical prote
167	202	5.1	167	2	S78549	notch3 protein - h	240	180.5	4.6	248	2	S55067	trypsin (EC 3.4.21
168	201.5	5.1	246	2	B25528	trypsin (EC 3.4.21	241	180.5	4.6	275	2	S55072	factor IX - rabbit
169	200.5	5.1	226	1	KCUF	brechhyrtn (EC 3.4	242	180.5	4.6	436	2	JX0172	acrosin (EC 3.4.21
170	200.5	5.1	231	1	TRGTR	trypsin (EC 3.4.21	243	180	4.6	254	2	S49329	trypsin-like prote
171	200.5	5.1	810	2	B30848	plasmin (EC 3.4.21	244	180	4.6	261	2	S01971	tissue kallikrein
172	199.5	5.1	247	2	A27547	trypsin (EC 3.4.21	245	180	4.6	275	2	S40005	trypsin (EC 3.4.21
173	199.5	5.1	257	2	S33772	tissue kallikrein	246	179.5	4.6	243	2	A35871	trypsin (EC 3.4.21
174	199.5	5.1	258	2	G02959	haptoglobin - rhes	247	179.5	4.6	259	1	WMMS28	complement factor
175	199.5	5.1	275	2	S40007	trypsin (EC 3.4.21	248	179.5	4.6	274	2	I47078	coagulation factor

249	179.5	4.6	728	2	150719	C-Delta-1 - chicke
250	179.5	4.6	1047	2	A55617	maquerade precurs
251	179	4.5	266	1	ELPG	pancreatic elastas
252	179	4.5	612	2	B42755	E-selectin precurs
253	178.5	4.5	402	2	JH0403	procollagen I C-pr
254	177.5	4.5	248	2	A43520	natural killer cel
255	177.5	4.5	420	2	A55283	acrosin (BC 3.4.21
256	177.5	4.5	1964	2	T09059	notch4 - mouse
257	177	4.5	268	2	J01473	pancreatic elastas
258	177	4.5	473	2	A56175	adhesive plaque pr
259	177	4.5	747	2	T51579	complement factor
260	176.5	4.5	1091	1	PL0009	complement C3d/Bps
261	176	4.5	261	2	A29745	tissue kallikrein
262	176	4.5	261	2	A31136	tissue kallikrein
263	176	4.5	264	2	S32794	trypsin-like prote
264	176	4.5	2318	2	S45306	notch 3 protein -
265	175.5	4.4	274	2	S40004	trypsin-related pr
266	175	4.4	270	2	A29934	pancreatic elastas
267	175	4.4	421	1	S11674	acrosin (BC 3.4.21
268	174.5	4.4	232	1	S32398	serine proteinase
269	174.5	4.4	246	1	TRDGC	trypsin (BC 3.4.21
270	174	4.4	259	2	A29746	tissue kallikrein
271	174	4.4	261	1	KQMS1	tissue kallikrein
272	174	4.4	1295	2	A32901	glpi protein precu
273	173.5	4.4	548	2	D82175	probable trypsin V
274	173	4.4	229	1	TRDFS	trypsin (BC 3.4.21
275	173	4.4	768	1	T53821	P-selectin - rat
276	172.5	4.4	248	1	PRMSC2	granzyme C (BC 3.4
277	172.5	4.4	277	2	S35340	trypsin (BC 3.4.21
278	172.5	4.4	431	2	S47538	acrosin (BC 3.4.21
279	172.5	4.4	449	2	A55362	procollagen I C-pr
280	172	4.4	254	2	S65465	trypsin-like prote
281	172	4.4	261	2	A24378	tissue kallikrein
282	172	4.4	415	1	A34170	acrosin (BC 3.4.21
283	171.5	4.3	230	2	A27802	hypodermis C (BC 3
284	171.5	4.3	262	1	KOHU	tissue kallikrein
285	171.5	4.3	2403	2	A59386	sanko - human
286	171	4.3	257	2	B45061	granzyme A (BC 3.4
287	171	4.3	260	2	A45061	pancreatic elastas
288	171	4.3	266	1	ELERT1	trypsin-related pr
289	171	4.3	273	2	S40003	crumbs protein - f
290	171	4.3	2139	2	A35672	granzyme-like prote
291	170	4.3	248	2	S33756	trypsin-like prote
292	170	4.3	266	2	JC4850	trypsin-like prote
293	169.5	4.3	251	2	T10262	maet cell serine p
294	169.5	4.3	261	1	S35711	benemogelase (BC 3
295	169.5	4.3	421	2	S29599	acrosin (BC 3.4.21
296	169.5	4.3	560	2	T16833	hypothetical prote
297	169	4.3	214	2	S17680	fibrinolytic prote
298	169	4.3	246	2	S64707	chymase (BC 3.4.21
299	169	4.3	259	2	B31136	tissue kallikrein
300	169	4.3	504	2	S56745	mucin (clone gpm31
301	168.5	4.3	248	2	S33755	granzyme-like prote
302	168	4.3	597	2	S71352	metalloproteinase
303	168	4.3	2014	1	S16936	complement recepto
304	167.5	4.2	261	1	A32997	semenogelase (BC 3
305	167.5	4.2	383	2	S53716	delta-like homeoci
306	167	4.2	247	2	S45113	granzyme-like prote
307	167	4.2	260	2	A37938	tissue kallikrein
308	166	4.2	265	2	T10495	chymotrypsin (BC 3
309	165	4.2	2043	2	T18524	scavenger receptor
310	164.5	4.2	449	1	NBRHHS	complement factor
311	164.5	4.2	1231	1	NBRHHS	complement factor
312	164	4.2	230	2	I46885	maet cell proteina
313	164	4.2	613	2	S15468	complement C3d/C4b
314	164	4.2	2871	2	A55624	fibrillin-1 precu
315	163	4.1	868	2	T20239	hypothetical prote
316	162.5	4.1	276	2	A47290	TSG-6 homolog p54
317	162.5	4.1	1290	2	A57190	ehnerin precursor
318	162.5	4.1	2083	2	T42721	CRP-ductin-alpha p
319	162	4.1	261	1	EGMSB	tissue kallikrein
320	161.5	4.1	226	2	S69370	duodenase - bovine
321	161.5	4.1	248	2	S01006	cytotoxic T-lympo
322	161.5	4.1	250	2	S31384	trypsin (BC 3.4.21
323	161.5	4.1	261	1	S40162	cathepsin G (BC 3.
324	161.5	4.1	265	2	T15451	hypothetical prote
325	161.5	4.1	832	2	A31246	neurogenic protein
326	161.5	4.1	880	2	S00676	neurogenic repetit
327	161.5	4.1	1025	1	A43526	complement C3d/Bps
328	161	4.1	1827	2	T34288	hypothetical prote
329	160.5	4.1	661	1	KFHU13	coagulation factor
330	160	4.1	262	1	A31372	granzyme A (BC 3.4
331	160	4.1	3002	2	A47321	fibrillin 1 precu
332	159.5	4.0	1722	2	B87753	protein P11C7.4 (i
333	159	4.0	244	2	A44284	tissue kallikrein
334	159	4.0	261	2	A28062	gamma-tenin (BC 3.
335	159	4.0	2907	2	A57278	fibrillin-2 precu
336	158.5	4.0	247	2	S59135	maet cell proteina
337	158.5	4.0	385	2	S53718	homeotic protein d
338	158.5	4.0	833	2	S19087	gene Delta protein
339	158	4.0	610	2	T16761	hypothetical prote
340	158	4.0	2918	2	A54105	fibrillin-2 precu
341	157.5	4.0	579	2	A56740	sperm-egg recognit
342	157.5	4.0	907	2	T27317	hypothetical prote
343	157	4.0	261	2	J50236	tissue kallikrein
344	157	4.0	610	2	A35046	E-selectin precurs
345	156.5	4.0	252	2	A36172	procytotoxic T-lym
346	156.5	4.0	275	2	JC6506	tumor necrosis fac
347	156.5	4.0	1429	2	S06434	homeotic protein 1
348	156.5	4.0	3635	2	T10053	laminin alpha 5 ch
349	156	4.0	259	1	KORTM	toxin (BC 3.4.21.-
350	156	4.0	261	2	A29586	tissue kallikrein
351	156	4.0	702	2	T16832	hypothetical prote
352	155.5	3.9	213	2	S17537	fibrinolytic prote
353	155.5	3.9	485	2	S36772	E-selectin - bovin
354	155.5	3.9	533	2	JC7985	brain-specific CUB
355	155	3.9	250	2	S15685	kallikrein, glandu
356	155	3.9	2489	2	T17012	complement C3d/C4b
357	154.5	3.9	252	2	A34877	C4b-binding protei
358	154	3.9	669	2	S65551	factor H - bovine
359	153.5	3.9	281	2	JC2125	chymase (BC 3.4.21
360	153.5	3.9	387	2	B49175	Morch A protein -
361	153.5	3.9	551	2	T46709	endothelial leukoc
362	153.5	3.9	1786	1	NMMSB1	laminin beta-1 cna
363	153	3.9	152	2	A53274	complement factor
364	153	3.9	254	3	TRWV37	trypsin-like prote
365	153	3.9	2871	2	A55567	fibrillin I - bovi
366	152.5	3.9	248	1	S01007	granzyme F (BC 3.4
367	152.5	3.9	264	2	S55663	granzyme 3 (BC 3.4
368	152.5	3.9	385	2	A54785	preadipocyte facto
369	152.5	3.9	422	1	KXHUZ	plasma protein Z p
370	152	3.9	281	1	A61021	granzyme B (BC 3.4
371	152	3.9	686	2	JC7569	Delta-4 protein -
372	151.5	3.8	261	2	A34079	tissue kallikrein
373	151.5	3.8	716	1	A40332	macrophage-stimula
374	151.5	3.8	977	2	I52657	seizure-related pr
375	151	3.8	249	1	A35842	chymase (BC 3.4.21
376	151	3.8	261	2	A41020	tissue kallikrein
377	151	3.8	1620	2	T27283	hypothetical prote
378	150.5	3.8	248	2	S43259	granzyme-like prote
379	150.5	3.8	277	2	A41735	hyaluronate-bindin
380	150.5	3.8	285	2	T35195	probable serine pr
381	150.5	3.8	685	2	JC7570	Delta-4 protein -
382	150.5	3.8	1053	2	S46199	probable complemen
383	150	3.8	263	1	NMVZSP	apolipoprotein H h
384	150	3.8	267	1	EHUHL	leukocyte elastase
385	150	3.8	601	2	B36346	fibrulin 1 precu
386	150	3.8	770	2	T00203	LDL receptor-relat
387	150	3.8	3712	2	S18253	laminin alpha-1 ch
388	149.5	3.8	236	1	A32121	snake venom factor
389	149.5	3.8	259	1	TRSMG	trypsin (BC 3.4.21
390	148.5	3.8	12388	2	T03099	mucin, submaxillar
391	149	3.8	216	1	KYVH20	chymotrypsin (BC 3
392	149	3.8	683	2	C36346	fibrulin 1 precu
393	149	3.8	770	2	T00204	LDL receptor relat
394	149	3.8	1408	2	S16148	gene serrate prote

395	148	3.8	218	1	KYH2C	468	134	3.4	3034	2	T14119	seven-pass transme
396	148	3.8	668	2	A46013	469	133.5	3.4	154	2	S35207	protease 7 - buf
397	18	3.8	1469	2	B36665	470	133.5	3.4	1687	2	T30176	EGF repeat transme
398	148	3.7	1480	2	A36665	471	133.5	3.4	3507	2	T34513	hypothetical prote
399	147.5	3.7	244	2	A34671	472	133	3.4	810	2	T10756	Nel-homolog prote
400	147.5	3.7	244	2	A34671	473	132.5	3.4	331	2	T27906	hypothetical prote
401	147.5	3.7	597	1	MMHUB1	474	132	3.3	246	2	A36678	mast cell proteina
402	147.5	3.7	1786	1	MMHUB1	475	132	3.3	372	2	JC5377	L-selectin precurs
403	147.5	3.7	4391	2	A38096	476	132	3.3	558	2	S57953	aggresecn precurs
404	147	3.7	236	2	A28566	477	132	3.3	2109	1	T50421	hypothetical prote
405	147	3.7	259	2	D23863	478	132	3.3	3871	2	T22812	hypothetical prote
406	147	3.7	262	1	JC4803	479	132	3.3	302	1	MMB81E	secretory comple
407	147	3.7	716	1	JC5861	480	131.5	3.3	1268	1	S52781	neurocan - mouse
408	147	3.7	1557	2	T28811	481	130.5	3.3	1257	2	S28764	neurocan precurs
409	147	3.7	3084	1	MMMSA	482	130.5	3.3	3672	2	T23433	hypothetical prote
410	146.5	3.7	236	1	B32121	483	130.5	3.3	3704	2	T37316	probable laminin a
411	146.5	3.7	3707	2	S18252	484	129.5	3.3	233	1	JG0169	L-selectin precurs
412	146	3.7	263	2	T28450	485	129.5	3.3	376	2	JC4892	venombin A (EC 3.4
413	145	3.7	256	1	TRPF	486	129.5	3.3	381	2	B26359	decay-accelerating
414	145	3.7	263	1	C36838	487	129.5	3.3	440	2	A26359	decay-accelerating
415	145	3.7	372	1	A32375	488	129	3.3	235	2	A27122	venombin AB (EC 3.
416	145	3.7	782	2	A61625	489	128.5	3.3	321	2	T33161	cathepsin G (EC 3.
417	144.5	3.7	246	2	B38678	490	128.5	3.3	219	1	TRPGAZ	hypothetical prote
418	144.5	3.7	303	2	T13598	491	128	3.2	5147	1	T42218	azurocidin - pig
419	144.5	3.7	360	2	T42921	492	127.5	3.2	1531	2	T42218	cadherin-related c
420	144	3.7	263	2	B72121	493	127.5	3.2	258	2	T56220	slit-1 protein hom
421	144	3.7	685	2	S78040	494	127	3.2	1609	1	MMHUB2	tryptase 2 - rat
422	143.5	3.6	247	2	S23504	495	127	3.2	1751	1	MMHUB2	laminin gamma-1 ch
423	143	3.6	3075	2	S14458	496	127	3.2	3106	1	S53868	laminin alpha-2 ch
424	142.5	3.6	260	2	S25043	497	127	3.2	1025	2	T42626	laminin alpha-2 ch
425	142	3.6	272	2	UC4170	498	126.5	3.2	265	2	A38894	secreted leucine-r
426	141.5	3.6	310	2	S41055	499	126	3.2	265	2	J50260	serine proteinase
427	141.5	3.6	385	1	A34015	500	126	3.2	330	2	T56100	serine proteinase
428	141	3.6	225	2	S45356	501	126	3.2	642	2	S53433	plasma protein S p
429	141	3.6	246	2	A32692	502	126	3.2	254	2	S35885	chymotrypsin-like
430	140.5	3.6	246	1	A46504	503	125.5	3.2	265	2	I48679	neutrophil elastas
431	140.5	3.6	1234	1	NBWSH	504	125.5	3.2	597	1	NBHUC4	Cab-binding protei
432	140.5	3.6	2406	2	A54148	505	125.5	3.2	152	2	S35209	serine proteinase
433	140.5	3.6	2515	2	S47008	506	125	3.2	333	1	MMFPR1	complement factor
434	140	3.5	396	1	KXBOZ	507	125	3.2	1790	1	MMFPR1	L-selectin precurs
435	139.5	3.5	258	1	S44184	508	125	3.2	248	2	A33412	laminin beta-1 cha
436	139.5	3.5	288	2	T33224	509	124.5	3.2	548	2	T46642	cytotoxic T-lympho
437	139.5	3.5	319	2	I51569	510	124.5	3.2	330	2	T46256	hypothetical prote
438	139	3.5	1820	2	A55494	511	124	3.1	1584	2	T29764	brevican - human (
439	138.5	3.5	244	2	S26042	512	124	3.1	710	1	I51283	hepatocyte growth
440	138.5	3.5	247	1	KYHUCM	513	124	3.1	883	2	S49126	brevican precurs
441	138.5	3.5	705	2	S34968	514	124	3.1	1221	2	A49457	fibulin-2 precurs
442	138.5	3.5	1111	2	T25972	515	124	3.1	1523	2	T13953	MEGF5 protein - ra
443	137.5	3.5	191	2	S54115	516	124	3.1	1584	2	T22674	hypothetical prote
444	137.5	3.5	808	2	D35069	517	124	3.1	2180	2	T29764	hypothetical prote
445	137	3.5	258	2	S57960	518	123.5	3.1	151	2	S35205	proteinae 5 - buf
446	137	3.5	372	2	S23936	519	123.5	3.1	259	1	S22124	L-selectin precurs
447	137	3.5	2823	2	F87908	520	123.5	3.1	370	2	T33375	hypothetical prote
448	137	3.5	2823	2	T23064	521	123.5	3.1	699	2	T33375	hypothetical prote
449	137	3.5	3102	2	T43291	522	123.5	3.1	1184	2	A55164	fibulin-2 precurs
450	136.5	3.5	247	1	PRRTG	523	123	3.1	248	2	S49323	chymotrypsin (EC 3
451	136.5	3.5	1274	1	T42017	524	123	3.1	340	2	JC7125	epidermal growth f
452	136	3.4	676	2	MMB82E	525	123	3.1	308	2	I56234	decay-accelerating
453	136	3.4	1574	2	T13954	526	123	3.1	798	2	T22793	hypothetical prote
454	136	3.4	1607	1	MMMSB2	527	123	3.1	2844	2	S68221	receptor tyrosine
455	136	3.4	226	2	JE0151	528	122.5	3.1	1081	2	T31329	hypothetical prote
456	135.5	3.4	372	2	T29359	529	122	3.1	152	2	S65206	serine proteinase
457	135.5	3.4	452	2	A35068	530	122	3.1	198	2	I46002	CAB beta chain -
458	135.5	3.4	469	1	NBWSM4	531	122	3.1	676	1	KXHS	plasma protein S p
459	135.5	3.4	159	2	G35070	532	122	3.1	1810	1	A32230	aggr precurs
460	135	3.4	343	1	NBHU	533	122	3.1	1955	1	ACGH	hypothetical prote
461	135	3.4	345	1	NBHU	534	121.5	3.1	245	2	A48598	aggr precurs
462	135	3.4	3051	2	S42373	535	121.5	3.1	416	2	T20448	hypothetical prote
463	134.5	3.4	601	2	D89711	536	121.5	3.1	610	1	I46001	Cab-binding protei
464	134.5	3.4	601	2	D89711	537	121.5	3.1	5376	2	T42215	zonadhesin - mouse
465	134	3.4	232	1	A54361	538	121	3.1	647	2	A43902	tenascin - eastern
466	134	3.4	232	1	A54361	539	121	3.1	1627	2	S65464	pregnancy-associat
467	134	3.4	2824	2	T22759	540	121	3.1	2409	1	A60979	versican precurs

541	120.5	3.1	247	2	S64708	614	112	2.8	228	1	S35689	venombin A (EC 3.4
542	120.5	3.1	252	2	T46247	615	112	2.8	918	2	JC4361	scavenger receptor
543	120.5	3.1	345	1	JN0465	616	112	2.8	1125	1	S57846	proteins-tyrosine k
544	120.5	3.1	497	2	JC2054	617	112	2.8	1353	1	JH0675	reticulin precurs
545	120.5	3.1	646	2	S38819	618	112	2.8	1639	1	NMFRB2	laminin gamma-1 ch
546	120.5	3.1	689	2	T42760	619	112	2.8	3562	2	A47171	chondroitin sulfat
547	120.5	3.1	712	2	T42990	620	112	2.8	4307	2	T20721	hypothetical prote
548	120.5	3.1	728	1	A60185	621	111.5	2.8	159	2	S35202	proteinae 2 - buf
549	120.5	3.1	1394	2	A35626	622	111.5	2.8	370	2	JC7592	spinal cord-deri
550	120.5	3.1	1801	1	NMRTS	623	111.5	2.8	651	2	T19477	hypothetical prote
551	120	3.0	257	1	UC2479	624	111.5	2.8	1328	2	T13060	agrin - electric r
552	120	3.0	363	2	B45900	625	111.5	2.8	1797	2	A55677	laminin beta-2 cha
553	120	3.0	493	2	JC5621	626	111.5	2.8	2019	1	JQ1322	tenascin precursor
554	120	3.0	589	2	T43210	627	111.5	2.8	2531	2	T16743	hypothetical prote
555	120	3.0	912	2	A54423	628	111.5	2.8	4351	2	T00252	MEGF1 protei
556	120	3.0	1548	2	S34583	629	111	2.8	231	2	A60468	venombin A (EC 3.4
557	120	3.0	1643	2	T14274	630	111	2.8	915	2	T21773	hypothetical prote
558	120	3.0	1937	1	A55535	631	110.5	2.8	234	1	S20407	venombin A (EC 3.4
559	120	3.0	3381	2	T42389	632	110.5	2.8	297	1	NBRT	apolipoprotein H p
560	119.5	3.0	161	2	I48158	633	110.5	2.8	408	2	T22801	hypothetical prote
561	119.5	3.0	482	2	A34924	634	110.5	2.8	583	2	A29154	complement factor
562	119.5	3.0	675	1	KXBOS	635	110.5	2.8	678	2	B48089	growth arrest-spec
563	119.5	3.0	835	2	JP0076	636	110.5	2.8	692	2	T2980	hypothetical prote
564	119.5	3.0	1247	1	MMHUND	637	110.5	2.8	961	1	TSHUP4	thrombospondin 4 p
565	119.5	3.0	1506	2	T30886	638	110.5	2.8	1217	1	BGMSMG	epidermal growth f
566	119	3.0	258	2	A57290	639	110.5	2.8	1894	2	JC4980	plexin 1 precursor
567	119	3.0	513	2	D88991	640	110	2.8	266	2	T19292	hypothetical prote
568	118.5	3.0	674	2	T55476	641	110	2.8	1124	1	T58368	protein-tyrosine k
569	118.5	3.0	728	1	A35644	642	110	2.8	1905	2	T15353	plexin - African c
570	118.5	3.0	728	1	JH0579	643	109.5	2.8	198	2	S06176	cytotoxic T-lympho
571	118	3.0	133	2	S21114	644	109.5	2.8	2215	2	T00348	LRI1 protein - mou
572	118	3.0	196	2	T08808	645	109	2.8	661	2	T42754	hypothetical prote
573	118	3.0	293	2	B26637	646	109	2.8	1808	2	T15099	hypothetical prote
574	118	3.0	838	2	T20125	647	109	2.8	2610	2	T20968	hypothetical prote
575	118	3.0	883	2	S57653	648	108.5	2.8	236	1	A41456	venombin A (EC 3.4
576	117.5	3.0	188	2	B32340	649	108.5	2.8	2825	2	T14271	Dcc4 protein, stre
577	117.5	3.0	259	2	T21011	650	108	2.7	251	1	TRHUA2	azurocidin precurs
578	117.5	3.0	642	2	S53434	651	108	2.7	1450	2	T30273	hypothetical prote
579	117.5	3.0	996	2	J50237	652	108	2.7	1700	2	S08167	Baldiani ring 3 pr
580	117.5	3.0	1160	2	P88369	653	108	2.7	2476	2	T34022	zonadhesin - pig
581	117.5	3.0	2295	2	C88369	654	107.5	2.7	640	2	T19346	hypothetical prote
582	117.5	3.0	3375	2	T19821	655	107.5	2.7	670	2	I65967	disintegrin-like m
583	116.5	3.0	256	1	PRHU3	656	107.5	2.7	3566	1	A40701	tenascin-X precurs
584	116.5	3.0	377	2	I54479	657	107.5	2.7	4544	1	S02392	alpha-2-macroglobu
585	116.5	3.0	378	2	B59180	658	107	2.7	280	2	G02741	skeleral muscle LI
586	116.5	3.0	384	2	S01896	659	107	2.7	497	2	T27827	hypothetical prote
587	116.5	3.0	1170	2	A53612	660	106.5	2.7	192	2	E70414	hypothetical prote
588	116	2.9	1376	2	G00043	661	106.5	2.7	362	2	JC5194	membrane cofactor
589	115.5	2.9	440	2	A43519	662	106.5	2.7	369	2	JC5138	hypothetical prote
590	115.5	2.9	1474	2	D88550	663	106.5	2.7	616	2	T29234	cartilage oligomer
591	115.5	2.9	1680	2	A43434	664	106.5	2.7	755	2	A44315	hypothetical prote
592	115	2.9	279	2	JG0164	665	106	2.7	417	2	T33376	hypothetical prote
593	115	2.9	1207	1	EGHU	666	106	2.7	657	2	T00859	hypothetical prote
594	114.5	2.9	270	2	I37278	667	106	2.7	927	2	T21772	epidermal growth f
595	114.5	2.9	349	2	G02913	668	106	2.7	1133	1	EGRT	hypothetical prote
596	114.5	2.9	369	2	I57998	669	106	2.7	1522	2	H88380	hypothetical prote
597	114.5	2.9	1798	2	S53869	670	106	2.7	1805	2	T11888	hypothetical prote
598	114	2.9	235	1	A28169	671	106	2.7	2195	2	T34264	variant-specific s
599	114	2.9	741	2	T46488	672	106	2.7	596	2	A45664	hypothetical prote
600	114	2.9	846	2	A30889	673	105.5	2.7	346	2	T46914	hypothetical prote
601	114	2.9	1069	2	T42681	674	105.5	2.7	673	2	A48089	growth arrest-spec
602	113.5	2.9	293	2	T22919	675	105.5	2.7	860	1	ORHUPD	LDL receptor precu
603	113.5	2.9	502	2	T20130	676	105	2.7	1107	2	T15884	hypothetical prote
604	113.5	2.9	558	2	T17324	677	105	2.7	1107	2	T15884	hypothetical prote
605	113.5	2.9	574	2	B88465	678	105	2.7	1746	1	S19694	tenascin precursor
606	113.5	2.9	879	1	ORRTLD	679	105	2.7	2201	2	A32160	tenascin-C - human
607	113.5	2.9	1712	2	A38261	680	104.5	2.6	1360	2	T33922	apolipoprotein H p
608	112.5	2.9	161	2	I62744	681	104.5	2.6	345	1	NBBO	hypothetical prote
609	112.5	2.9	264	2	A28942	682	104	2.6	345	1	NBBO	transcription fact
610	112.5	2.9	370	2	UC7591	683	104	2.6	360	1	A55198	apolipoprotein H p
611	112.5	2.9	677	2	C42125	684	104	2.6	379	2	A59180	Wnt inhibitory fac
612	112.5	2.9	1228	2	A57384	685	104	2.6	473	2	T32326	Wnt inhibitory fac
613	112.5	2.9	1797	2	T21889	686	104	2.6	2101	2	S57245	neuulin receptor (

687	104	2.6	4135	2	T42629	760	98	2.5	102	2	B55885	chondroitin sulfat
688	103.5	2.6	381	2	T21946	761	98	2.5	357	2	S23403	sperm surface prot
689	103	2.6	333	2	A45222	762	98	2.5	909	1	ORX1L1	LDL receptor 1 pre
690	103	2.6	412	2	S72579	763	98	2.5	937	2	I53282	gene PACFA protein
691	103	2.6	1296	2	T16859	764	98	2.5	1087	2	T31100	probable potaasium
692	103	2.6	2148	1	A56081	765	98	2.5	1748	1	JN0786	integrin beta-4 ch
693	102.5	2.6	153	2	S35204	766	98	2.5	2580	2	T14342	NSD1 protein - mou
694	102.5	2.6	473	2	I49283	767	98	2.5	4660	2	T42737	GP330 protein prec
695	102.5	2.6	565	2	T16408	768	97.5	2.5	537	2	A60501	thrombospondin pre
696	102.5	2.6	873	1	ORRVD	769	97.5	2.5	837	1	A29512	LDL receptor precu
697	102	2.6	149	2	S35208	770	97.5	2.5	878	2	B71460	probable outer mem
698	102	2.6	280	2	G01884	771	97.5	2.5	884	2	T18649	hypothetical prote
699	102	2.6	380	2	G01639	772	97.5	2.5	1162	2	T21557	hypothetical prote
700	102	2.6	411	2	D88087	773	97.5	2.5	2946	2	T15840	hypothetical prote
701	102	2.6	718	2	T29448	774	97	2.5	126	2	A23473	hypocryptein-like
702	102	2.6	863	1	S51789	775	97	2.5	27350	2	T27350	hypothetical prote
703	102	2.6	1168	2	I56985	776	97	2.5	429	2	T21113	hypothetical prote
704	102	2.6	1713	2	A55347	777	97	2.5	626	2	T27319	hypothetical prote
705	102	2.6	4006	2	T09070	778	97	2.5	799	1	I0MSP8	fibronectin recept
706	101.5	2.6	379	2	T16213	779	97	2.5	808	2	T23129	hypothetical prote
707	101.5	2.6	1106	2	T18739	780	97	2.5	862	2	S43922	versican - pig-cal
708	101.5	2.6	1959	1	AGRT	781	97	2.5	915	1	A48225	subtilisin-like pr
709	101.5	2.6	2415	1	A39086	782	97	2.5	1138	1	S24066	protein-tyrosine k
710	101	2.6	377	2	C88710	783	97	2.5	1193	2	A44018	laminin B2 chain
711	101	2.6	463	2	T26655	784	97	2.5	1292	2	T09229	galactose binding
712	101	2.6	557	2	A48434	785	96.5	2.4	149	1	K0MSM	tissue kallikrein
713	101	2.6	1371	2	A33837	786	96.5	2.4	317	2	D42526	B5R protein - vacc
714	101	2.6	1378	1	I48751	787	96.5	2.4	613	2	A69535	aldehyde ferredoxi
715	101	2.6	1875	2	A36429	788	96.5	2.4	956	2	A57121	thrombospondin 3 p
716	100.5	2.5	417	2	T20199	789	96.5	2.4	1149	2	I18006	M30 antigen precu
717	100.5	2.5	670	2	S77463	790	96.5	2.4	1193	2	T21133	hypothetical prote
718	100.5	2.5	802	2	T24293	791	96.5	2.4	1297	2	T30274	proteolisin - ae
719	100.5	2.5	949	2	T24294	792	96.5	2.4	3133	2	S52093	hemocytin - silkw
720	100.5	2.5	956	1	A46016	793	96	2.4	116	2	S17567	AOX-3 protein - pi
721	100.5	2.5	1252	2	S36016	794	96	2.4	116	2	S39434	spermadhesin AOX-3
722	100.5	2.5	1356	2	A45445	795	96	2.4	286	2	A65934	cyprin-related pr
723	100	2.5	152	2	S35203	796	96	2.4	392	2	T25213	hypothetical prote
724	100	2.5	421	2	T25383	797	96	2.4	798	2	A28193	integrin beta-1+ c
725	100	2.5	667	2	A48579	798	96	2.4	798	2	B28193	integrin beta-1+ c
726	100	2.5	873	1	A49729	799	96	2.4	886	2	A57172	probable hormone r
727	100	2.5	1122	2	I54237	800	96	2.4	4753	1	A47437	LDL-receptor-relat
728	100	2.5	1123	1	JN0712	801	96.5	2.4	177	2	S33505	chymase (EC 3.4.21
729	100	2.5	1125	1	JH0771	802	96.5	2.4	218	2	H70770	probable regulator
730	100	2.5	1151	2	I13804	803	95.5	2.4	330	2	B82415	probable serine pr
731	100	2.5	1156	2	I13805	804	95.5	2.4	427	2	JC4915	age protein precu
732	100	2.5	1251	2	A57293	805	95.5	2.4	561	2	T27318	hypothetical prote
733	100	2.5	1299	2	T43251	806	95.5	2.4	1042	2	A57534	mucin SAC (clone L
734	99.5	2.5	330	2	I55975	807	95.5	2.4	1135	1	J01928	G2-G1 polypeptin
735	99.5	2.5	640	1	A30452	808	95.5	2.4	1135	2	T22615	hypothetical prote
736	99.5	2.5	686	2	S43562	809	95.5	2.4	3191	2	T22945	hypothetical prote
737	99.5	2.5	914	1	S07047	810	95	2.4	463	2	T29621	peptidyl prollyl ci
738	99.5	2.5	1280	2	A39117	811	95	2.4	850	2	S56015	gastric mucin MUC5
739	99.5	2.5	1350	2	S00647	812	95	2.4	869	1	JC4858	VDL receptor prec
740	99.5	2.5	1766	2	A42125	813	95	2.4	989	2	T01519	hypothetical prote
741	99.5	2.5	1847	2	T18308	814	95	2.4	1245	1	MMMSND	nldogen precursor
742	99.5	2.5	1984	2	T13171	815	95	2.4	1321	2	JE0352	mucin MUC5B, trach
743	99	2.5	589	2	B38128	816	94.5	2.4	111	2	S21211	spermadhesin AOX-1
744	99	2.5	591	2	I48141	817	94.5	2.4	643	2	T25473	hypothetical prote
745	99	2.5	675	1	KXMS	818	94.5	2.4	736	2	S47645	tMDC 1 protein - c
746	99	2.5	675	1	KXRTS	819	94.5	2.4	862	1	QMSLUD	LDL receptor precu
747	99	2.5	805	2	S68441	820	94.5	2.4	1216	2	T26104	hypothetical prote
748	99	2.5	892	2	S68439	821	94.5	2.4	1416	2	E88550	protein ZC84.1 (im
749	99	2.5	894	2	S68437	822	94.5	2.4	1717	1	A45558	epidermal growth f
750	99	2.5	900	2	S68440	823	94	2.4	258	1	B37252	insulin-like growt
751	99	2.5	1162	2	S68438	824	94	2.4	370	2	JC7998	platelet-derived g
752	99	2.5	1558	2	A82457	825	94	2.4	634	2	T02594	hypothetical prote
753	99	2.5	2809	2	T30213	826	94	2.4	713	2	T44447	neuregulin-3 (lipo
754	98.5	2.5	317	2	T28605	827	94	2.4	736	2	T06757	hypothetical prote
755	98.5	2.5	317	2	F72172	828	94	2.4	899	2	G02428	subtilisin-like pr
756	98.5	2.5	437	2	G36855	829	94	2.4	915	2	JC6148	subtilisin-like pr
757	98.5	2.5	427	2	S74211	830	94	2.4	932	2	I52527	PACFA - mouse (fr
758	98.5	2.5	1178	2	A39804	831	94	2.4	1381	2	T31063	paranodin - rat
759	98	2.5	82	2	T46510	832	94	2.4	1385	2	T14158	neurexin IV - mou

833	94	2.4	3097	2	T00021	DN-cadherin - fru1
834	93.5	2.4	258	2	A45403	insulin-like growt
835	93.5	2.4	317	2	T01799	BSR protein precu
836	93.5	2.4	449	2	T35048	probable ATP /GTP
837	93.5	2.4	456	2	T31483	hypothetical prote
838	93.5	2.4	486	2	S49820	PR1 protein - Ara
839	93.5	2.4	612	2	JH0799	laminin-related pr
840	93.5	2.4	739	2	B88553	protein K04H4.2b [
841	93.5	2.4	1115	2	S40241	G protein-coupled
842	93.5	2.4	1136	1	S57845	protein-tyrosine k
843	93	2.4	104	2	T19868	hypothetical prote
844	93	2.4	329	2	A48805	insulin-like growt
845	93	2.4	873	1	I48952	VDL receptor prec
846	93	2.4	995	2	A56599	embryo kinase 5 -
847	93	2.4	2767	1	U1HU	chryoglobulin proc
848	93	2.4	4545	1	S25111	alpha-2-macroglobu
849	92.5	2.3	211	2	A46458	human CRI homolog
850	92.5	2.3	736	2	T19366	hypothetical prote
851	92.5	2.3	756	2	S47656	TMDC II protein -
852	92.5	2.3	803	1	IJCCH3	integrin, band 3 p
853	92.5	2.3	955	2	A45441	thrombospondin 4
854	92.5	2.3	1367	1	I6HUR1	insulin-like growt
855	92	2.3	334	2	T23027	hypothetical prote
856	92	2.3	650	2	A34498	glycoprotein antig
857	92	2.3	719	2	T00266	hypothetical prote
858	92	2.3	915	2	B48225	probable proprotei
859	92	2.3	964	2	UC5545	integrin beta-4 pr
860	92	2.3	1097	2	S68685	adenylate cyclase
861	92	2.3	1444	2	T18856	angiogenesis inh
862	92	2.3	1895	2	T15881	hypothetical prote
863	92	2.3	2533	2	T28675	alpha-51D immob
864	92	2.3	3869	2	A48205	All-1 protein +GTR
865	91.5	2.3	237	2	I47031	insulin-like growt
866	91.5	2.3	250	2	T30124	hypothetical prote
867	91.5	2.3	303	2	H35068	apolipoprotein H-r
868	91.5	2.3	511	2	T17298	hypothetical prote
869	91.5	2.3	588	2	T33815	hypothetical prote
870	91.5	2.3	640	2	S49932	MET30 protein - ye
871	91.5	2.3	1101	2	T16840	hypothetical prote
872	91.5	2.3	1161	2	D83076	type 4 fibrinolyt
873	91.5	2.3	2144	2	S71490	ash1 protein - fru
874	91.5	2.3	2672	2	A48126	translational activa
875	91.5	2.3	2910	2	T42214	otogelin - mouse
876	91	2.3	94	2	PC3013	tissue kallikrein
877	91	2.3	293	2	T08065	hypothetical prote
878	91	2.3	319	1	I50370	transcription fact
879	91	2.3	398	2	E71539	hypothetical prote
880	91	2.3	435	2	I54182	tumor necrosis fac
881	91	2.3	478	2	S47040	gene Tf52 protein
882	91	2.3	909	1	ORXL12	LDL receptor 2 pre
883	91	2.3	2543	2	T31687	surface antigen - p
884	91	2.3	4543	1	A53102	alpha-2-macroglobu
885	90.5	2.3	53	2	S17294	epidermal growth f
886	90.5	2.3	330	1	JN0561	urokinase-type pla
887	90.5	2.3	642	1	JPU079	LIM protein kinase
888	90.5	2.3	746	1	HYHUMA	mepin A (EC 3.4.2
889	90.5	2.3	776	2	S28258	androgen-regulated
890	90.5	2.3	960	2	JE0356	gamma-aminobutyric
891	90.5	2.3	1104	2	I38869	transcription fact
892	90.5	2.3	1148	1	GNVUNE	M polypeptide proc
893	90.5	2.3	1357	2	T16860	hypothetical prote
894	90.5	2.3	1436	2	A45496	antigen WC1.1 prec
895	90.5	2.3	2813	1	VHNU	von Willebrand fac
896	90	2.3	156	2	B23863	tissue kallikrein
897	90	2.3	340	2	T34423	hypothetical prote
898	90	2.3	409	2	T11743	PP47 protein - pig
899	90	2.3	417	2	T29864	hypothetical prote
900	90	2.3	522	2	T29767	hypothetical prote
901	90	2.3	577	2	B37057	integrin beta-6 ch
902	90	2.3	814	1	I39627	nicotinic dehydroge
903	90	2.3	2533	1	T28674	alpha-51D-immobil
904	89.5	2.3	417	2	T39939	DNA binding protei
905	89.5	2.3	748	2	S24134	endopeptidase 2 (E

LDL receptor precu	906	89.5	2.3	854	1	ORHYLD
RNA-directed DNA p	907	89.5	2.3	1164	2	T01871
WD-repeat protein	908	89.5	2.3	1258	2	A12155
MEGR2 protein - hu	909	89.5	2.3	1364	2	T00250
folliclestatin - Afr	910	89	2.3	319	2	A53502
hypothetical prote	911	89	2.3	354	2	T22274
histone deacetylase	912	89	2.3	369	2	F81178
hypothetical prote	913	89	2.3	390	2	C90208
exo-alpha-sialidas	914	89	2.3	469	1	NMTV27
hypothetical prote	915	89	2.3	525	2	T21357
p508/p97 (lyc-10)	916	89	2.3	907	2	I50404
G2-G1 polypeptide	917	89	2.3	1110	1	B42544
thrombospondin 1 p	918	89	2.3	1170	2	A40558
EBV gp42/ps/hr pro	919	88.5	2.2	317	2	T37442
hypothetical prote	920	88.5	2.2	356	2	T20656
lim domain protein	921	88.5	2.2	438	2	T40509
zinc finger protei	922	88.5	2.2	693	2	I37570
transketolase-like	923	88.5	2.2	754	2	T47886
fertilin alpha-I -	924	88.5	2.2	905	2	S55059
probable cysteine-	925	88.5	2.2	1077	2	T41146
thrombospondin 1 p	926	88.5	2.2	1096	2	T16875
acetyl-CoA carboxy	927	88.5	2.2	1170	1	TSHUP1
low density lipopr	928	88.5	2.2	1978	2	T07081
integrin beta-5 ch	929	88	2.2	621	2	I38467
fibronectin recept	930	88	2.2	656	2	JC2005
integrin beta-5 ch	931	88	2.2	798	2	B27079
subtilisin-like pr	932	88	2.2	799	2	A38308
unknown protein (I	933	88	2.2	962	2	JC5571
E-selectin ligand-	934	88	2.2	1085	2	C96797
laminin gamma 2 ch	935	88	2.2	1175	2	S52417
cyclolestin precurs	936	88	2.2	1192	2	S69000
spermatogenesis pr	937	87.5	2.2	554	2	A45818
complement C8 alph	938	87.5	2.2	580	2	A37107
hypothetical prote	939	87.5	2.2	584	1	CBHUA
iodide peroxidase	940	87.5	2.2	667	2	T01999
integrin beta-4 ch	941	87.5	2.2	914	1	JN0550
laminin alpha-4 ch	942	87.5	2.2	1807	2	JC6319
extracellular prot	943	87.5	2.2	1816	1	S68960
hypothetical prote	944	87	2.2	387	2	I38449
hypothetical prote	945	87	2.2	706	2	S74610
hypothetical prote	946	87	2.2	743	2	I40521
hypothetical prote	947	87	2.2	970	2	T16892
receptor protein-t	948	87	2.2	975	2	JC5570
subtilisin-like pr	949	87	2.2	975	2	JC5570
hypothetical prote	950	87	2.2	1042	2	T26644
hypothetical prote	951	87	2.2	1056	2	A53761
protein-tyrosine k	952	87	2.2	1134	1	JN0711
plexin A - fruit f	953	87	2.2	1945	2	T13937
fibronectin - Afr	954	87	2.2	2481	2	A43908
trithorax homolog	955	87	2.2	3968	2	A44265
hypothetical prote	956	86.5	2.2	222	2	S72795
hypothetical prote	957	86.5	2.2	264	2	T16271
polyferredoxin 4x2	958	86.5	2.2	336	2	D69074
hypothetical prote	959	86.5	2.2	391	2	T34284
alkaline phosphata	960	86.5	2.2	471	2	I79528
complement compone	961	86.5	2.2	585	2	I46865
hypothetical prote	962	86.5	2.2	632	2	T21602
hypothetical prote	963	86.5	2.2	638	2	T22288
flagellar protein	964	86.5	2.2	632	2	AP3463
type III DNA modif	965	86.5	2.2	641	2	F71810
hypothetical prote	966	86.5	2.2	651	2	T05869
protein kinase C (967	86.5	2.2	700	2	A32392
isocitrate dehydro	968	86.5	2.2	734	2	C81399
thrombospondin 2 p	969	86.5	2.2	1172	2	A42587
E2 glycoprotein pr	970	86.5	2.2	1376	1	J01534
ribonucleoside-dip	971	86.5	2.2	1418	2	D75281
ovostatin precursor	972	86.5	2.2	1473	2	A20872
alpha-aminoadipyl-	973	86.5	2.2	3712	1	YGC9VC
conserved hypothet	974	86	2.2	455	2	B85525
major surface-labe	975	86	2.2	713	2	A35502
hypothetical prote	976	86	2.2	738	2	S40992
hypothetical prote	977	86	2.2	905	2	T23229
probable resistanc	978	86	2.2	906	2	A71438

979	86	2.2	933	1	OPHUT	1052	83.5	2.1	311	2	JC7873	l-rhamnose-binding
980	86	2.2	969	1	A39490	1053	83.5	2.1	344	2	A31241	foliistratin 1 prec
981	86	2.2	1487	2	phospholipase-A(2)	1054	83.5	2.1	348	2	T28623	hypothetical prote
982	86	2.2	1572	2	T00027	1055	83.5	2.1	354	2	G64475	GFP-binding protei
983	86	2.2	1550	2	S53457	1056	83.5	2.1	358	1	A55973	transcription fact
984	86	2.2	2233	2	T28669	1057	83.5	2.1	366	2	I55035	trithorax homolog
985	85.5	2.2	317	1	A38493	1058	83.5	2.1	491	2	H83770	hypothetical prote
986	85.5	2.2	340	1	B55973	1059	83.5	2.1	579	2	H84192	pyruvate kinase [i
987	85.5	2.2	344	1	A27701	1060	83.5	2.1	589	2	C38128	epithelin/granulin
988	85.5	2.2	358	2	B64427	1061	83.5	2.1	697	2	H66457	78.1k hypothetica
989	85.5	2.2	463	1	A36479	1062	83.5	2.1	873	2	D88482	protein COSD11.8 [
990	85.5	2.2	515	2	T05863	1063	83.5	2.1	1106	2	T19338	gene Shuicle craft
991	85.5	2.2	638	2	S22491	1064	83.5	2.1	2120	2	T130243	alpha tectorin - c
992	85.5	2.2	663	2	T21010	1065	83.5	2.1	2704	2	S09118	G surface protei
993	85.5	2.2	798	2	S01659	1066	83.5	2.1	4302	2	A38971	polycystic kidney
994	85.5	2.2	1162	2	PC4184	1067	83.5	2.1	13055	2	T16580	hypothetical prote
995	85.5	2.2	1229	2	H84465	1068	83.5	2.1	304	2	A83513	probable transcrip
996	85.5	2.2	2452	1	RN202L	1069	83	2.1	351	2	S20078	NOV protein - chic
997	85.5	2.2	2457	2	T18492	1070	83	2.1	372	2	T39244	probable phospho-2
998	85	2.2	200	2	T42678	1071	83	2.1	451	2	F83747	denosylmethionine-
999	85	2.2	291	2	I38098	1072	83	2.1	492	2	D35114	anthranilate synth
1000	85	2.2	318	2	H86342	1073	83	2.1	593	1	GYHU	granulin precursor
1001	85	2.2	343	2	S53369	1074	83	2.1	770	2	S04847	leukocyte adhesion
1002	85	2.2	359	1	I51734	1075	83	2.1	770	2	D89447	protein F57C12.1 [
1003	85	2.2	413	2	T23098	1076	83	2.1	771	2	A45839	leukocyte adhesio
1004	85	2.2	542	2	A84554	1077	83	2.1	800	2	S54623	probable mitochon
1005	85	2.2	552	2	F83417	1078	83	2.1	816	2	C69493	hypothetical prote
1006	85	2.2	606	2	S43118	1079	83	2.1	1046	2	F71432	hypothetical prote
1007	85	2.2	638	2	S23490	1080	83	2.1	1066	2	B85037	hyaluronidase [imp
1008	85	2.2	653	2	G96675	1081	83	2.1	1111	2	T00324	hypothetical prote
1009	85	2.2	671	1	URPV15	1082	83	2.1	1373	2	JB0095	gastric mucin MUC5
1010	85	2.2	752	2	T26508	1083	83	2.1	2116	1	ZLVNSY	genome polypeptin
1011	85	2.2	794	2	H88508	1084	83	2.1	3020	2	A43932	mucin 2 precursor,
1012	85	2.2	895	2	S74225	1085	82.5	2.1	328	2	F83599	hypothetical prote
1013	85	2.2	1021	2	S26985	1086	82.5	2.1	429	2	A42972	coagulation factor
1014	85	2.2	1078	2	F97907	1087	82.5	2.1	486	2	S29302	alliin lyase (EC 4
1015	85	2.2	1148	1	UQ1604	1088	82.5	2.1	591	1	C8HUB	complement C8 beta
1016	85	2.2	1533	2	T00344	1089	82.5	2.1	751	2	T19338	hypothetical prote
1017	85	2.2	1538	2	S73296	1090	82.5	2.1	763	2	B82223	ribonucleoside-dip
1018	85	2.2	2150	2	T32497	1091	82.5	2.1	781	2	S43534	integrin beta3 - c
1019	84.5	2.1	271	2	S12783	1092	82.5	2.1	984	2	T00326	hypothetical prote
1020	84.5	2.1	337	2	I47079	1093	82.5	2.1	1175	2	I75349	adenosine deaminas
1021	84.5	2.1	344	2	I45894	1094	82.5	2.1	1372	2	A34157	insulin receptor p
1022	84.5	2.1	429	2	T16656	1095	82	2.1	188	2	A39787	teratocarcinoma-de
1023	84.5	2.1	494	2	A59683	1096	82	2.1	235	2	AE0114	deoxyribonuclease
1024	84.5	2.1	494	2	B85533	1097	82	2.1	318	2	S65019	foliistratin - mous
1025	84.5	2.1	505	2	A46570	1098	82	2.1	343	2	S45321	G2R protein - mous
1026	84.5	2.1	615	2	S06546	1099	82	2.1	349	2	D72175	cabon storage regu
1027	84.5	2.1	634	2	T30136	1100	82	2.1	432	2	D83904	4-chlorobenzoate-C
1028	84.5	2.1	666	2	A12849	1101	82	2.1	528	2	B42560	steroid/choyloid/re
1029	84.5	2.1	696	2	G97626	1102	82	2.1	583	2	T34121	formate-tetrahydro
1030	84.5	2.1	744	2	A43353	1103	82	2.1	599	2	B82439	hypothetical prote
1031	84.5	2.1	746	2	F87243	1104	82	2.1	711	2	T27358	D2 protein homolog
1032	84.5	2.1	760	2	A40195	1105	82	2.1	868	2	T02635	neurexin I - alpha
1033	84.5	2.1	788	2	A46547	1106	82	2.1	1530	2	I45944	F44E2.4 protein -
1034	84.5	2.1	789	2	S28259	1107	82	2.1	1609	2	S44821	head-activator bin
1035	84.5	2.1	864	2	T49574	1108	82	2.1	1661	2	T31330	hypothetical prote
1036	84.5	2.1	917	2	I48950	1109	82	2.1	2214	2	T16305	giant protein p619
1037	84.5	2.1	950	2	T28793	1110	82	2.1	4861	2	S71752	hypothetical prote
1038	84	2.1	278	2	T21718	1111	81.5	2.1	209	2	T02394	cysteine-rich prot
1039	84	2.1	335	2	T32657	1112	81.5	2.1	251	2	A55035	polyferredoxin 4x2
1040	84	2.1	349	2	D36858	1113	81.5	2.1	349	2	S57453	protein F56B3.2 [i
1041	84	2.1	413	2	T34123	1114	81.5	2.1	383	2	D88633	klirps protein - f
1042	84	2.1	471	2	A84741	1115	81.5	2.1	429	2	S01919	env polypeptin, r
1043	84	2.1	520	2	G88846	1116	81.5	2.1	432	2	A25483	hypothetical prote
1044	84	2.1	567	2	T49942	1117	81.5	2.1	443	2	T29147	hypothetical prote
1045	84	2.1	972	2	A30363	1118	81.5	2.1	460	2	S67174	lysine decarboxyla
1046	84	2.1	1034	2	JC5358	1119	81.5	2.1	482	2	A83655	probable finger pr
1047	84	2.1	1047	2	T34946	1120	81.5	2.1	496	2	T08674	transketolase (EC
1048	84	2.1	1599	2	T16210	1121	81.5	2.1	519	2	S54300	hemagglutinin - ca
1049	84	2.1	2153	2	T14893	1122	81.5	2.1	604	1	HMN2CD	hematopoietic grow
1050	83.5	2.1	202	1	A44247	1123	81.5	2.1	625	2	S35317	proto-oncogene - m
1051	83.5	2.1	278	2	AH0282	1124	81.5	2.1	626	2	S37622	

1125	81.5	2.1	724	2	A48569	antigen Em100 - E1	1198	80	2.0	644	2	184634	Tamm-Horsfall prot
1126	81.5	2.1	977	2	S49004	tyrosine kinase Mp	1199	80	2.0	656	1	S59631	endo-1,4-beta-xyla
1127	81.5	2.1	1187	2	T18355	hypothetical prote	1200	80	2.0	680	2	PN0510	integrin beta-3 ch
1128	81.5	2.1	1210	2	D88013	protein K10B4.1 (i	1201	80	2.0	713	2	UC6012	glutamine-fructose
1129	81.5	2.1	1507	2	A40228	neurexin I-alpha p	1202	80	2.0	741	2	G84888	probable transket
1130	81	2.1	180	2	AE1010	conserved hypothet	1203	80	2.0	746	2	G84605	hypothetical prote
1131	81	2.1	296	2	C81906	hypothetical prote	1204	80	2.0	753	2	JC7386	retinovin - chicke
1132	81	2.1	348	2	A56247	natural killer cel	1205	80	2.0	817	2	T24063	hypothetical prote
1133	81	2.1	428	2	T04472	probable porphobil	1206	80	2.0	902	2	T01127	curly leaf protein
1134	81	2.1	491	2	I40455	pentacillin binding	1207	80	2.0	1136	2	T36406	hypothetical prote
1135	81	2.1	501	2	UC7181	maternal transcrip	1208	80	2.0	1184	2	A96638	hypothetical prote
1136	81	2.1	554	2	A31300	perforin precursor	1209	80	2.0	1342	2	A36223	kinase-related tra
1137	81	2.1	560	2	S25092	jaemonate-induced	1210	80	2.0	1385	2	H88569	protein K03H1.5 (i
1138	81	2.1	732	2	T52588	wall-associated se	1211	80	2.0	1409	2	I41028	hypothetical prote
1139	81	2.1	735	2	G02937	fertilin beta - cr	1212	80	2.0	2219	2	T27684	hypothetical prote
1140	81	2.1	735	2	I48101	ADAM 6 protein pre	1213	80	2.0	2229	2	T16199	hypothetical prote
1141	81	2.1	769	1	UC1121	leukocyte adhesion	1214	80	2.0	2643	2	T29149	hypothetical prote
1142	81	2.1	787	1	T49614	related to tol pro	1215	80	2.0	3140	2	S47508	genome polypeptin
1143	81	2.1	799	2	JC4126	integrin beta olig	1216	80	2.0	71	2	A59412	KCP-bearing placel
1144	81	2.1	821	1	A39667	brain-derived neur	1217	79.5	2.0	217	2	D90033	conserved hypothet
1145	81	2.1	1166	1	S06142	protein-tyrosine k	1218	79.5	2.0	254	2	I48599	hypothetical prote
1146	81	2.1	1344	2	H84557	hypothetical prote	1219	79.5	2.0	254	2	UC1464	hypothetical prote
1147	81	2.1	1365	2	T00833	RNA-directed DNA p	1220	79.5	2.0	317	2	D64167	insulin-like growt
1148	81	2.1	1438	2	A48216	neurexin III - alpha	1221	79.5	2.0	318	2	S43317	transaldolase (EC
1149	81	2.1	1471	2	B48218	neurexin III - alpha	1222	79.5	2.0	324	2	S20981	chitinase (EC 3.2.
1150	81	2.1	1578	2	I48216	neurexin III - alpha	1223	79.5	2.0	356	2	A25918	chitinase (EC 3.2.
1151	81	2.1	1895	2	T06609	disease resistance	1224	79.5	2.0	391	2	S49300	chromomodulin - b
1152	81	2.1	3898	2	S57437	genome polypeptin	1225	79.5	2.0	457	2	C66464	hypothetical prote
1153	80.5	2.0	371	2	B72461	hypothetical prote	1226	79.5	2.0	474	2	A57480	hypothetical prote
1154	80.5	2.0	390	2	T27256	hypothetical prote	1227	79.5	2.0	614	2	T40652	hypothetical prote
1155	80.5	2.0	409	2	B87661	conserved hypothet	1228	79.5	2.0	661	2	C85758	hypothetical prote
1156	80.5	2.0	416	2	A37877	hemorrhagic protei	1229	79.5	2.0	661	2	B90861	hypothetical prote
1157	80.5	2.0	431	2	S49821	PR2 protein - Ara	1230	79.5	2.0	694	2	S58083	transketolase (EC
1158	80.5	2.0	454	2	T26654	hypothetical prote	1231	79.5	2.0	700	2	HRH0MB	weprin A (EC 3.4.2
1159	80.5	2.0	471	1	PAECA	alkaline phosphata	1232	79.5	2.0	713	2	I65253	diintegrin-like t
1160	80.5	2.0	479	2	D86182	protein F13M7.11 (1233	79.5	2.0	741	2	T09015	transketolase (EC
1161	80.5	2.0	502	2	T16716	hypothetical prote	1234	79.5	2.0	868	2	G84674	probable selenium-
1162	80.5	2.0	509	2	T22238	hypothetical prote	1235	79.5	2.0	952	2	T28792	disicylglycerol kin
1163	80.5	2.0	516	2	S53007	citrate synthase -	1236	79.5	2.0	1161	1	S31213	nirogen precursor
1164	80.5	2.0	555	2	T21028	hypothetical prote	1237	79.5	2.0	1178	2	S08405	hypothetical prote
1165	80.5	2.0	570	2	T46261	hypothetical prote	1238	79.5	2.0	1239	2	A86323	protein F14D16.3 (
1166	80.5	2.0	604	2	T15796	hypothetical prote	1239	79.5	2.0	1390	2	S51364	sperm tail-specific
1167	80.5	2.0	627	2	T00603	hypothetical prote	1240	79.5	2.0	1402	2	T24664	hypothetical prote
1168	80.5	2.0	656	2	B49423	semaphorin I - fru	1241	79.5	2.0	2261	2	T07084	acetyl-CoA carboxy
1169	80.5	2.0	658	2	A86828	transketolase (EC	1242	79.5	2.0	2499	1	A30788	mannose 6-phosphat
1170	80.5	2.0	673	2	A49878	coagulation factor	1243	79	2.0	171	2	S57894	lanthan - Hydra vu
1171	80.5	2.0	704	2	A48040	meprin A (EC 3.4.2	1244	79	2.0	188	2	A30362	teratocarcinoma-de
1172	80.5	2.0	741	2	B81143	isocitrate dehydro	1245	79	2.0	192	1	B57143	thiosulfate-dithio
1173	80.5	2.0	742	2	I37225	leucocyte antigen	1246	79	2.0	192	2	AC0763	thiosulfate reduct
1174	80.5	2.0	773	2	I46059	beta-1 integrin su	1247	79	2.0	206	2	D97285	ribosomal protein
1175	80.5	2.0	1055	2	T05663	hypothetical prote	1248	79	2.0	360	2	S32695	Wnt-2 protein - Ca
1176	80.5	2.0	1119	2	A88481	protein C16A3.6 (i	1249	79	2.0	364	2	T24153	hypothetical prote
1177	80.5	2.0	1245	1	VHNV82	structural polypep	1250	79	2.0	392	2	T33444	hypothetical prote
1178	80.5	2.0	1376	1	VGHIJ2	E2 glycoprotein pr	1251	79	2.0	403	2	A64036	hypothetical prote
1179	80.5	2.0	1382	1	INHUR	insulin receptor p	1252	79	2.0	415	2	D87020	probable membrane
1180	80.5	2.0	1526	2	T19473	hypothetical prote	1253	79	2.0	417	2	T08724	hypothetical prote
1181	80.5	2.0	1558	2	C89114	protein C37C3.6a (1254	79	2.0	587	2	C85044	hypothetical prote
1182	80.5	2.0	1611	2	G84493	probable retroelem	1255	79	2.0	602	2	B81420	GTP-binding protei
1183	80.5	2.0	2167	2	T34395	hypothetical prote	1256	79	2.0	606	2	T22105	hypothetical prote
1184	80.5	2.0	2262	2	T30890	calcium channel al	1257	79	2.0	630	2	T48369	hypothetical prote
1185	80.5	2.0	2262	2	T30890	beta-crystallin B3	1258	79	2.0	660	2	S71949	metalloproteinase
1186	80	2.0	243	2	T27036	hypothetical prote	1259	79	2.0	687	2	T16352	hypothetical prote
1187	80	2.0	284	2	T25938	hypothetical prote	1260	79	2.0	729	2	A45716	Leukemia virus cel
1188	80	2.0	290	2	T46470	hypothetical prote	1261	79	2.0	738	2	T41730	hypothetical prote
1189	80	2.0	335	2	A39743	u-plaemogen acti	1262	79	2.0	753	2	B36268	platelet glycoprot
1190	80	2.0	395	2	S64299	probable membrane	1263	79	2.0	773	2	JB0387	exo-alpha-stilidas
1191	80	2.0	398	1	S24802	polyferredoxin 6x2	1264	79	2.0	788	2	A60798	platelet glycoprot
1192	80	2.0	437	2	S05478	propenidin - mouse	1265	79	2.0	790	2	I77349	phenylalanine-tRNA
1193	80	2.0	464	2	H82928	ATP synthase beta	1266	79	2.0	790	2	D81668	monocyte surfact a
1194	80	2.0	500	2	A36388	RNA-directed RNA p	1267	79	2.0	826	2	A60385	hypothetical prote
1195	80	2.0	589	2	I38598	zinc finger protei	1268	79	2.0	871	2	T04867	disintegrin and me
1196	80	2.0	642	2	C89124	protein K07C11.9 (1269	79	2.0	952	2	T18900	
1197	80	2.0	644	1	A40212	uromodulin precurs	1270	79	2.0	1023	2	T30257	

1271	79	2.0	1289	1	RMXRR3	mRNA guanylyltrans	1344	78	2.0	4085	2	S28600	hypothetical prote
1272	79	2.0	1391	2	T20406	hypothetical prote	1345	77.5	2.0	46	2	JT0747	epiregulin - rat
1273	79	2.0	1531	2	A54895	mucin 2, intestine	1346	77.5	2.0	162	2	S68401	epiregulin precurs
1274	79	2.0	1522	2	T00028	brain-specific ang	1347	77.5	2.0	244	2	AB2505	histidine kinase-1
1275	79	2.0	1642	2	T19130	hypothetical prote	1348	77.5	2.0	255	2	H6776	hypothetical prote
1276	79	2.0	1777	2	T00490	nonstructural prote	1349	77.5	2.0	295	2	UC5559	lectin-B - Virginl
1277	79	2.0	1777	2	AC2088	serine/threonine k	1350	77.5	2.0	296	2	G81111	conserved hypotet
1278	78.5	2.0	1166	2	S65875	spermathecin psp-1	1351	77.5	2.0	400	2	A56111	phyllodop - fruit
1279	78.5	2.0	307	1	S18523	fructokinase (EC 2	1352	77.5	2.0	402	2	S02099	phosphoribulokinase
1280	78.5	2.0	327	2	A55356	urokinase-type pla	1353	77.5	2.0	407	2	C82428	glucose-1-phosphat
1281	78.5	2.0	341	2	T161725	natural killer fas	1354	77.5	2.0	413	4	FOH022	retrovirus-related
1282	78.5	2.0	344	2	I57698	folliclestatin - rat	1355	77.5	2.0	457	2	B85749	ATP-dependent RNA
1283	78.5	2.0	355	2	C70457	hypothetical prote	1356	77.5	2.0	457	2	G90869	ATP-dependent RNA
1284	78.5	2.0	363	1	C55973	transcription fact	1357	77.5	2.0	457	2	B64884	ATP-dependent RNA
1285	78.5	2.0	376	2	E70361	chaperone DnaJ - A	1358	77.5	2.0	469	2	T36362	probable DNA repai
1286	78.5	2.0	389	2	D75180	hypothetical prote	1359	77.5	2.0	488	2	T21701	hypothetical prote
1287	78.5	2.0	401	2	S65138	glycoprotein anti-g	1360	77.5	2.0	546	2	B75375	probable amidease -
1288	78.5	2.0	436	2	S06884	viid2 protein - Ag	1361	77.5	2.0	548	2	S38864	Ig epsilon chain C
1289	78.5	2.0	474	2	B38634	tumor necrosis fac	1362	77.5	2.0	569	2	B85076	probable transposo
1290	78.5	2.0	495	2	A57053	germ cell nuclear	1363	77.5	2.0	645	2	S20138	probable protein k
1291	78.5	2.0	507	2	T06452	probable legumin A	1364	77.5	2.0	717	2	B32838	DNA-directed RNA p
1292	78.5	2.0	517	1	FMEPMLA	legumin A precuro	1365	77.5	2.0	721	2	A39707	erythrocyte membra
1293	78.5	2.0	552	2	C45710	R transactivator h	1366	77.5	2.0	729	2	A69202	conserved hypotet
1294	78.5	2.0	600	2	I49281	feritin alpha pre	1367	77.5	2.0	767	2	B85079	hypothetical prote
1295	78.5	2.0	638	2	D86477	protein F1504.27 f	1368	77.5	2.0	809	2	A57283	integrin beta chai
1296	78.5	2.0	658	2	F85024	probable GTP-rich	1369	77.5	2.0	845	2	G82773	phage-related prot
1297	78.5	2.0	662	2	I37892	IL12 receptor comp	1370	77.5	2.0	848	2	AF0020	nitrile reductase
1298	78.5	2.0	717	2	T25431	hypothetical prote	1371	77.5	2.0	913	2	A31930	cytoactin - chick
1299	78.5	2.0	748	2	T00732	hypothetical prote	1372	77.5	2.0	1017	2	D75028	h+-transporting AT
1300	78.5	2.0	757	2	T05688	hypothetical prote	1373	77.5	2.0	1079	1	TFVW1	gag-Rn11-env poly
1301	78.5	2.0	763	2	T49089	hypothetical prote	1374	77.5	2.0	1142	2	A45031	cysteine-rich fibr
1302	78.5	2.0	842	2	T04555	hypothetical prote	1375	77.5	2.0	1323	2	B88257	protein let-23 (lm
1303	78.5	2.0	1119	2	T16720	hypothetical prote	1376	77.5	2.0	1374	2	S70712	protein-tyrosine k
1304	78.5	2.0	1121	2	S57058	probable membrane	1377	77.5	2.0	2895	2	T08437	hyperplastic discs
1305	78.5	2.0	1131	2	T30951	hypothetical prote	1378	77.5	2.0	3085	2	T00327	polyprotein - infe
1306	78.5	2.0	1137	2	T18625	actrial natriuretic	1379	77	2.0	194	2	S70663	lectin heavy chain
1307	78.5	2.0	1188	2	JC4889	phosphatidylinosit	1380	77	2.0	230	2	T31722	hypothetical prote
1308	78.5	2.0	3473	1	A46112	genome polyprotein	1381	77	2.0	230	2	A44074	probable EGF-like
1309	78.5	2.0	3473	2	S27927	polyprotein - rice	1382	77	2.0	279	2	T46201	hypothetical prote
1310	78.5	2.0	3864	2	D87757	protein C4E4.1a f	1383	77	2.0	317	2	T45984	hypothetical prote
1311	78	2.0	247	2	T27775	hypothetical prote	1384	77	2.0	375	2	F70691	hypothetical prote
1312	78	2.0	334	2	T03157	probable capid as	1385	77	2.0	452	2	H84772	probable serine ca
1313	78	2.0	360	2	T26037	hypothetical prote	1386	77	2.0	476	2	T19786	hypothetical prote
1314	78	2.0	360	2	G82994	glycine-cleavage s	1387	77	2.0	500	2	A52032	glycerol kinase [i
1315	78	2.0	372	2	T31060	hypothetical prote	1388	77	2.0	502	2	T41148	trp-asp repeat con
1316	78	2.0	385	2	A81926	hypothetical prote	1389	77	2.0	535	2	T19706	hypothetical prote
1317	78	2.0	401	2	C89102	protein P25E5.10 f	1390	77	2.0	540	1	OYHUCR	natriuretic peptid
1318	78	2.0	404	2	T40553	trp-asp repeat pro	1391	77	2.0	591	2	S33542	catechol oxidase f
1319	78	2.0	415	2	B83377	probable alcohol d	1392	77	2.0	713	2	T40729	WD repeat-containi
1320	78	2.0	441	2	AH2930	oxidoreductase Atu	1393	77	2.0	729	2	A49120	fibroblast growth
1321	78	2.0	446	2	P98351	probable oxidoredu	1394	77	2.0	768	2	A87722	protein ZC123.1 [i
1322	78	2.0	454	1	GOMST1	tumor necrosis fac	1395	77	2.0	821	1	S06943	brain-derived neur
1323	78	2.0	468	2	B40228	neurexin I-beta pr	1396	77	2.0	1019	2	IC7538	neuronal different
1324	78	2.0	468	2	S26741	T-cell glycoprotei	1397	77	2.0	1302	2	T00038	hypothetical prote
1325	78	2.0	482	2	T17250	transmembrane glyc	1398	77	2.0	1498	2	B97355	DNA segregation AT
1326	78	2.0	522	2	A46103	hypothetical prote	1399	77	2.0	1552	2	G86344	T2211.2 protein-l
1327	78	2.0	523	2	C95303	conserved hypotet	1400	77	2.0	1723	2	S58880	receptor DEC-205 -
1328	78	2.0	527	2	T04329	importin alpha - t	1401	77	2.0	1743	2	T26859	hypothetical prote
1329	78	2.0	599	2	JH0258	prostaglandin-endo	1402	77	2.0	2165	2	T21371	hypothetical prote
1330	78	2.0	723	2	FW0509	integrin beta-3 ch	1403	77	2.0	2584	2	T24158	hypothetical prote
1331	78	2.0	725	2	T27148	hypothetical prote	1404	77	2.0	2606	2	T24157	thryoglobulin prec
1332	78	2.0	843	2	A27131	epidermal growth f	1405	77	2.0	2769	1	UIBO	hypothetical prote
1333	78	2.0	957	2	T15976	hypothetical prote	1406	77	2.0	3033	1	GNMWJ8	genome polyprotein
1334	78	2.0	989	2	T47503	hypothetical prote	1407	77	2.0	3660	2	S02041	dystrophin, muscle
1335	78	2.0	1016	2	G86295	hypothetical prote	1408	77	2.0	4957	2	T03455	AKR protein - huma
1336	78	2.0	1131	2	T38744	hypothetical prote	1409	77	2.0	5262	2	T03454	AKR protein - huma
1337	78	2.0	1245	1	YHMB	structural polypro	1410	76.5	1.9	71	2	A59413	platelet-aggregati
1338	78	2.0	1260	1	TVRTNV	protein-tyrosine k	1411	76.5	1.9	146	2	G95995	platelet-aggregati
1339	78	2.0	1330	1	GOFFS	epidermal growth f	1412	76.5	1.9	216	2	JX0265	platelet aggregati
1340	78	2.0	1339	2	JC4387	epidermal growth f	1413	76.5	1.9	224	2	AD2115	phosphoribosylform
1341	78	2.0	1369	2	S70713	protein-tyrosine k	1414	76.5	1.9	254	2	I48603	insulin-like growt
1342	78	2.0	1658	2	D75489	hypothetical prote	1415	76.5	1.9	264	2	T22380	hypothetical prote
1343	78	2.0	3224	1	S58884	Ran-binding protei	1416	76.5	1.9	272	2	AG2669	enoyl-(acyl-carrie

1417 76.5 1.9 272 2 E97451 hypothetical prote
1418 76.5 1.9 279 2 J06565 four-and-a-half li
1419 76.5 1.9 302 2 E86267 hypothetical prote
1420 76.5 1.9 322 1 S37344 chitinase (EC 3.2.
1421 76.5 1.9 323 2 T24836 hypothetical prote
1422 76.5 1.9 327 2 AC0156 probable cobalam
1423 76.5 1.9 359 2 T36050 probable histidin
1424 76.5 1.9 359 2 E83622 hypothetical prote
1425 76.5 1.9 385 2 AH0793 probable lipopoly
1426 76.5 1.9 385 2 T12527 hypothetical prote
1427 76.5 1.9 388 1 EHMS Ig epsilon chain C
1428 76.5 1.9 420 2 S74388 gamma-glutamyl pho
1429 76.5 1.9 435 2 T25350 hypothetical prote
1430 76.5 1.9 481 2 A56346 transcription fact
1431 76.5 1.9 483 2 T48328 importin alpha-lik
1432 76.5 1.9 487 2 T23384 hypothetical prote
1433 76.5 1.9 504 2 T33404 hypothetical prote
1434 76.5 1.9 518 2 G88961 protein F59A7.8 [l
1435 76.5 1.9 520 2 C70311 hypothetical prote
1436 76.5 1.9 536 1 A39036 H+-transporting tw
1437 76.5 1.9 545 1 PM8YA H+-transporting tw
1438 76.5 1.9 601 2 T34396 hypothetical prote
1439 76.5 1.9 623 2 S56206 probable membrane
1440 76.5 1.9 658 2 T47960 hypothetical prote
1441 76.5 1.9 707 2 S68858 finger protein - m
1442 76.5 1.9 712 2 T16338 hypothetical prote
1443 76.5 1.9 722 2 S32659 integrin beta 2 ch
1444 76.5 1.9 837 2 A42112 mucin-like peptide
1445 76.5 1.9 849 2 I50617 protein-tyrosine k
1446 76.5 1.9 1000 2 S47243 starch phosphoryla
1447 76.5 1.9 1004 2 T31665 hypothetical prote
1448 76.5 1.9 1056 2 T33167 hypothetical prote
1449 76.5 1.9 1071 2 T18307 suppressor protein
1450 76.5 1.9 1153 2 T00615 DNA polymerase III
1451 76.5 1.9 1201 2 AD1107 RNA polymerase (be
1452 76.5 1.9 1361 2 T01699 aldehyde oxidase (l
1453 76.5 1.9 1561 2 S46200 acetyl-CoA carboxy
1454 76.5 1.9 1660 2 T18561 vitellinogen vit-6
1455 76.5 1.9 1738 2 C84507 hypothetical prote
1456 76.5 1.9 1985 2 T61776 Munc13-2 - rat
1457 76.5 1.9 2098 2 T18397 protein CRP - mal
1458 76.5 1.9 2155 2 T30197 alpha tectorin - m
1459 76.5 1.9 2395 1 S50820 surface protein ty
1460 76.5 1.9 2562 2 T14266 Xin protein - chic
1461 76.5 1.9 3828 2 T13857 trihorax protein
1462 76.5 1.9 4550 2 T18440 hypothetical prote
1463 76.5 1.9 4836 2 T14346 hec2 protein - mo
1464 76.5 1.9 96 2 A05308 sperm motility inh
1465 76.5 1.9 136 2 S72508 tissue kallikrein
1466 76.5 1.9 171 2 T49612 teratocarcinoma-de
1467 76.5 1.9 233 2 T23396 RNA methylase, YS
1468 76.5 1.9 261 2 G97190 paired box transcr
1469 76.5 1.9 269 2 S36166 conserved hypochet
1470 76.5 1.9 287 2 A11072 hypothetical prote
1471 76.5 1.9 333 2 T15257 transcription fact
1472 76.5 1.9 349 1 I51739 membrane-associate
1473 76.5 1.9 374 2 A42264 hypothetical prote
1474 76.5 1.9 415 2 T32467 hypothetical prote
1475 76.5 1.9 418 2 T23450 oxidoreductase - D
1476 76.5 1.9 454 2 D75446 probable ADA-like
1477 76.5 1.9 490 2 T35948 purh bifunctional
1478 76.5 1.9 512 1 D785PH hypothetical prote
1479 76.5 1.9 531 2 T22021 2-aminobenzoyl pro
1480 76.5 1.9 603 2 S22402 metallopeptidase
1481 76.5 1.9 605 2 S71630 WD-repeat protein
1482 76.5 1.9 612 2 T39666 probable RNA-dirce
1483 76.5 1.9 616 1 RRVOMA hypothetical prote
1484 76.5 1.9 626 2 T09345 probable DEAD box
1485 76.5 1.9 634 2 AG0252 transkeolase (imp
1486 76.5 1.9 670 2 A12223 furin (EC 3.4.21.7
1487 76.5 1.9 837 2 S43656 Erbb kinase activa
1488 76.5 1.9 860 2 J05702 hypothetical prote
1489 76.5 1.9 897 2 S67283

1490 76 1.9 908 2 T27117 hypothetical prote
1491 76 1.9 925 2 T37475 lipoprotein recept
1492 76 1.9 926 1 OPPGIT iodide peroxidase
1493 76 1.9 934 1 A34372 complement C6 prec
1494 76 1.9 967 2 T48210 hypothetical prote
1495 76 1.9 1001 2 AG1979 hypothetical prote
1496 76 1.9 1084 2 T18292 nicotinamide nucle
1497 76 1.9 1097 2 S17308 leukemia inhibitor
1498 76 1.9 1206 2 T18557 probable hydrogna
1499 76 1.9 1245 1 VHWVB2 structural polypro
1500 76 1.9 1385 2 S34230 156k protein - Pla

ALIGNMENTS

RESULT 1
T08805
hypothetical protein DKFZP586H2123.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T08805
R:Ansoerge, W.; Winkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A:Reference number: Z16472
A:Accession: T08805
A:Molecule type: mRNA
A:Residues: 1-181 <MS>
A:Cross-References: UNIPROT:Q9Y432; UNIPARC:UPI0000070151; EMBL:AL050214
A:Experimental source: adult uterus; clone DKFZP586H2123
C:Genetics:
A>Note: DKFZP586H2123.1

Query Match 24.1%; Score 949; DB 2; Length 181;
Best Local Similarity 99.4%; Pred. No. 6, 8e-57;
Matches 180; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 540 SIQISAIHPHYDPIILDADIAIKLIDKARISTRVOPICLAASRDLSFQESHITVA 599
1 SRIISNIHPHYDPIILDADIAIKLIDKARISTRVOPICLAASRDLSFQESHITVA 60
DB 600 GNNVLADVRSPPGKNDTLRSVGVSVYDLSLCEQHEHDGIPVSYTDNMCASMEPTAPSD 659
61 GNNVLADVRSPPGKNDTLRSVGVSVYDLSLCEQHEHDGIPVSYTDNMCASMEPTAPSD 120
QY 660 ICTAETGCIANVSPPGRASPPPRMILMGIVNSYDKTCSHRISTATKTLPRKDWIERNM 719
121 ICTAETGCIANVSPPGRASPPPRMILMGIVNSYDKTCSHRISTATKTLPRKDWIERNM 180
DB
QY 720 K 720
181 K 181
DB

RESULT 2

A38738
coagulation factor C precursor - horseshoe crab (Tachyples tridentatus)
N:Alternate names: coagulation factor C; Limulus factor C
N:Contains: coagulation factor C heavy chain; coagulation factor C light chain peptide A;
C:Species: Tachyples tridentatus
C:Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 09-Jul-2004
R:Muta, T.; Miyata, T.; Misumi, Y.; Tokunaga, F.; Nakamura, T.; Toh, Y.; Ikehara, Y.; Iw
J. Biol. Chem. 266, 6554-6561, 1991
A:Title: Limulus factor C. An endotoxin-sensitive serine protease zymogen with a mosaic
A:Reference number: A38738; MUID:91177916; PMID:2007602
A:Accession: A38738
A:Molecule type: mRNA
A:Residues: 1-1019 <MT>
A:Cross-References: UNIPROT:P28175; UNIPARC:UPI000012B5D2; GB:D90271; NID:9217396; PID:d
A:Accession: B38738
A:Molecule type: mRNA
A:Residues: 1-466, 516, 'DN', 619-620, 'A', 622 <MU2>

125 C-MRCSQVLRAPKQIIL-----ESYPLNACSEMTIHAKEPGVQLRFRVMLSEEDYM-- 176
 A:Residues: 18-166, 'X', 168-463 <ARL>
 A:Cross-references: UNIPARC:UPI0000172BC5
 A>Note: 152-Leu was also found
 R:Arlaud, G.J.; van Dorsselaer, A.; Bell, A.; Mancini, M.; Aude, C.; Gagnon, J.
 FBS Lett. 222, 129-134, 1987
 A:Title: Identification of erythro-beta-hydroxyasparagine in the EGF-like domain of human
 A:Reference number: S02422; MUID:88005128; PMID:2820791
 A:Accession: S02422
 Db 233 YEITACSSSPCFHDTGCVLDKAGSYKACACLAGYGCRCENILERRNCSDPGCPVNGYOK 292
 A:Molecule type: protein
 A:Residues: 152-186 <AR3>
 A:Cross-references: UNIPARC:UPI0000172BC6
 A>Note: 152-Leu was also found
 R:Arlaud, G.J.; Gagnon, J.
 Biochemistry 22, 1758-1764, 1983
 A:Title: Complete amino acid sequence of the catalytic chain of human complement subcomp
 A:Reference number: A00916; MUID:83204782; PMID:6303394
 A:Accession: A00916
 Db 293 ITGGPGLNGHAKIGTVSF-----CNNSY-VLSNGER-----TQONGMSGKQ 339
 A:Molecule type: protein
 A:Residues: 464-705 <AR2>
 A:Cross-references: UNIPARC:UPI000015033B
 R:Thielens, N.M.; Aude, C.A.; Lacroix, M.B.; Gagnon, J.; Arlaud, G.J.
 J. Biol. Chem. 265, 14463-14475, 1990
 A:Title: Ca(2+) binding properties and Ca(2+)-dependent interactions of the isolated NH-;
 A:Reference number: A37820; MUID:90354439; PMID:2387866
 A:Accession: A37820
 Db 340 PIC-1KACREPKISDLVRRVLPMQVSRERPLHQLYSAPSKQLQSAPTKKPALPRGD 398
 A:Molecule type: protein
 A:Residues: 18-26, 'L', 153-160, 'XX', 252-255 <THI>
 A:Cross-references: UNIPARC:UPI0000172BC8; UNIPARC:UPI0000172BC9
 A:Cross-references: UNIPARC:UPI0000172BC7; UNIPARC:UPI0000172BC8; UNIPARC:UPI0000172BC9
 R:Belloc, S.; Thielens, N.M.; Hudry-Clergeon, G.; Peticol, Y.; Filhol, O.; Arlaud, G.J.
 FBS Lett. 386, 15-20, 1996
 A:Title: Identification of a cryptic protein kinase CK2 phosphorylation site in human com
 A:Reference number: S68830; MUID:965221263; PMID:8635594
 A:Accession: S68830
 Db 433 LPVCLPFRSKRLMARIRN-GRPAOKGTT-PIAIHL-----SHANGPF--CGGS 478
 A:Molecule type: protein
 A:Residues: 133-137, 187-211, 610-613 <PEL>
 A:Cross-references: UNIPARC:UPI0000172BCA; UNIPARC:UPI0000172BCB; UNIPARC:UPI0000172BCC
 A:Experimental source: plasma
 A:Comment: C1r is a dimer of identical chains, each of which is activated by cleavage int
 A chain, while fragment gamma remains disulfide-bonded to the B chain to form C1r II.
 C:Comment: This protein is a serine protease that combines with C1q and C1s to form C1, t
 n, activate C2 and C4.
 C:Genetics:
 A:Gene: GDB:C1R
 A:Cross-references: GDB:119729; OMIM:216950
 A:Map position: 12p13-12p13
 C:Superfamily: complement-activating serine proteases C1r/C1s/MASP; C1r/C1s repeat homol
 C:Keywords: acute phase; beta-hydroxyasparagine; calcium binding; complement pathway; dui
 F:1-17/Domain: signal sequence #status predicted <SIG>
 F:17-138/Domain: C1r/C1s repeat homology <C1R1>
 F:18-463/Product: complement C1r chain A #status experimental <ACH>
 F:146-189/Domain: EGF homology <EGF>
 F:193-302/Domain: C1r/C1s repeat homology <C1R2>
 F:297-463/Product: C1r gamma fragment #status experimental <GFR>
 F:309-371/Domain: complement factor H repeat homology <FH1>
 F:376-447/Domain: complement factor H repeat homology <FH2>
 F:464-705/Product: complement C1r chain B #status experimental <BGH>
 F:464-697/Domain: trypsin homology <TRY>
 F:71-89, 146-165, 161-174, 176-189, 193-220, 250-268, 309-358, 338-371, 376-429, 406-447, 451-577, 4
 F:125, 221, 514, 581/Binding site: carboxylate (Asn) (covalent) #status experimental
 F:167/Modified site: erythro-beta-hydroxyasparagine (Asn) #status experimental
 F:206/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status experimental
 F:463-466/Cleavage site: Arg-Ile (autolytic) #status experimental
 F:502, 557, 654/Active site: His, Asp, Ser #status predicted
 A:Accession: A29769
 A:Reference number: A29769; MUID:8715625; PMID:3030286
 A:Accession: A29768
 A:Reference number: A29768; MUID:8715625; PMID:3030286
 A:Title: Cloning and sequencing of full-length cDNA encoding the precursor of human comp
 A:Accession: A29769
 A:Reference number: A29769; MUID:87241248; PMID:3036070
 A:Accession: A29769
 A:Molecule type: protein

RESULT 4
 C1HURB
 Complement subcomponent C1r (EC 3.4.21.41) precursor [validated] - human
 C:Species: Homo sapiens (man)
 C:Date: 15-Nov-1984 #sequence revision 30-Jun-1991 #text change 09-Jul-2004
 C:Accession: A24170; A29768; A29769; S02422; A00916; A37820; S68830
 R:Levy, S.P.; Kurachi, K.; Sakuraba, K.S.; Davie, E.W.
 Biochemistry 25, 4855-4863, 1986
 A:Title: Nucleotide sequence of the cDNA coding for human complement C1r.
 A:Reference number: A24170; MUID:87026566; PMID:3021205
 A:Accession: A24170
 A:Molecule type: mRNA
 A:Residues: 1-705 <LEX>
 A:Cross-references: UNIPROT:P00736; UNIPARC:UPI00000422ED; GB:M14058; NID:g179643; PIDN:
 R:Journet, A.; Tosi, M.
 Biochem. J. 240, 783-787, 1986
 A:Title: Cloning and sequencing of full-length cDNA encoding the precursor of human comp
 A:Accession: A29768
 A:Reference number: A29768; MUID:8715625; PMID:3030286
 A:Accession: A29768
 A:Molecule type: mRNA
 A:Residues: 1-151, 'L', 153-705 <JOU>
 A:Cross-references: UNIPARC:UPI0000001C2B; GB:X04701; NID:295538; PIDN:CAA28407.1; PID:9
 R:Arlaud, G.J.; Willis, A.C.; Gagnon, J.
 Biochem. J. 241, 711-720, 1987
 A:Title: Complete amino acid sequence of the A chain of human complement-classical-pathw
 A:Reference number: A29769; MUID:87241248; PMID:3036070
 A:Accession: A29769
 A:Molecule type: protein

A:Residues: 18-166, 'X', 168-463 <ARL>
 A:Cross-references: UNIPARC:UPI0000172BC5
 A>Note: 152-Leu was also found
 R:Arlaud, G.J.; van Dorsselaer, A.; Bell, A.; Mancini, M.; Aude, C.; Gagnon, J.
 FBS Lett. 222, 129-134, 1987
 A:Title: Identification of erythro-beta-hydroxyasparagine in the EGF-like domain of human
 A:Reference number: S02422; MUID:88005128; PMID:2820791
 A:Accession: S02422
 A:Molecule type: protein
 A:Residues: 152-186 <AR3>
 A:Cross-references: UNIPARC:UPI0000172BC6
 A>Note: 152-Leu was also found
 R:Arlaud, G.J.; Gagnon, J.
 Biochemistry 22, 1758-1764, 1983
 A:Title: Complete amino acid sequence of the catalytic chain of human complement subcomp
 A:Reference number: A00916; MUID:83204782; PMID:6303394
 A:Accession: A00916
 A:Molecule type: protein
 A:Residues: 464-705 <AR2>
 A:Cross-references: UNIPARC:UPI000015033B
 R:Thielens, N.M.; Aude, C.A.; Lacroix, M.B.; Gagnon, J.; Arlaud, G.J.
 J. Biol. Chem. 265, 14463-14475, 1990
 A:Title: Ca(2+) binding properties and Ca(2+)-dependent interactions of the isolated NH-;
 A:Reference number: A37820; MUID:90354439; PMID:2387866
 A:Accession: A37820
 A:Molecule type: protein
 A:Residues: 18-26, 'L', 153-160, 'XX', 252-255 <THI>
 A:Cross-references: UNIPARC:UPI0000172BC8; UNIPARC:UPI0000172BC9
 A:Cross-references: UNIPARC:UPI0000172BC7; UNIPARC:UPI0000172BC8; UNIPARC:UPI0000172BC9
 R:Belloc, S.; Thielens, N.M.; Hudry-Clergeon, G.; Peticol, Y.; Filhol, O.; Arlaud, G.J.
 FBS Lett. 386, 15-20, 1996
 A:Title: Identification of a cryptic protein kinase CK2 phosphorylation site in human com
 A:Reference number: S68830; MUID:965221263; PMID:8635594
 A:Accession: S68830
 A:Molecule type: protein
 A:Residues: 133-137, 187-211, 610-613 <PEL>
 A:Cross-references: UNIPARC:UPI0000172BCA; UNIPARC:UPI0000172BCB; UNIPARC:UPI0000172BCC
 A:Experimental source: plasma
 A:Comment: C1r is a dimer of identical chains, each of which is activated by cleavage int
 A chain, while fragment gamma remains disulfide-bonded to the B chain to form C1r II.
 C:Comment: This protein is a serine protease that combines with C1q and C1s to form C1, t
 n, activate C2 and C4.
 C:Genetics:
 A:Gene: GDB:C1R
 A:Cross-references: GDB:119729; OMIM:216950
 A:Map position: 12p13-12p13
 C:Superfamily: complement-activating serine proteases C1r/C1s/MASP; C1r/C1s repeat homol
 C:Keywords: acute phase; beta-hydroxyasparagine; calcium binding; complement pathway; dui
 F:1-17/Domain: signal sequence #status predicted <SIG>
 F:17-138/Domain: C1r/C1s repeat homology <C1R1>
 F:18-463/Product: complement C1r chain A #status experimental <ACH>
 F:146-189/Domain: EGF homology <EGF>
 F:193-302/Domain: C1r/C1s repeat homology <C1R2>
 F:297-463/Product: C1r gamma fragment #status experimental <GFR>
 F:309-371/Domain: complement factor H repeat homology <FH1>
 F:376-447/Domain: complement factor H repeat homology <FH2>
 F:464-705/Product: complement C1r chain B #status experimental <BGH>
 F:464-697/Domain: trypsin homology <TRY>
 F:71-89, 146-165, 161-174, 176-189, 193-220, 250-268, 309-358, 338-371, 376-429, 406-447, 451-577, 4
 F:125, 221, 514, 581/Binding site: carboxylate (Asn) (covalent) #status experimental
 F:167/Modified site: erythro-beta-hydroxyasparagine (Asn) #status experimental
 F:206/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status experimental
 F:463-466/Cleavage site: Arg-Ile (autolytic) #status experimental
 F:502, 557, 654/Active site: His, Asp, Ser #status predicted
 A:Accession: A29769
 A:Reference number: A29769; MUID:8715625; PMID:3030286
 A:Accession: A29768
 A:Reference number: A29768; MUID:8715625; PMID:3030286
 A:Title: Cloning and sequencing of full-length cDNA encoding the precursor of human comp
 A:Accession: A29769
 A:Reference number: A29769; MUID:87241248; PMID:3036070
 A:Accession: A29769
 A:Molecule type: protein

Query Match 10.2%; Score 403.5; DB 1; Length 705;
 Best Local Similarity 22.9%; Pred. No. 1.6e-19;
 Matches 178; Conservative 96; Mismatches 259; Indels 245; Gaps 41;
 44 ECCEFDQIQC-----VC-----PGKEVVGCTITPC-----RNEBND 77
 Db 69 ECFDYDYKISADKSLGRFCQGLSPGNPGKKEFMSQGNMLTTHTPDSNEN--G 126
 78 SCLIRPGCTIF---ENCKSCRWGSGTLD-----DFYKGFYCAECRAGW----- 120

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Db 127 TIMEFKGLAYQAQVLDLBECASRKSGBEDPPOCQHLCNHYGGYFCS-CPRPYELQED 185
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Db 186 RHSCQAC-C-SEELYTEASGVYISLSEYPRSPYDRLCNYSIRVERGLTLHLFLE---PF 240
Qy 174 D-----YMCQDYUEVANDGDRDGOIIRKVCGRNRPAPIGISGSLNVLPHSDSGKPD 227
Db 241 DIDHQVHCPYDQOI-----YANGKNIGEFCKGRPRPDLTSSNAVVDLFFPTDSSGSR 296
Qy 228 GFHAIV-SEITACSSSPCFHDGTCVLDAAGSYKACLAGYTGORCENLLEBRNCSDPGGP 286
Db 297 GMLKRYTTEIHKCPKPLDBETIIQNIQPOVQ---FRDYFATCK----- 339
Qy 287 VNGYOKITGSGPEGLNGRHAKITGVVSPFCNNSYVLSGNEKRTCOONGEMSGKOPIC-IKA 345
Db 340 -QGYYLLEGNQVL-----HSFT-----AVCQDDGTNHRAMPCKIKD 375
Qy 346 CREPRISLVVRRVLPVMOVSRPETHQLYSAAPSKQLQSPRTKRLPFRDL-----PM 401
Db 376 CGQRP-----NLPNQDFRYTTM 393
Qy 402 GYONLHTQLOYESIPFYR---RLGSSRR---TCLRTGKWSG---RAPSCPIGCK 448
Db 394 GVNTYKARIQYCHPEPYTKMOTRAGSRSEGOVYTCTGQIKMKEQKBEKIPCLPVGCK 453
Qy 449 IEN-----ITAEKTOGLRMPQAAIYRRTSGVHDSLHKGANFLVCSGALVNERTV 500
Db 454 PNVPEGRORIIGGKAKGNPNMQV-----FTNIHG-----GGALLDGRWIL 498
Qy 501 VAARCVTDLQKVTMTKTDADLVVLGKPYRDDDRDKETQSLD-----ISAILHPN- 552
Db 499 TAAHTLVYKEHQAQ-SNBSLDVFLG-----HTNVEELMKLGNHDIRRVSVAHPDYRQ 548
Qy 553 -DPIILLDADIAILKLLDBKARISTRVOPICLAASRDLSTSPQESH-TYAGMNVLAD----- 606
Db 549 DESTNFEEDIALLELENSVTLGPNLLPCLP---DNDFYDLGLMGVYSGGVEWEKTAH 605
Qy 607 ---VRSBGFKNDTLRSGVSVSVDSLLCEQHEDHGIPIVSVYTDNMFCASWEPTASDICT 662
Db 606 DLREVRLEP-----VANPQACENMLRGKNRDVSQNNFCAG-HPSLKQDACQ 651
Qy 663 AETGIGIAVSPFGAASPERRWHLMGLVSWSDTKCSHSLSTAFTKVLVLPKOWIEANMK 720
Db 652 GDSGSGVAVRDPN---TDRNVAVGIVSWGIG-CS-RGYFPYTKVLNVYVMIKKEME 702

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RESULT 5
A:59271
Ra:reactive factor (EC 3.4.21.-) 2 precursor - human
N:Alternate names: mannose binding protein-associated serine proteinase 2 (MASP-2)
C:Species: Homo sapiens (man)
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C:Accession: A59271
R:Hitel, S.; Vorup-Jensen, T.; Stover, C.M.; Schwaible, W.J.; Laursen, S.B.; Poulsen, K.
Nature 386, 506-510, 1997
A:Title: A second serine protease associated with mannan-binding lectin that activates C
A:Reference number: A59271; PMID:97242412; PMID:9087411
A:Accession: A59271
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-686 <JEN6>
A:Cross-references: UNIPROT:O00187, UNIPARC:UPI0000047562; GB:Y09926; NID:G4007626; PIDRC:
A:Experimental source: tissue liver
A:Note: submitted to Genbank, December 1996
A:Note: parts of this sequence, including the amino end of the mature protein, were deter
C:Genetics:
A:Gene: GDB:MASP2
A:Cross-references: GDB:6071500
A:Map position: 1p36.2-1p36.3
C:Superfamily: complement-activating serine proteases C1r/C1s/MASP; C1r/C1s repeat homol
C:Keywords: beta-hydroxyaspartagine; complement pathway; duplication; hydrolase; serine p

F.1-15/Domains: signal sequence #status predicted <SIG>
F.16-444,445-686/Product: Ra-reactive factor 2 #status predicted <MAT>
F.19-134/Domains: C1r/C1s repeat homology <C1R1>
F.142-180/Domains: EGF homology <EGF>
F.184-293/Domains: C1r/C1s repeat homology <C1R2>
F.300-361/Domains: complement factor H repeat homology <FH1>
F.366-430/Domains: complement factor H repeat homology <FH2>
F.445-679/Domains: trypsin homology <TRY>
F.72-90,142-156,157-165,167-180,184-211,241-259,300-348,328-361,366-412,396-430,434-552,555-583,584-600,601-629,630-658,659-686/Products: cytochrome-beta-hydroxypargine (Asn) #status predicted
F.158/Modified site: Arg-116 (autolytic) #status predicted
F.444,445/Cleavage site: Arg-116 (autolytic) #status predicted
F.483,537,633/Active site: His, Asp, Ser #status predicted

Query Match	10.2%	Score 400.5	DB 1	Length 686
Best Local Similarity	32.7%	Pred. No. 2.5e-19		
Matches 173, Conservative	78	Mismatches 245	Indels 267	Gaps 34

QY	128	CGGVL-R--APK-----CGILLSEYP-----LNAHCENMTHAKPGVIGLRLRVMLSLSEBDY	178
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QY	176	MCQDYVERVDGNDNRDQIIRKVCNE-----RPAP-----IOSIGSSLHLVHFSQGS--KN	222
Db	71	LCEYDFVKLSSG--AKVIALTLCSQESTDTERAGCKDTFSLSGSLDITPRSDYSEKRP	126
QY	226	PDEFNHAIY--EELTACSSSP-----CFHDGTCVLDKASYSYCACLAAGTQGR-----CENL	277
Db	127	FTSGFEAFYAABEDIDECOVAPGAFTCDHH--CHNHGLGFFCYCSRAGVLRHNRKTCAL	183
QY	275	-----LBE-----	277
Db	184	CSGOVFTQSGSELSEPEYRPFPKLSSCTYSISLEBGSVLDLPVESTFDEVTHERETLCPY	244
QY	278	-----RNCSDP	281
Db	244	DPLKIQDREBHGPFCKTLPRIETKSNVTYITFVTDSEGDHGMKIHYSMAACPYP	303
QY	284	GGVNGVQKLTGTGPGLLINGRAK--IGTVSPFCNNIS-VLSG-----NEKRTQONGEW	333
Db	304	MAPPNH-----VSPVQAKYILKQSFISFCTGYELLQGHPLKSPFAVQCKQGSW	35
QY	336	SGKQPI-C-IKACBEPKISDLYRRARVLPMQOVGRFETPLQLYLSAFAFSKQIQASAPTKKRAL	394
Db	355	DRMPKACSLVDCGP--DLPBSGRV-----EYITGP-----	38
QY	395	PFGDLPMGYOHLHTLOVEYCISPFY--RLRGSRRTCRLTKGMSG----RAPSCPICGK	448
Db	384	-----GVTYTKAVIQVSCBETFTYMKKNDQKVCBADGFMTSSKGEKSLPVCBEPVCGL	436
QY	449	IEHTLPKTOGLR-----WPMQAAIYRTSGVNDGSLHKAMFLVCSGALVNERITYVA	50
Db	437	SARTTGRRYGGOKAKKPGDFPMQVILIGTT-----AAGALLVYNMWLTA	483
QY	503	AHCVTDLGKVTMIKTADLKVVLGKFEYRDDDRDEKTIQSLQ-----ISAILHPNY--DP	554
Db	482	AHAAYVE-----QKHDSALDIRMG-----TLKLSLPHYTQAMSEAVFHIEGTHD	528
QY	555	ILLDADIALIKLIDKARISTRVQPICLASBDLSFQESHITVAGNVLADVRSPPGKN	614
Db	527	AGDNQDIALIKNNKVVINSNTIPLCRKEASEPMRTDIDIGTASGNG----LTRQGFILA	582
QY	615	DTLRGSVSVVDSLCEBOEDHDGIP--VSVDNNFCSWEPTABSDICTMETGIAAVSF	673
Db	583	RNLMTYDIDIVHOKCTAAVEKRPVPRGSLVANNMLCGLLE--SGKDSGCRGSGG--ALVF	639
QY	674	PGASBPBRWMLMGIVMSYDKTCSHRSLSTAFTVLPKQDIE	716
Db	640	--LDSETERWEVGGIVSWGNNAGCEAGQGVAYTIAKINITPITE	680

RESULT 6
S05008
Complement subcomponent C1s (EC 3.4.21.42) precursor [similarity] - golden hamster

C.Species: Mesocricetus auratus (golden hamster)
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C.Accession: S05008
R.Kinoshita, H.; Sakiyama, H.; Tokunaga, K.; Imajob-Ohmi, S.; Hamada, Y.; Isono, K.; Sak
PEBS Lett. 250, 411-415, 1989
A.Title: Complete primary structure of a calcium-dependent serine proteinase capable of
A.Reference number: S05008; MUID:89325606; PMID:2753140
A.Accession: S05008
A.Molecule type: mRNA
A.Residues: 1-695 <KIN>
A.Cross-references: UNIPROT:P15156; UNIPARC:UPI000012700B; EMBL:X16160; NID:g49621; PIDN
A.Note: part of this sequence, including the amino ends of both the heavy and light chain
C:Superfamily: complement-activating serine proteases C1r/C1s/MASP; C1r/C1s repeat homol
C:Keywords: beta-hydroxyasparagine; calcium binding; duplication; glycoprotein; hydrolyas
F.1-21/Domain: signal sequence #status predicted <SIG>
F.17-133/Domain: C1r/C1s repeat homology <C1R1>
F.22-444/Product: serine proteinase heavy chain #status experimental <HC1>
F.141-177/Domain: EGF homology <EGF>
F.181-293/Domain: C1r/C1s repeat homology <C1R2>
F.300-360/Domain: complement factor H repeat homology <FH1>
F.365-428/Domain: complement factor H repeat homology <FH2>
F.445-682/Domain: trypsin homology <TRY>
F.446-695/Product: serine proteinase light chain #status experimental <LC1>
F.71-89,141-153,164-167,181-208,240-257,300-347,327-360,365-410,392-428,432-556,
F.155/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F.180,413/Binding site: carbohydrate (Asn) (covalent) #status predicted
F.482,536,638/Active site: His, Asp, Ser #status predicted

Query Match 9.6%; Score 378.5; DB 1; Length 695;
Best Local Similarity 21.8%; Pred. No. 7.6e-18;
Matches 168; Conservative 81; Mismatches 227; Indels 293; Gaps 35;
QY 137 GOILL-----ESYPLNACSWTHAKPGFVIOLEFVWMLSEPFYMCQYDVEVRDGDNRG 192
DB 27 GEILSPNTPOALPNEKMTWIDIEPBGFVRLYFTHLDELSENCEYDSVQIIISGVEBG 86
QY 193 QIIRKVCNERNP-----API-----OSIGSLHVLPHSDGS--KNPDGFHAIY-----EET 237
DB 87 -----RLCGRTSKNANSPIVEEFQIPYNKLOVIFPSDFENBERFTGFAVYALVDNBE 142
QY 238 ACSSSPCHDGTCLDKAGSYKACIAGY----- 266
DB 143 DFTDPCSHFCNNFT-----GGYFCSPEPEYFLHDMKNCVNCGNVFTALIGEISSPNYP 199
QY 267 -----TGRCEN-----LLEB-----RNCSDP----- 283
DB 200 NPYENSRCYQIILEBGFQVVTTQREDPDVEPADSGNCDLSLFAAKNQFGPCGN 259
QY 284 -----GAPVNGYOKITGCP----- 297
DB 260 GPPGLTIEHTSNTLDIVFQDLEQKKGMKLRYHGDPIPCPKETANSVMAPEKAYVF 319
QY 298 -----GLNGRHAKIGTVVSFFCNSYVLSGNEKRTCOQNGEMSGK-----OPICIKACR 347
DB 320 KDVAKISCVDGFEAEGVNGSTFFYS-----TCQSNQGMNSRLRCQPV---DCG 366
QY 348 EPKISDLYRRRLPMQOVOSRETFHLQVLSAASFKOKLSAPTKKALPFGDLPMEGYQLH 407
DB 367 IPE-----PIQNGKVDPDENTLFGSV----- 387
QY 408 TQLOECISPFY-----RRIGSGRRCTCLRTGKWSG-----RAPSCIPIGKIENITAPKTO 458
DB 388 --IHSCSEPTIYMHAEHGEYR--CAANGSVNDELIGELPKCYPVCG-----VPLE 437
QY 459 GLRMEWQAIYRRTSGVHDSLHKAM-----FLVCSGALVNERTVVAACVTDLGKVT 513
DB 438 PFR-----IQGRIGGFPKAKIQSPFQVFEFPRAAGALIGEHVWLTAAHVEGNSDPS 491
QY 514 M-IKTRADIKVVLGKRYRDDREKTIQSLQISAILLHPYDP-----ILLDAIILIK 565
DB 492 MIVGTSVFM-----ENLAVVQKLTJTDVILIHGMKPGDGLSTRTFNDNDIALVR 541
QY 566 LDKARISTRVOPICLAASRDISTSFQESH---ITVAGW-----NLADVRSFGFKNDT 616

QY 542 LKD PYMGPTVSPICLPFT-----SSSEYBSEGLIGLISGGRTERRNIVQLR----- 590
DB 617 LNSGVSVSDSL-----LCEQHEHDGIFVSTLDNMFCSWEPTRASDICTMETGSIANV 671
QY 591 ---GAKLPVTSLEKCRQYVENPKARADDVFTSNKICGEGV---DSCQDSGSAFAL 644
DB 672 SPPGRASPEPRWHLNGLVSWSYDKTCSHRLSTAFKVLPEFKWIERNMK 720
QY 645 PVPN---VNDPKFYVAGVSWG---KKCG---TYGIVTKVKNVYKWMILQTMQ 667
DB
RESULT 7
T30337
polyprotein - African clawed frog
C.Species: Xenopus laevis (African clawed frog)
C.Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C.Accession: T30337
R.Yang, J.C.; Lindsey, L.L.; Hedrick, J.L.
submitted to the EMBL Data Library, March 1998
A.Description: cDNA cloning of ovochymase, a chymotrypsin-like protease released from Xer
A.Reference number: Z20829
A.Accession: T30337
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residues: 1-1524 <YAN>
A.Cross-references: UNIPROT:Q91674; UNIPARC:UPI000009BA76; EMBL:U01290; NID:g2981640; PII
C:Superfamily: trypsin related polyprotein; trypsin homology

Query Match 9.0%; Score 354; DB 2; Length 1524;
Best Local Similarity 22.3%; Pred. No. 8e-16;
Matches 166; Conservative 101; Mismatches 260; Indels 216; Gaps 39;
QY 55 CPGRKENVGY-----TIFCCRNENBECDSCLHPCSTIFENCKSRNGSGTLDFFYK 109
DB 214 CHAVLEPIGHVLDPTMLCAGFEGMDACQDSGAPFV---CRR-RSGVW-----FLA 263
QY 110 GFYCAE-----CRAGW-----YGGDCMKCGVLRAP 135
DB 264 G---CVSMGLGCRSGAKQIIRSGSGSPAIRSVSVLDLFRPPLTGTGCKSKKGTITQ 321
QY 136 KGOI---LLESYPLNACSWTHAKPGFVIOLEFVWMLSEPFYMCQYDVEVRDGDNRG 192
DB 322 NGTVARYPLSGNVNSVCRMWMLAVOKAKTIEIRFLQIDIEDHATCFDVLSTVNE--- 377
QY 193 QIIRKVCNERNPAPIQSIGSLHVLPHSDGSKNPDGFHAIYBEITACSSSPCHDGTCL 252
DB 378 KMIKRYCGSTIPSPILVSNKVTYTFPSDGTFTGFGFIOFLAIPTKASAC--GSAKL 435
QY 253 DRAGSYKACIAGYTGRCENLLEBNCSDP-----GAPVNGYOKITGPGGLIN 301
DB 436 KKKG-----MIVSPNYPDPYPRKLTQSMITEADENHIVLKLFEDFVNE 478
QY 302 GRHAKIGTVVSFFCNSYVLSGNEKRTCOQNGEMSGKOPICIKACREPKISDLVER---R 358
DB 479 YGHGCTYAVS-----YVDGAEK-----QLIARLGY 506
QY 359 VLPQOVOSRE-----TPHLQVLSAASFKOKLSAPTKK--ALPFGDLPMEGYQLHTQ 409
DB 507 TLPLPISSPENTMLIRFTDMENSYPG--FYKFSFVPEKQFSLPVDVDTPT--ISMELPR 563
QY 410 ---LQYECISPFYRRLTSGSRRTCLRTGKWSGRAPSCIP--IGKIENITAPKTOGLRWPQ 465
DB 564 AIALDVCGMAAPV-----TPRW-----WLPRIYGEER--ASPNS---WPMQ 598
QY 466 AAI-YRRTSGVHDSLHKAMFLVCSGALVNERTVVAACVTDLGKVTMTKTD---LK 521
DB 599 VQIFPLRT-----FH-----CEGALISPPQWILTAHC-----IRAAEPSYWT 635
QY 522 VVLGKFYDDDR--DEKTIQSLQISAILLHPYDPILLDADIALIKLDKARISTRVOP 579
DB 636 VIAG---DHNRMNTESTEQIRIKITRIHDNYSSETYDNDIALLYLEBPDLANDFVRPV 691

QY 580 CLAASRDLSSTFOESHITTAGNNVLADVRSFGKNDLTSGVSVSDSLCEQEHDEGI 639
 Db 692 CLPEBEVLT--PASVCVVTGWTGNTAEDQPALGLQLO---LPIDSLITCNTSYSG-- 744
 QY 640 PVSVDNMFCASMEPTAPSDICTAETGTAASFPBRASPERPWHLMGVMSYDTCGH 699
 Db 745 --ELTDHMLCAPSPSKKQACQDGGGGLVCO---NEKQFSLYGLVSWG--EGCG- 794
 QY 700 RLST--AFTKVLPRKDMIERNNK 720
 Db 795 RVSKRGVTKVRLPFTWIONTOQ 817

RESULT 8

complement subcomponent C1s (EC 3.4.21.42) precursor [similarity] - rat
 C.Species: Rattus norvegicus (Norway rat)
 C.Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
 C.Accession: J06554
 C.Sakai, H.; Nakashima, S.; Yoshimura, S.; Nishimura, Y.; Sakai, N.; Nozawa, Y.
 Gene 209, 87-94, 1998
 A.Title: Molecular cloning of a cDNA encoding a serine protease homologous to complement
 A.Reference number: J06554; MUID:98192519; PMID:9524231
 A.Accession: J06554
 A.Molecule type: mRNA
 A.Residues: 1-694 <SAR>
 A.Cross-references: UNIPROT:070542; UNIPARC:UP10000066CA8; DDBJ:D88250; NID:93080541; PI
 C.Comment: This protein is involved in glial cell differentiation and cartilage remodeling
 C.Genetics:
 A.Gene: F-99P
 C.Superfamily: complement-activating serine proteases C1r/C1s/MASP; C1r/C1s repeat homol
 C.Keywords: differentiation; glycoprotein; hydrolase; serine proteinase
 F.1-21/Domin: signal sequence #status predicted <SIG>
 F.17-133/Domin: C1r/C1s repeat homology <C1r>
 F.122-694/Product: serine protease homolog #status predicted <MAT>
 F.141-177/Domin: EGF homology <EGF>
 F.300-360/Domin: complement factor H repeat homology <FHR>
 F.444-681/Domin: tryptsin homology <TRY>
 F.180,412/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F.481,535,637/Active site: His, Asp, Ser #status predicted

Query Match 8.6%; Score 340.5; DB 2; Length 694;
 Best Local Similarity 21.2%; Pred. No. 2.7e-15;
 Matches 167; Conservative 98; Mismatches 244; Indels 277; Gaps 40;
 QY 44 ECCEVDIOECVCPGRK-----VVGITPCCR-----NEE----- 73
 Db 69 ENCAVDVQIISGIEERLCQGRSSKSPNSPTVEFQPKRLQVFTSPDSNEBRFTG 128
 QY 74 -----NECDSLHPGCTTFENCKSCRNWSGGTLDFYVKGFGYCAECRAGWYG 123
 Db 129 FAAYSAVDVNECTDFTDVP-CSHF-----CNN-----FIGYFCS-CPEYFLH 171
 QY 124 DCMR-----CGOVLRAKQGLLES---YPLNAHCETTHAKGFIQGLFVWLSLEF 173
 Db 172 DDMRTCGVNCSDVFTALIGELASPNYPENRRCYQIRLQGF--RLVLTTRRDPF 229
 QY 174 DYMCQYDVVEYVDGDN-----DGOIKRVCGNERPAP--TOSIGSSLHVLPHSDG 222
 Db 230 D-----VEPADSEGNCHDSITFAAKQOQFGPYCGNGFPGLTKTKTSNTLDIVFQIDL 282
 QY 223 SKNPDGFPAIY-----EBITACS-----SPCFHDGTCVLDKAGSYKACLAGTGTG 268
 Db 283 TGQKQKWLRIHGDPIPCPKESANSIWEPEAKAVFPD-----VVKITC----- 327
 QY 269 QRCENLEERNCSDBGVNGYQKTGTGPGGLINGHAHIGIVVSFFCANNVYLSGNEKRT 328
 Db 328 -----VDGFEVVEGVNG-----STSPY-----ST 346
 QY 329 COONGEMSGK-----QPICTIKACREPKISDLVRRVLPWQVQSRERPLHQLVSAARSKQL 384
 Db 347 COSNGQMSNRLKCPV--DCGVPE-----PIENGKVEDPBDTVEGVSV----- 387

QY 385 QSAPTKPPALPFGDLPWGYOHLHTLOLYECISPFY--RRLGSSRRPTCLRTGWSG----- 437
 Db 388 -----IHTCEPFYYMEQEGEGYHCANGSWVNDQGV 422
 QY 438 RAPSCIPICG-----KIEN--ITAPKQGLRMPQAAIYRTSGVHOSLHKGMFLVC 489
 Db 423 ELPKCIPVCGVTEPEPKYQOIRLFGYSTKIQSPFQVYFESPRG----- 467
 QY 490 SGALVNERTVVAACHYT-DLGKVTMTKADKLVLGKFRYRDDDEKTIQSLQISAIL 548
 Db 468 -GALIDEYVLTAAIVVEGNSDPVNYVSGSTLTK-----ERLNAQGLITERVYI 516
 QY 549 HPNYDP-----ILLDDIALILKLDKARISTRVOPICLAASRDLSSTFOESHI--TV 598
 Db 517 HPSWKQBDLNTRTNFDNDIALVQLKDPVKQPTVAPICLP---ETPSDYNSEVDLGI 573
 QY 599 AGWNVLDVRSFGKNDLTSGVSVSDSLCE---EQEHDEGI-PVSVTDMFCASMEP 654
 Db 574 SGWG-RTEIRTVIQ--LRGAKLPITSLERKQOQVKNPNKARSNDYFTDMICAGEKG 629
 QY 655 TAPSDICTAETGTAASFPBRASPERPWHLMGVMSYDTCSHRLSTAFKVLPRKDM 714
 Db 630 V---DSCGDSGGAFLVFPN--VDPKRYAGLVSWG--KKCG--TYGITTKVKNYVDM 680
 QY 715 IERNNK 720
 Db 681 ILKTMQ 686

RESULT 9

C1HUS

complement subcomponent C1s (EC 3.4.21.42) precursor [validated] - human
 N.Alternate names: C1 esterase precursor
 C.Species: Homo sapiens (man)

C.Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-May-2004
 C.Accession: A40496; A27381; S00224; S26732; S05634; A05140; A25396; A36407; B37820
 C.Kusumoto, H.; Hirosewa, S.; Sallier, J.P.; Hagen, F.S.; Kurachi, K.
 Proc. Natl. Acad. Sci. U.S.A. 85, 7307-7311, 1988
 A.Title: Human genes for complement components C1r and C1s in a close tail-to-tail arrang
 A.Reference number: A40496; MUID:8901187; PMID:2459702
 A.Accession: A40496
 A.Molecule type: mRNA
 A.Residues: 1-688 <KUS>
 A.Cross-references: UNIPARC:UP10000126BF6; GB:J04080; NID:9179645; PIDN:AA51852.1; PID:G
 R.Tosti, M.; Duponchel, C.; Meo, T.; Jullier, C.
 Biochemistry 26, 8516-8524, 1987
 A.Title: Complete cDNA sequence of human complement C1s and close physical linkage of the
 A.Reference number: A27381; MUID:88163522; PMID:2831944
 A.Accession: A27381
 A.Molecule type: mRNA
 A.Residues: 1-688 <TOS>
 A.Cross-references: UNIPARC:UP10000126BF6; GB:M18767; NID:9179647; PIDN:AA51853.1; PID:G
 R.Mackinnon, C.M.; Carter, P.E.; Smyth, S.J.; Dunbar, B.; Fothergill, J.E.
 Eur. J. Biochem. 169, 547-553, 1987
 A.Title: Molecular cloning of cDNA for human complement component C1s. The complete amin
 A.Reference number: S00224; MUID:88082788; PMID:3500856
 A.Accession: S00224
 A.Molecule type: mRNA
 A.Residues: 1-688 <MAC>
 A.Cross-references: UNIPARC:UP10000126BF6; EMBL:X06596; NID:929542; PIDN:CAA29817.1; PID:
 A.Accession: S26732
 A.Molecule type: protein
 A.Residues: 16-38; 68-116; 170-236; 246-262; 265-280; 282-284; 287-308; 315-363; 384-394; 421-435;
 A.Cross-references: UNIPARC:UP1000015033A; UNIPARC:UP10000172BCD; UNIPARC:UP10000172BCE;
 B03; UNIPARC:UP10000172BD4; UNIPARC:UP10000172BDS
 R.Tosti, M.; Duponchel, C.; Meo, T.; Couture-Tosti, E.
 J. Mol. Biol. 208, 709-714, 1989
 A.Title: Complement genes C1r and C1s feature an intronless serine protease domain (close)
 A.Reference number: S05634; MUID:90040704; PMID:2553984
 A.Accession: S05634
 A.Status: not compared with conceptual translation
 A.Molecule type: DNA
 A.Residues: 356-513, 'G', 514-688 <T02>

A:Cross-references: UNIPARC:UPI0000172BD6
 R:Cartier, P.E.; Dunbar, B.; Fothergill, J.E.
 Biochem. J. 215, 565-571, 1983
 A:Title: The serine proteinase chain of human complement component C1s. Cyanogen bromide
 A:Reference number: A05140; MUID:84104122; PMID:6362661
 A:Accession: A05140
 A:Molecule type: protein
 A:Residues: 438-483, 'X', 485-500, 503-534, 542-558, 561-572, 'A', 574-601, 617-623, 626-644, 647-
 A:Cross-references: UNIPARC:UPI0000172BD7; UNIPARC:UPI0000172BD8; UNIPARC:UPI0000172BD9;
 R:Spicher, S.E.; Nick, H.; Rickli, E.E.
 Eur. J. Biochem. 156, 49-57, 1986
 A:Title: Human complement component C1s. Partial sequence determination of the heavy cha
 A:Reference number: A25396; MUID:86164350; PMID:3007145
 A:Accession: A25396
 A:Molecule type: protein
 A:Residues: 16-61, 168-219, 287-293, 'K', 295-334, 384-445 <SPY>
 A:Cross-references: UNIPARC:UPI0000172BDE; UNIPARC:UPI0000172BDF; UNIPARC:UPI0000172BE0;
 R:Hees, D.; Schaller, J.; Rickli, E.E.
 Biochemistry 30, 2827-2833, 1991
 A:Title: Identification of the disulfide bonds of human complement C1s.
 A:Reference number: A38407; MUID:91175725; PMID:2007122
 A:Accession: A38407
 A:Molecule type: protein
 A:Residues: 131-134, 'X', 136-146, 'X', 148-150, 155, 'X', 157-162, 166-170, 'X', 172-174, 'X', 176-
 'X', 387-402, 'X', 404-408, 416-424, 'X', 426-431, 547-556, 592-597, 617, 'X', 619-627, 'X', 629-635
 A:Cross-references: UNIPARC:UPI0000172BE2; UNIPARC:UPI0000172BE3; UNIPARC:UPI0000172BE4;
 BE9; UNIPARC:UPI0000172BEA; UNIPARC:UPI0000172BEB; UNIPARC:UPI0000172BEC; UNIPARC:UPI000
 R:Thelens, N.M.; Aude, C.A.; Lacroix, M.B.; Gagnon, J.; Arlaud, G.J.
 J. Biol. Chem. 265, 14469-14475, 1990
 A:Title: Ca(2+) binding properties and Ca(2+)-dependent interactions of the isolated NH-
 A:Reference number: A37820; MUID:90354439; PMID:2387866
 A:Accession: B37820
 A:Molecule type: protein
 A:Residues: 16-25; 'X', 203-207 <THI>
 A:Cross-references: UNIPARC:UPI0000172BF2; UNIPARC:UPI0000172BF3
 R:Thelens, N.M.; Van Dorsselaer, A.; Gagnon, J.; Arlaud, G.J.
 Biochemistry 29, 3570-3578, 1990
 A:Title: Chemical and functional characterization of a fragment of C1s containing the ef
 A:Reference number: A32672; MUID:90283368; PMID:2141278
 A:Contents: annotation: erythro-beta-hydroxyasparagine site, content
 A:Note: about half of the A chains contain erythro-beta-hydroxyasparagine
 C:Comment: This protein is a serine proteinase that combines with C1q and C1r to form C1
 s C2 and C4.
 C:Comment: C1s is a dimer of identical chains, each of which is activated by cleavage in
 C:Genetics:
 A:Gene: GDB:C1S
 A:Cross-references: GDB:119730; OMIM:120580
 A:Map position: 12p13-12p13
 A:Introns: 291/1; 329/3; 356/1; 399/1; 424/1
 A:Note: the list of introns may be incomplete
 C:Superfamily: complement-activating serine proteases C1r/C1s/MASP; C1r/C1s repeat homol
 C:Keywords: acute phase; beta-hydroxyasparagine; calcium binding; complement pathway; du
 F:1-15/Domain: signal sequence #status predicted <SIG>
 F:11-127/Domain: C1r/C1s repeat homology <C1R1>
 F:16-688/Product: complement subcomponent C1s #status experimental <MAT>
 F:16-437/Product: complement subcomponent C1s chain A (heavy chain) #status experimental
 F:135-171/Domain: BGF homology <BGF>
 F:175-287/Domain: C1r/C1s repeat homology <C1R2>
 F:294-354/Domain: complement factor H repeat homology <FH1>
 F:359-421/Domain: complement factor H repeat homology <FH2>
 F:438-668/Product: complement subcomponent C1s chain B (light chain) #status experimental
 F:438-675/Domain: trypsin homology <TRY>
 F:65-83, 135-147, 143-156, 158-171, 175-202, 234-251, 294-341, 321-354, 359-403, 386-421, 425-549,
 F:1174, 406/Binding site: erythro-beta-hydroxyasparagine (Asn) (partial) #status experimental
 F:1174, 406/Cleavage site: carboxylate (Asn) (covalent) #status experimental
 F:437-438/Cleavage site: Arg-1le (complement subcomponent C1r) #status experimental
 F:475, 529, 632/Active site: His, Asp, Ser #status predicted

Query Match 8 5%; Score 334; DB 1; Length 688;
 Best Local Similarity 21.7%; Pred. No. 7, 4e-15;
 Matches 163; Conservative 83; Mismatches 246; Indels 260; Gaps 37;

Db
 21 GELISPNYPOAVPSEVEKSMIEVEGEGIHLYFHLIDIEISENCAVDSVOIISGDTSEG 80
 193 QIKKVCNNERPAPV-----QSIGSLHYLFIHSDGS--KNPQGFHAY--EETIACS---S 241
 81 RLCCGRSSNNPHSPFVEEFQVPYNNQLQVIFXSDFSNERRFTGFAPVAVYATDINECTD 140
 242 SPCFIDGTCVLDKASGYCACIAGY----- 266
 141 VPCSHFCNNFT---GGYFCSCPEYFLHDMKNGCNGSGVFTALMIGIASPNPKPYV 197
 267 TGQRCENLL-----EERNCSN-----PGGPNYQKIT 294
 198 ENSRCEYQIRLEKGFQVVVTLREDDFVEADASAGNCLDSLFAVAGDRQFGYCGH----- 253
 295 GGRGLN-----GRAK--I 307
 254 GPPGLNLETYSNALDIIFGTDLTGCKKWKLRHYHDMPCPKEDTPNSVWEPAKATYV 313
 308 GTVAFPCNNSTY-VLSG-----NEKRTQONGEMSGK-----QPICIKAREPKISDLVR 357
 314 RDVQITLIDGFEVVEGKVGATSPYSTQSGKNSNLTCKQPV---DCGIP----- 362
 358 RVLPMQVQSRETPLHQLYSAAFSKQKQASAPTKP-ALPFGDLPMGYHLHTQIYECIS 416
 363 -----ESINGKVEDESTLFGSV-----IRYTCBE 388
 417 PFY--RLIGSSRRITCLRTGKNSGRA-----PSCIFICKEINHTAPKQGLRMPQAAIY 469
 389 PYYVWENGGGEYHACANGSWNEVLAGELPKVCVCG-----VPE-----REPBEK-- 435
 470 RRTSGVHDGSLHKGMFLV-----CSGALVNERVTVAACHCTDGLKTYMTITADLKVYL 524
 436 QRITGSDADIKNPFQVFPDNPMAAGALLINEYWLTLAAHVEGAREPTM-----YV 487
 525 GKPYRDDDRDEKTIQSLQISALIIHPNYDPIIL-----DADIALKLKDKARISTRVQ 577
 488 GSTVQTSRLAKS-KMLPPEHVFIHPKMLEVEPGRTNFDNDIALVRLDKVKKGPVTS 546
 578 PICLAASDLSTSPESHITTAQWNVLDVSPGRND---TLRSGVSYVDSLLICEBH 634
 547 PICLPGTSSDYNLMDGDLISGWG---RTE--KRRAVRLKARLPVAPLRCKEYK 599
 635 EDHGIPVS-----VTDNMFCAWSEPTAPSDICTAETGIAVSPFGNASPEPRHMLML 688
 600 VEK--PTDAEAHYVTPMNICAGE--KQMSCKDSSGAPVQDP---NDKTKFYAGL 652
 689 VSWSYDKTCSHRLSTAFTRKVLFPKDMIRNMK 720
 653 VSWG--PQCG--TYGLYTRVKNYVDWIKKTQ 680

Db
 689 VSWSYDKTCSHRLSTAFTRKVLFPKDMIRNMK 720
 653 VSWG--PQCG--TYGLYTRVKNYVDWIKKTQ 680

RESULT 10
 A56318
 N:Enteropeptidase (EC 3.4.21.9) precursor [validated] - human
 M:Alternate names: enterokinase
 C:Species: Homo sapiens (man)
 C:Date: 19-May-1995 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
 C:Accession: A56318; B43090
 R:Kitemoto, Y.; Velle, R.A.; Donis-Keller, H.; Sadler, J.E.
 Biochemistry 34, 4562-4568, 1995
 A:Title: cDNA sequence and chromosomal localization of human enterokinase, the proteolyti
 A:Reference number: A56318; MUID:95234679; PMID:7718557
 A:Accession: A56318
 A:Molecule type: mRNA
 A:Residues: 1-1019 <KIT>
 A:Cross-references: UNIPROT:P98073; UNIPARC:UPI000003PF65; GB:U09860; NID:G746412; PIDN:
 R:Kitemoto, Y.; Yuan, X.; Wu, O.; McCourt, D.W.; Sadler, J.E.
 Proc. Natl. Acad. Sci. U.S.A. 91, 7588-7592, 1994
 A:Title: Enterokinase, the initiator of intestinal digestion, is a mosaic protease compo
 A:Reference number: A43090; MUID:94329561; PMID:8052624
 A:Accession: B43090
 A:Status: nucleic acid sequence not shown

A: Molecule type: mRNA
A: Residues: 749-1019 <KI2>
A: Cross-references: UNIPARC:UPI000017280B; GB:U09860
C: Comment: The mechanism of association with the membrane of the intestinal brush border coated below) or with amino-terminal myristoylation of the heavy chain.
C: Genes: GDB: PRSS7
A: Cross-references: GDB: 384083; OMIM: 226200
A: Map position: 21q21-21q21
C: Complex: Mature enteropeptidase is variously reported to contain two (heavy and light) ed by a disulfide bond. Possibly, conversion from membrane-bound to soluble forms involve ducts.
C: Function:
A: Description: cleaves activation peptide from trypsinogen to produce active trypsin
A: Pathway: intestinal digestive hydrolase cascade
C: Superfamily: enteropeptidase; C1r/C1s repeat homology; LDL receptor ligand-binding rep
C: Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein; zymogen
F: 1-784/Product: enteropeptidase heavy chain #status predicted <HCH>
F: 122-38/Domain: transmembrane #status predicted <TM>
F: 184-221/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F: 342-504/Domain: MAM homology <MAM>
F: 526-631/Domain: C1r/C1s repeat homology <C1r>
F: 643-677/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F: 785-1019/Domain: scavenger receptor cysteine-rich domain homology #status atypical <SRC
F: 785-1019/Product: enteropeptidase light chain #status predicted <LCH>
F: 116-147, 119, 328, 335, 388, 440, 470, 503, 534, 630, 682, 706, 725, 848, 887, 909, 949/Binding site:
F: 772-896, 810-926, 910-977, 941-956, 967-995/Disulfide bonds: #status predicted
F: 825, 876, 971/Active site: His, Asp, Ser #status predicted

Query Match 8.4%; Score 331.5; DB 1; Length 1019;
Best Local Similarity 22.9%; Pred. No. 1.7e-14;
Matches 136; Conservative 90; Mismatches 225; Indels 143; Gaps 27;
Db 143 SYPLAHCEWTHAKRGVYIOLRFVMLSLERPMQYDVVVRGDNDRDGIIRKVCNE 202
Db 545 SYPLAHCEWTHAKRGVYIOLRFVMLSLERPMQYDVVVRGDNDRDGIIRKVCNE 598
Qy 203 RPAPIQSIGSS-----LVLFHSDGSKNF-DGFHAIEEITACSSSPCFPHD 251
Db 599 -PGPKVDVFTTNMTVLTITNDVLARGSPKANTTGHILGIP-----PC----- 643
Qy 252 LDKAGSYVC--ACLA-----GYTGRCENLLEERNCSDPGPNVGYOKITGGGLING 302
Db 644 --KADHFOCKNGECVPLVNLCDGHL--HCEDESDADC-----VRFNGTINNNGLVRF 693
Qy 303 RHAKIGTVSFFCNNSVYLSGNEKRTCOONGEMSGKQPCIKACREKISDLVRRRLVPM 362
Db 694 RIQSIW-----HTACAEWTTQTISNDVC-----QLLGL 721
Qy 363 QVOSREPLHQLYSAFSAFQKQLOAPTKKRALPFGDLPMGYOHLTOLQYECISPFYRL 422
Db 722 GSGNSKRIFFSTDPGF--VKLTNAPD-----GHLLTFSQCLQDSILRL 765
Qy 423 GSSRTCTLRGKMSGRAPSCIPGCKIENITAPKTOGLRMPQAAIYRTSGVHDSLHK 482
Db 766 QCNKSKC-----GKLLAODITPKI--VGSNAKEGAMPVWVGLY-----YGR-- 807
Qy 483 GAWFLVSGALVNERTVVVAHCVTDLGKVTMIKADLKVVLGKFRYDDDRDEKTIQSLQ 542
Db 808 ---LTCASIVSSDMLVSAHCV--YGR--NLEBSKATALLGLHMSKNLTPQIVPL- 858
Qy 543 ISAILHPNDYPLLDADIALIKLIDKARISTRVOPICLAASRDLSFOSHSITVAAMN 602
Db 859 IDELVINPHVRRKKNDIANMHLBFKNYTYDIQPICLPRENOVFPFGR--NCSIAQMG 916
Qy 603 VLADYRBPFGKNDTLRSGVSVVDSLLCEQHEHDGILPVSVTDMNFCAWEPAPSDICT 662
Db 917 T---VVVQGTANILQENDVPLLSNERCOQMPREY---NITENNICAGYE-EGGIDSCQ 968
Qy 663 AETGSIADVSPFGASPERRHHMLGLVMSYDKTCSHRLSTAFKVLVLFKMWIE 716
Db 969 GDSGG-----PLMCEENRWFAGVTSFGKCALPKN-PGVYARVSRFTMIQ 1015

RESULT 11

A53663

enteropeptidase (EC 3.4.21.9) precursor [validated] - pig

N/Alternate names: enterokinase

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 07-Oct-1994 #sequence_revision 09-Aug-1996 #text_change 28-Apr-2003

A53663

R/Matsumura, M.; Ichinose, M.; Yahagi, N.; Kakei, N.; Tsukada, S.; Miki, K.; Kurokawa, J.

J. Biol. Chem. 269, 19976-19982, 1994

A: Title: Structural characterization of porcine enteropeptidase.

A: Reference number: A53663; MUID: 94327548; PMID: 8051081

A53663

A: Accession: A53663

A: Molecule type: mRNA

A: Residues: 1-1034 <MAT>

A: Cross-references: UNIPARC:UPI000017280C; GB: D30799; NID: g505122; PIDN: BAA06459.1; PID: 5

A: Note: parts of this sequence, including the amino ends of three chains isolated from ti

C: Comment: The mechanism of association with the membrane of the intestinal brush border

C: Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein; zymogen

F: 1-784/Product: enteropeptidase heavy chain #status predicted <HCH>

F: 122-38/Domain: transmembrane #status predicted <TM>

F: 184-221/Domain: LDL receptor ligand-binding repeat homology <LDL1>

F: 342-504/Domain: MAM homology <MAM>

F: 526-631/Domain: C1r/C1s repeat homology <C1r>

F: 643-677/Domain: LDL receptor ligand-binding repeat homology <LDL2>

F: 785-1019/Domain: scavenger receptor cysteine-rich domain homology #status atypical <SRC

F: 785-1019/Product: enteropeptidase light chain #status predicted <LCH>

F: 116-147, 119, 328, 335, 388, 440, 470, 503, 534, 630, 682, 706, 725, 848, 887, 909, 949/Binding site:

F: 772-896, 810-926, 910-977, 941-956, 967-995/Disulfide bonds: #status predicted

F: 825, 876, 971/Active site: His, Asp, Ser #status predicted

Query Match 8.4%; Score 330.5; DB 1; Length 1034;
Best Local Similarity 22.9%; Pred. No. 2e-14;
Matches 137; Conservative 86; Mismatches 224; Indels 151; Gaps 27;
Db 143 SYPLAHCEWTHAKRGVYIOLRFVMLSLERPMQYDVVVRGDNDRDGIIRKVCNE 202
Db 560 NYPOAFVWMLNMQKGNLQHF-----BFDLENIDVVEIRGEBDSLLLVYTG-- 613
Qy 203 RPAPIQSIGSS-----LVLFHSDGSKNF-DGFHAIEEITACSSSPCFPHD----- 247
Db 614 -PGVEDVFTTNMTVLTITNDALTKGSPKANTTGHILGIP-----PCEDNPOC 665
Qy 248 --GTVIDKAGSYVCACLAGYTGRCENLLEERNCSDPGPNVGYOKITGGGLINGRHA 305
Db 666 ENGEVCV-----LVNLCDFGSHCKDGSDEACVRLPANGTANNSGLVORPIQ 711
Qy 306 KIGTVSFFCNNSVYLSGNEKRTCOONGEMSGKQPCIKACREKISDLVRRRLVPMQV 365
Db 712 SIW-----HTACAEWTTQTISDVC-----QLLGLGTG 739
Qy 366 SRETRPLHQLYSAFSAFQKQLOAPTKKRALPFGDLPMGYOHLTOLQYECISPFYRLGSS 425
Db 740 NSSMPFSSSGGPR--VKLTNAPGSLITNASE-----QCEBDSILILQCN 783
Qy 426 RRTCLRTGKMSGRAPSCIPGCKIENITAPKTOGLR-----WPMQAAIYRTSGVHDS 479
Db 784 HKSC--GK-----KQVAGEVSPKIVGANDSRGAWPVVALY-----YNGQ 822
Qy 480 LHKAWFLVSGALVNERTVVVAHCVTDLGKVTMIKADLKVVLGKFRYDDDRDEKTIQ 539
Db 823 -----LTCASIVSSDMLVSAHCV--YGR--NLEPSKAKILG-LHMTSNLTSPOIV 870

QY 540 SLQISAILHPNYDPIILDADIALIKLADKARISTRVQDICAASRLDSTFSQESH1-TV 598
 DB 871 TRLEIDELVFNPHNRRKSDIAMMHLKFNKVTYDQICLPEBNQV---FPPGICSI 927
 QY 599 AGMNVADVRSPGFKNDRILRSQVSVVDSLLCEBQEDHEDGIVSVTDNNFCSWETAPS 658
 DB 928 AGMGVIVYQGSPPA---DILQEDVPLLSNEKCOQOQPEX---NTTENMKCAGYE-EGGI 979
 QY 659 DICTATGTGIAAVSPFGRASPEPRMHLMLGLVMSYDKTCSHRLSTAFTVLPFKWIE 716
 DB 960 DSCGDSG-----PLMKLENNRMLLAGVTSFGYCALPNR-PCGYARVAPKFTMTIQ 1030
 RESULT 12
 JX0210
 protein C (activated) (EC 3.4.21.69) precursor - mouse
 N:Alternate names: vitamin K-dependent serine proteinase
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: JX0210
 R:Tada, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.
 J. Biochem. 111, 491-495, 1992
 A:Title: Isolation and characterization of a mouse protein C cDNA.
 A:Reference number: JX0210; MUID:92316897; PMID:1618739
 A:Accession: JX0210
 A:Molecule type: mRNA
 A:Residues: 1-461 <TAB>
 A:Cross-references: UNIPROT:P33587; UNIPARC:UPI0000027800; GB:D10445; NID:g220385; PIND:
 A:Experimental source: liver
 C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re
 8.
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam
 F:1-33/Domain: signal sequence #status predicted <SIG>
 F:27-85/Domain: Gla domain homology <Gla>
 F:34-41/Domain: propeptide #status predicted <PRO>
 F:42-196/199-461/Product: protein C #status predicted <PRC>
 F:42-196/Domain: light chain #status predicted <PCL>
 F:91-130/Domain: EGF homology <EG1>
 F:139-174/Domain: EGF homology <EG2>
 F:199-461/Domain: heavy chain #status predicted <PCH>
 F:199-211/Domain: activation peptide #status predicted <ACT>
 F:212-461/Product: vitamin K-dependent serine proteinase #status predicted <VIT>
 F:212-445/Domain: trypsin homology <TRY>
 F:47 48 55 57 60 61 66 67 70 76/Modified site: gamma-carboxylglutamic acid (Glu) #status
 F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
 F:121-130,139-150,146-159,161-174,182-219,238-254,373-387,398-426/Disulfide bonds: #stat
 F:214,290,355/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:253,299,402/Active site: His, Asp, Ser #status predicted
 Query Match 8.1%; Score 320; DB 1; Length 461;
 Best Local Similarity 23.9%; Pred. No. 4,2e-14;
 Matches 145; Conservative 70; Mismatches 174; Indels 218; Gaps 29;
 QY 152 WT-----HAKGPF-----VIOLEFVLSLEFDYMCQYDVEVRDNDNRGOIKRV 198
 DB 14 MGISSTIRPHDPVFSSESHAHQVLAVRANSFL-----EMREC-SLERCEMEIRI 62
 QY 199 CGNERPADT-OSIGSSLHLVPHSDSKNPFGEFHAITEITACSSPPCFHDTGVLDKAGS 257
 DB 63 CDFEBAQRIQVNVEDTLAFWI-----KYFDGQCSAPRLDHCDBPCCHGTIC-DGIGS 116
 QY 258 YKCACTAGYTGRCNMLEBRVCSDPGCRVNGYKQITGPGI-----INGHAATGIVV 311
 DB 117 FSCSCDKMEGKFCQQLERFQDC-----RVNNGGCLAHYCLIESNGRCA----- 160
 QY 312 SFFCNSVYLSGNER-----TCQNGEMSGKOPICIKACREPKISDLVRRVLPQV 364
 DB 161 ---CAPGELADNHRKSTNVFPGCKLGRWLEK-----KRLK----- 196
 QY 365 QSRETPLHOLYSAAFSKQKLGAPTKKRALPFGDLPMGYQHLTQLQYECISPPYRRLGS 424
 DB 197 -KRDTL-----EDLELBDP----- 210

QY 425 SRRTCLRTGKMGSRAPSCIPICIKIENTTAPKTOGLRMPQAAIYRTSGVHDSLHKGA 484
 DB 211 -----RIVNGTLTK-QG-DSWQAILL-----DSKCK-- 235
 QY 485 WFLVSGALVNERTVVAACHVTDLGKVTMTKTAQKLVYLGKPYRDDDEKTIQSLQIS 544
 DB 236 --LACGGVLIRHSWVLTAAHCVEGTRKLT-----VILGEY--DLRRRDHWELELDIK 283
 QY 545 AIIHPNDPILLDADIALIKLADKARISTRVQICL-----AASRLDSTFSQESH1TVAG 600
 DB 284 ELIVHNPTRSSSDNDIALRLAQPATLSKTIVPICLPNNGLAQOELTQAGGETVLT--G 341
 QY 601 WNVLDVRSPPGFKNDRILRSQVSVVDSLLCEBQEDHEDGIVSVTDNNFCSWETAPS 649
 DB 342 MCGQSDRIKDGRRNRTFILTRIRPLVARNCEVEMKRV-----VSENMIC 387
 QY 650 ASWETAPSDICTATGTGIAAVSPFGRASPEPRMHLMLGLVMSYDKTCSHRLSTA-FTKV 708
 DB 388 AGIIGNT-RDACDGDGSGGPMVVFVRG-----TWFLVGLVSWG--EGCGHTNNYGYITKV 438
 QY 709 LPFKDWT 715
 DB 439 GSYLTKMI 445
 RESULT 13
 A43090
 enteropeptidase (EC 3.4.21.9) precursor [validated] - bovine
 N:Alternate names: enterokinase
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: A43090; A48874; A61436
 R:Kitamoto, Y.; Yuan, X.; Wu, Q.; McCourt, D.W.; Sadler, J.E.
 Proc. Natl. Acad. Sci. U.S.A. 91, 7588-7592, 1994
 A:Title: Enterokinase, the initiator of intestinal digestion, is a mosaic protease compo
 A:Reference number: A43090; MUID:94329561; PMID:8052624
 A:Accession: A43090
 A:Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1035 <KIT>
 A:Cross-references: UNIPROT:P98072; UNIPARC:UPI000004BBB5; GB:U09859; NID:g746410; PIND:
 A:Experimental source: small intestine
 R:Alavallie, E.R.; Rehmetulla, A.; Reale, L.A.; DiBlasio, E.A.; Ferez, C.; Grant, K.L.; I
 J. Biol. Chem. 268, 23311-23317, 1993
 A:Title: Cloning and functional expression of a cDNA encoding the catalytic subunit of b
 A:Reference number: A48874; MUID:94043122; PMID:8226855
 A:Accession: A48874
 A:Molecule type: mRNA
 A:Residues: 801-1035 <LAV>
 A:Cross-references: UNIPARC:UPI00001133D; GB:U19663; NID:g416131; PIND:AAA16035.1; PID:
 A:Note: parts of this sequence, including the amino end of the mature protein, were confi
 R:Light, A.; Janska, H.
 J. Protein Chem. 10, 475-480, 1991
 A:Title: The amino-terminal sequence of the catalytic subunit of bovine enterokinase.
 A:Reference number: A61436; MUID:92189715; PMID:1799406
 A:Accession: A61436
 A:Molecule type: protein
 A:Residues: 801-807, 'Y', 809-827 <LIG>
 A:Cross-references: UNIPARC:UPI00001468A0
 C:Comment: The mechanism of association with the membrane of the intestinal brush border
 membrane attachment using a signal-anchor sequence.
 C:Complex: conversion from membrane-bound to soluble forms may involve further processing
 C:Function: mature enteropeptidase is variously reported to contain two (heavy and light)
 C:Function: cleaves propeptide from trypsinogen to produce active trypsin
 A:Pathway: intestinal digestive hydrolase cascade
 C:Superfamily: enteropeptidase, C1/C1s repeat homology; LDL receptor ligand-binding rep
 C:Keywords: glycoprotein; hydrolyase; intestine; serine proteinase; transmembrane protein;
 F:52-117/Domain: transmembrane #status predicted <TM>
 F:52-117/Product: enteropeptidase mini chain #status predicted <MCH>
 F:118-800/Product: enteropeptidase heavy chain #status predicted <HCH>

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2006, 06:49:46 ; Search time 304 Seconds
(without alignments)
2190.826 Million cell updates/sec

Title: US-10-063-546-38
Perfect score: 3945
Sequence: 1 MELGWTQLGLTFLQLLIS.....LSTAFKYLPRKWIERNMK 720

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : UniProt_7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3945	100.0	720	2	Q6UXH9 HUMAN
2	3941	99.9	720	2	O5JPI4 HUMAN
3	3936	99.8	720	2	O6N062_HUMAN
4	3926.5	99.5	737	2	O5EBL7_HUMAN
5	3921.5	99.4	737	2	O6UJW2_HUMAN
6	3898	98.8	720	2	O5RDI1_PONPY
7	3616	91.7	720	2	O5E9P5_BOVIN
8	3612	91.6	720	2	O8BU25_MOUSE
9	3612	91.6	720	2	O8K2B8_MOUSE
10	2823	71.6	722	2	O6DIV5_XENTR
11	2059	59.7	417	2	O7IRB9_HUMAN
12	1566	39.7	1009	2	O4SAP4_TETNG
13	1122.5	28.5	488	2	O4SHD4_TETNG
14	949	24.1	181	2	O9Y432_HUMAN
15	678	17.2	1019	1	O8T9S1_TACTR
16	672	17.0	1019	1	LFC_TACTR
17	665	16.9	1019	1	LFC_CARRO
18	665	15.9	1083	2	O26423_CARRO
19	608.5	15.4	680	2	O868H7_BRABE
20	604	15.3	680	2	O868H5_BRABE
21	597	15.1	688	2	O868H6_BRABE
22	576.5	14.6	688	2	O868H4_BRABE
23	507.5	12.9	698	2	O6GPF9_XENLA
24	490.5	12.4	730	2	O6QIQ8_CHICK
25	489.5	12.4	698	2	O9PU71_XENLA
26	483	12.2	701	2	O9JJS9_RAT
27	482.5	12.2	703	2	O8CHN8_RAT
28	482	12.2	717	2	O8AXR1_XENLA
29	478	12.1	699	1	MASPI1_HUMAN
30	475	12.0	704	1	MASPI1_MOUSE
31	468	11.9	728	2	O96RS4_HUMAN

32	467	11.8	697	2	O8CG43_RAT	O8CG43 rattus norv
33	466	11.8	717	2	O8AXR0_XENLA	O8AXR0 xenopus lae
34	459	11.6	733	2	O8CD27_MOUSE	O8CD27 mus musculu
35	457	11.6	719	2	O9PVY2_TRISC	O9PVY2 trielkie scy
36	452	11.5	733	2	O920S0_MOUSE	O920S0 mus musculu
37	450.5	11.4	687	2	O5XHB9_XENTR	O5XHB9 xenopus tro
38	448	11.4	745	2	O9PVY3_CYPCA	O9PVY3 cyprinus ca
39	447	11.3	686	2	O6QIQ9_CHICK	O6QIQ9 gallus gall
40	436.5	11.1	681	2	O7ET70_LAMJA	O7ET70 lampetra ja
41	432.5	11.0	745	2	O4SB45_TETNG	O4SB45 tetraodon n
42	428	10.8	707	1	C1RA_MOUSE	O8EG16 mus musculu
43	428	10.8	707	2	O56616_MOUSE	O56616 mus musculu
44	423	10.7	685	1	MASP2_RAT	O9J188 r mannan-bl
45	422.5	10.7	713	2	O5DVT1_EPRBU	O5DVT1 epactreus lae
46	421.5	10.7	688	2	O9PVY4_XENLA	O9PVY4 xenopus lae
47	417	10.6	685	1	MASP2_MOUSE	O91WP0 m mannan-bl
48	416.5	10.6	706	1	C1RB_MOUSE	O8CT99 mus musculu
49	414	10.5	708	2	O2VPN1_XENLA	O2VPN1 xenopus lae
50	404.5	10.3	705	2	O5JHT9_HUMAN	O5JHT9 homo sapien
51	403.5	10.2	705	1	C1R_HUMAN	P00736 homo sapien
52	403.5	10.2	705	2	O6BD77_HUMAN	O6BD77 homo sapien
53	401.5	10.2	496	2	O8CHP7_CAVPO	O8CHP7 cavia porce
54	401.5	10.2	746	2	O8TAD8_HALRO	O8TAD8 halocynthia
55	400.5	10.2	686	1	MASP2_HUMAN	O00187 h mannan-bl
56	400.5	10.2	746	2	O01654_HALRO	O01654 halocynthia
57	398.5	10.1	686	2	O9DGC2_CYPCA	O9DGC2 cyprinus ca
58	395.5	10.0	705	2	O5JHU9_HUMAN	O5JHU9 homo sapien
59	395	10.0	721	2	O7ET69_LAMJA	O7ET69 lampetra ja
60	394.5	10.0	705	1	C1R_PANTR	O51W43 pan troglod
61	394.5	10.0	705	1	C1R_PONPY	O51W44 pongo pygma
62	390.5	9.9	702	2	O4SNB6_TETNG	O4SNB6 tetraodon n
63	390.5	9.9	705	2	O4R577_MACFA	O4R577 macaca fasc
64	384	9.7	688	1	C51B_MOUSE	O8CF68 mus musculu
65	382.5	9.7	752	2	O01655_HALRO	O01655 halocynthia
66	382	9.7	722	2	O8AW90_LAMJA	O8AW90 lampetra ja
67	381	9.6	722	2	O9PSZ5_LAMJA	O9PSZ5 lampetra ja
68	378.5	9.6	695	1	CASF_MESAU	P15156 meoscoricetu
69	378	9.6	676	2	O4SB51_TETNG	O4SB51 tetraodon n
70	373.5	9.5	688	2	O4SNB7_TETNG	O4SNB7 tetraodon n
71	373.5	9.5	752	2	O8TAD7_HALRO	O8TAD7 halocynthia
72	368	9.3	685	2	O9DGC1_CYPCA	O9DGC1 cyprinus ca
73	366	9.3	685	2	O9DGC0_CYPCA	O9DGC0 cyprinus ca
74	364	9.2	688	1	C51A_MOUSE	O8CG14 mus musculu
75	364	9.2	685	2	O6UUT6_CYPCA	O3V5G0 cyprinus ca
76	359	9.1	675	2	O91674_XENLA	O91674 xenopus lae
77	357	9.0	676	2	O6UUT5_CYPCA	O6UUT5 cyprinus ca
78	354	9.0	1524	2	O91674_XENLA	O91674 xenopus lae
79	346	8.8	690	2	O5E3N3_CHICK	O5E3N3 gallus gall
80	340.5	8.6	688	1	C1S_RAT	O6E6T1 rattus norv
81	340	8.6	688	2	O3T5K1_MOUSE	O3T5K1 mus musculu
82	339.5	8.6	707	2	O7OWJ1_ONCMY	O7OWJ1 oncorhynch
83	337.5	8.6	479	2	O5HYM1_HUMAN	O5HYM1 homo sapien
84	337.5	8.6	668	2	O7EY92_ANOGA	O7EY92 anopheles g
85	335	8.5	606	2	O69BLO_MANSE	O69BLO brachydanio
86	334	8.5	503	2	O8AYE4_BRABE	O8AYE4 brachydanio
87	334	8.5	688	1	C1S_HUMAN	P09891 homo sapien
88	333	8.4	730	2	O4RH70_TETNG	O4RH70 tetraodon n
89	331.5	8.4	1019	2	ENTK_HUMAN	P98073 homo sapien
90	331.5	8.4	1019	2	O2NKLT_HUMAN	O2NKLT homo sapien
91	330.5	8.4	1034	1	ENTK_PIG	P98074 sus scrofa
92	329.5	8.4	3565	1	CSMDI1_HUMAN	O96PZ7 homo sapien
93	329	8.3	3564	1	CSMDI1_MOUSE	O92313 mus musculu
94	328.5	8.3	2966	2	O59FF6_HUMAN	O59FF6 mus sapien
95	328	8.3	855	1	ST14_HUMAN	O9J5Y6 homo sapien
96	325	8.2	483	1	FA10_TROCA	O4XCT9 ratiopichis
97	324	8.2	3564	1	O45NC2_RAT	O45NC2 rattus norv
98	319.5	8.1	455	1	FA10V_TROCA	P81428 trochichis
99	318.5	8.1	445	2	O4F875_TROCA	O4F875 trochichis
100	318	8.1	3487	1	CSMD2_HUMAN	O7Z408 homo sapien
101	318	8.1	3631	2	O53TV4_HUMAN	O53TV4 homo sapien
102	317.5	8.0	455	2	O58L92_HOPST	O58L92 holocephal
103	317.5	8.0	1035	2	ENTK_BOVIN	P98072 bos taurine
104	316.5	8.0	460	1	PROC_MOUSE	P33587 m vitamin k

105	315	8.0	444	1	FA7_RABIT	P98139	oryctolagus	178	281	7.1	483	2	Q3MH2_BOVIN	Q3mh2	bos taurus
106	314.5	8.0	454	2	Q58L93_PSEPO	Q58193	pseudocichis	179	281	7.1	492	1	FA10_BOVIN	P00743	bos taurus
107	314.5	8.0	475	1	FA10_CHICK	P25155	gallus galli	180	281	7.1	492	2	Q3TDB9_MOUSE	Q3tdb9	bos taurus
108	314	8.0	855	1	ST14_MOUSE	P56677	mus musculus	181	281	7.1	493	2	Q3U3V1_MOUSE	Q3u3v1	m musculus
109	314	8.0	855	2	Q543E3_MOUSE	Q543e3	m 0 day neo	182	280.5	7.1	264	1	CTRL_HUMAN	P40113	homo sapien
110	313	7.9	855	2	Q9J177_RAT	Q9j177	rattus norv	183	280.5	7.1	269	2	Q81UW0_HUMAN	P08750	homo sapien
111	312.5	7.9	885	2	Q32N65_XENLA	Q32n65	xenopus lae	184	280	7.1	562	1	TPA_HUMAN	P08750	homo sapien
112	312	7.9	467	2	Q58L95_OXYMI	Q58195	oxytratus m	185	278.5	7.1	466	1	FA7_HUMAN	P08750	homo sapien
113	311	7.9	446	1	FA7_RAT	Q773B6	brachydantio	186	278.5	7.1	466	2	Q5JVF2_HUMAN	Q5jvf2	homo sapien
114	310.5	7.9	434	2	Q773B6_BRARE	Q773b6	brachydantio	187	278.5	7.1	824	2	Q61CC2_HUMAN	Q61cc2	homo sapien
115	310.5	7.9	453	1	Q58L94_9SAUR	Q58194	notechis bc	188	278	7.0	408	2	Q9YW15_DROME	Q9ywl5	drosophila
116	310.5	7.9	461	1	PROC_HUMAN	P04070	h vitamin k	189	278	7.0	433	2	Q804X5_CHICK	P00742	homo sapien
117	310.5	7.9	461	2	Q53S74_HUMAN	Q53s74	homo sapien	190	278	7.0	488	1	FA10_HUMAN	P00742	homo sapien
118	309.5	7.8	689	2	Q4VA78_XENTR	Q4va78	xenopus tiro	191	278	7.0	488	2	Q5JVE7_HUMAN	Q5jve7	homo sapien
119	309.5	7.8	799	1	TMPS6_MOUSE	Q9db10	mus musculus	192	278	7.0	562	2	Q503B0_HUMAN	Q503b0	homo sapien
120	309.5	7.8	799	2	Q6PE94_MOUSE	Q6pe94	mus musculus	193	278	7.0	1113	1	CORIN_MOUSE	P98219	mus musculus
121	309.5	7.8	811	2	Q3KN88_MOUSE	Q3kn88	mus musculus	194	277	7.0	559	1	TPA_RAT	P19637	rattus norv
122	305	7.7	456	1	PROC_CANFA	Q28278	c vitamin k	195	277	7.0	562	2	Q5R8J0_PONPY	Q5r8j0	pongo pygma
123	304	7.7	1069	1	ENTR_MOUSE	P97435	mus musculus	196	276.5	7.0	264	2	Q5JFV9_HUMAN	Q5jfv9	homo sapien
124	302.5	7.7	446	1	FA7_MOUSE	P70375	mus musculus	197	276.5	7.0	625	2	Q3MHK7_BOVIN	Q3mhk7	bos taurus
125	302.5	7.7	446	2	Q54ZC2_MOUSE	Q54Zc2	m b6-derivate	198	276.5	7.0	655	1	HGFA_HUMAN	Q04756	homo sapien
126	301.5	7.6	433	2	Q8UHD0_BRARE	Q8jhd0	brachydantio	199	276.5	7.0	655	2	Q53X47_HUMAN	Q53x47	homo sapien
127	300.5	7.6	463	2	Q6T110_PSETE	Q6t110	pseudonaja	200	276.5	7.0	679	2	Q6EPQ8_HUMAN	Q6epq8	homo sapien
128	299.5	7.6	433	2	Q504H3_BRARE	Q504h3	brachydantio	201	276	7.0	559	2	Q6E7U0_HUMAN	Q6e7u0	m plaeimnog
129	299.5	7.6	467	2	Q6T109_PSETE	Q6t109	pseudonaja	202	275.5	7.0	444	2	Q5JVF1_HUMAN	Q5jvf1	homo sapien
130	299	7.6	1111	2	Q80YN4_RAT	Q80yn4	rattus norv	203	275.5	7.0	498	2	Q4RP66_TETNG	Q4rp66	tetracodon n
131	298.5	7.6	433	2	Q90YK1_BRARE	Q90yk1	brachydantio	204	275.5	7.0	655	2	Q2M1W7_HUMAN	Q2m1w7	homo sapien
132	298.5	7.6	553	2	Q6P7K1_XENLA	Q6p7k1	xenopus lae	205	275.5	7.0	1134	2	Q7RTY7_HUMAN	Q7rty7	homo sapien
133	298	7.6	449	2	Q56VRS_PSETE	Q56vrs	pseudonaja	206	275.5	7.0	3247	2	Q4RFCL_TETNG	Q4rfcl	tetracodon n
134	297.5	7.5	777	2	Q8C8N9_MOUSE	Q8c8n9	mus musculus	207	275	7.0	497	2	Q4SVF9_TETNG	Q4svf9	tetracodon n
135	297.5	7.5	3239	2	Q4S0Y8_TETNG	Q4s0y8	tetracodon n	208	275	7.0	1047	2	Q566K6_MOUSE	Q566k6	mus musculus
136	297	7.5	456	2	Q5FVZ2_XENTR	Q5fvz2	xenopus tiro	209	274.5	7.0	445	2	Q504J5_BRARE	Q504j5	brachydantio
137	297	7.5	459	1	PROC_PIG	Q9g1p2	s vitamin k	210	274.5	7.0	547	2	Q5BKJ3_XENTR	Q5bkj3	xenopus tiro
138	296	7.5	458	1	PROC_PIG	Q28661	o vitamin k	211	274.5	7.0	566	2	Q2KJG9_BOVIN	Q2kjg9	bos taurus
139	296	7.5	485	2	Q4VA71_XENTR	Q4va71	xenopus tiro	212	274.5	7.0	625	1	THRB_BOVIN	P00735	bos taurus
140	295.5	7.5	336	2	Q8C1R5_MOUSE	Q8c1r5	mus musculus	213	274.5	7.0	654	1	HGFA_CANFA	Q6m9f4	canis fam1
141	295.5	7.5	441	2	Q804X2_FUGRU	Q804x2	fugu rubrip	214	274.5	7.0	1235	2	Q659T9_CIOIN	Q659t9	clona intes
142	295.5	7.5	505	2	Q4SB52_TETNG	Q4sb52	tetracodon n	215	274.5	7.0	3670	1	CSMD3_HUMAN	Q74C07	homo sapien
143	295	7.5	425	2	Q804X7_CHICK	Q804x7	gallus galli	216	273.5	6.9	443	2	H8JHC9_BRARE	Q8jh9c	brachydantio
144	294	7.5	461	2	Q68FY8_RAT	Q68fy8	rattus norv	217	273.5	6.9	517	2	Q3V1J8_MOUSE	Q3v1j8	bos taurus
145	293.5	7.4	364	2	Q4G030_RAT	Q4g030	rattus norv	218	273.5	6.9	566	1	TPA_BOVIN	Q28198	bos taurus
146	293.5	7.4	407	1	FA7_BOVIN	P22457	bos taurus	219	273	6.9	394	2	Q5SIX0_IKOSC	Q5slix0	ixodes scap
147	293.5	7.4	446	2	Q3BU75_CANFA	Q3bu75	canis fam1	220	273	6.9	560	1	HABP2_HUMAN	Q14520	h hyaluron
148	293.5	7.4	447	2	Q58DL3_BOVIN	Q58dl3	bos taurus	221	273	6.9	2796	1	CSMD3_MOUSE	Q80C79	mus musculus
149	293.5	7.4	1331	2	Q4S572_TETNG	Q4s572	tetracodon n	222	273	2972	2	Q4S1Z1_TETNG	Q4s1z1	tetracodon n	
150	293	7.4	430	2	Q804X0_FUGRU	Q804x0	fugu rubrip	223	272.5	6.9	321	2	Q6M2L2_HUMAN	Q6m2l2	homo sapien
151	292	7.4	461	1	PROC_RAT	P31394	r vitamin k	224	271.5	6.9	244	1	KIK6_HUMAN	Q92876	homo sapien
152	291.5	7.4	390	2	Q69DJ3_PIG	Q69dj3	bos taurus	225	271.5	6.9	244	2	Q6H301_HUMAN	Q6h301	homo sapien
153	291	7.4	475	2	Q804M9_FUGRU	Q804m9	fugu rubrip	226	271.5	6.9	461	2	Q61E64_RAT	Q61e64	rattus norv
154	290	7.4	464	1	Q5FW21_XENTR	Q5fw21	xenopus tiro	227	271	6.9	433	2	Q8MHY7_RABIT	Q8mhy7	oryctolagus
155	289.5	7.3	466	1	FA9_FELICA	Q6ea95	felis silve	228	271	6.9	433	2	Q8MHY7_RABIT	Q8mhy7	oryctolagus
156	287.5	7.3	802	1	TMPS6_HUMAN	Q6u180	homo sapien	229	271	6.9	559	1	TPA_MOUSE	P11214	mus musculus
157	287.5	7.3	980	2	Q6ETN7_BUPAR	Q6etn7	bute arenar	230	270.5	6.9	375	2	Q5WIK5_NITLU	Q5wik5	nitellu
158	287	7.3	467	2	Q58L96_9SAUR	Q58l96	oxytratus b	231	270.5	6.9	1022	2	Q4T9V1_TETNG	Q4t9v1	tetracodon n
159	287	7.3	504	2	Q4V971_BRARE	Q4v971	brachydantio	232	270	6.8	477	1	URTL_DEBRO	Q4t9v1	tetracodon n
160	285.5	7.2	452	1	FA9_CANFA	P19540	canis fam1	233	270	6.8	490	1	FA10_RABIT	Q19045	deemodus ro
161	285	7.2	504	2	Q6EGM7_BRARE	Q6egm7	brachydantio	234	269	6.8	261	2	Q6DHD9_BRARE	Q6dhd9	brachydantio
162	284	7.2	432	2	Q6GNA2_XENLA	Q6gna2	xenopus lae	235	269	6.8	265	2	Q561U4_BRARE	Q561u4	brachydantio
163	284	7.2	974	2	Q90WD8_BUFJA	Q90wd8	bute japoni	236	269	6.8	643	2	Q97506_PIG	Q97506	bos taurus
164	283.5	7.2	482	1	FA10_RAT	Q63207	rattus norv	237	269	6.8	833	2	Q96442_STRPU	Q96442	strongyloce
165	283.5	7.2	589	2	Q6UJAS_HUMAN	Q6ujas	homo sapien	238	268.5	6.8	833	2	Q8E077_XENLA	Q8e077	xenopus lae
166	283	7.2	376	1	FA10V_HOPST	Q83170	hoplcephal	239	268	6.8	558	1	HABP2_BOVIN	Q56929	h hyaluron
167	282.5	7.2	320	2	Q8C1R7_RAT	Q8c1r7	rattus norv	240	268	6.8	558	2	Q3MHK6_BOVIN	Q3mhk6	bos taurus
168	282.5	7.2	636	2	Q2KJ63_BOVIN	Q2kj63	bos taurus	241	268	6.8	740	2	Q4T8J3_TETNG	Q4t8j3	tetracodon n
169	282	7.1	456	1	PROC_BOVIN	P00745	b vitamin k	242	267.5	6.8	268	2	Q6GQ89_XENLA	Q6gq89	xenopus lae
170	282	7.1	469	2	Q9GMD9_ORNAN	Q9gmd9	ornithorhyn	243	267	6.8	455	2	Q7S1E6_XENLA	Q7s1e6	xenopus lae
171	282	7.1	1466	2	Q7Z241_BRARE	Q7z241	brachydantio	244	267	6.8	463	2	Q5M8Y0_XENTR	Q5m8y0	xenopus tiro
172	281.5	7.1	476	2	Q6GLK4_XENLA	Q6glk4	xenopus lae	245	267	6.8	868	2	Q9Y1V3_POLMI	Q9y1v3	polyandroc
173	281.5	7.1	558	1	HABP2_MOUSE	Q80Cdc	m hyaluron	246	266.5	6.8	441	2	Q4SUJ2_TETNG	Q4suj2	tetracodon n
174	281.5	7.1	558	1	HABP2_RAT	Q61711	r hyaluron	247	266	6.7	352	2	Q7KWM3_DROME	Q7kwm3	drosophila
175	281	7.1	481	1	FA10_MOUSE	Q88947	mus musculus	248	266	6.7	359	2	Q4SUG9_TETNG	Q4sug9	tetracodon n
176	281	7.1	481	1	Q3TBR2_MOUSE	Q3tbr2	m mod-deriv	249	266	6.7	889	2	Q5GCC1_CARRO	Q5gcc1	carcinogeor
177	281	7.1	481	2	Q4FJST_MOUSE	Q4fjst	m musculus	250	265.5	6.7	250	2	Q9V514_DROME	Q9v514	drosophila

251	265.5	6.7	264	2	Q4SEW3	tetracton n	324	253	6.4	1070	2	P91972	APLCA	P91972	aplysia cal
252	265	6.7	311	2	Q50214	brachydanto	325	253.5	6.4	241	2	Q4QY79	SPAU	Q4QY79	spatue aura
253	265	6.7	2	Q4SUAT	TEING	Q4suat tetracton n	326	252.5	6.4	487	2	Q53GX9	HUMAN	Q53GX9	homo sapien
254	264.5	6.7	431	1	URTB	DESRO	327	252	6.4	260	2	Q6P2Y9	XENTR	Q6P2Y9	xenopus tro
255	264.5	6.7	618	1	THRB	MOUSE	328	252	6.4	261	2	Q6H9E	BRARE	Q6H9E	brachydanto
256	264.5	6.7	618	1	Q3U94	MOUSE	329	252	6.4	600	2	Q5R976	PONPY	Q5R976	pongo pygma
257	264	6.7	653	1	HGPA	MOUSE	330	252	6.4	607	2	Q6DFJ5	XENLA	Q6DFJ5	xenopus lae
258	264	6.7	653	2	Q545J3	MOUSE	331	251.5	6.4	267	2	Q7PG94	ANOCA	Q7PG94	anophelis g
259	264	6.7	653	2	Q5EBA7	RAT	332	251	6.4	263	2	Q51029	XENTR	Q51029	xenopus tro
260	264	6.7	910	2	Q4RBD7	TEING	333	251	6.4	295	2	Q8C1P7	RAT	Q8C1P7	rattus norv
261	263.5	6.7	263	2	Q7SX97	BRARE	334	251	6.4	343	2	Q504K1	BRARE	Q504K1	brachydanto
262	263	6.7	431	2	Q53X83	HUMAN	335	251	6.4	407	2	Q7QK1	ANOCA	Q7QK1	anophelis g
263	263	6.7	431	2	Q5SW9	HUMAN	336	251	6.4	537	2	Q804W8	FUGRU	Q804W8	fugu rubrip
264	263	6.7	431	2	Q8VCS4	MOUSE	337	251	6.4	1215	2	Q4H2P2	CIOIN	Q4H2P2	ciona inte
265	263	6.7	3239	2	Q4S1T9	TEING	338	250.5	6.3	347	1	HPT	RABIT	HPT	RABIT
266	262.5	6.7	300	2	Q819P4	AURAU	339	250.5	6.3	548	2	Q502D2	BRARE	Q502D2	brachydanto
267	262.5	6.7	461	1	FAS	HUMAN	340	250.5	6.3	875	1	NETR	PANTR	NETR	PANTR
268	262.5	6.7	461	1	FAS	PANTR	341	250	6.3	306	1	BSSP4	MOUSE	Q5E271	pan trogliod
269	262.5	6.7	461	2	Q5JYJ8	HUMAN	342	250	6.3	562	2	Q8SQ23	PIG	Q5E271	pan trogliod
270	262.5	6.7	1042	1	CORIN	HUMAN	343	250	6.3	845	2	Q63Z06	XENLA	Q63Z06	xenopus lae
271	262.5	6.7	1042	2	Q2TBD2	HUMAN	344	250	6.3	1379	2	Q9V4N6	DROME	Q9V4N6	drosophila
272	262	6.6	477	1	URT2	DESRO	345	250	6.3	1397	2	Q7KQ9	DROME	Q7KQ9	drosophila
273	262	6.6	653	2	Q3TDB	MOUSE	346	249.5	6.3	400	2	Q27081	TRACTR	Q27081	rachypne
274	261.5	6.6	284	2	Q8AXQ8	XENLA	347	249.5	6.3	435	2	Q4TBY8	TEING	Q4TBY8	tetracton n
275	261.5	6.6	442	1	UROK	PIG	348	249.5	6.3	875	1	NETR	HUMAN	Q6GP11	homo sapien
276	261	6.6	431	1	UROK	HUMAN	349	249	6.3	263	2	Q9CR35	MOUSE	Q9CR35	m adult mal
277	261	6.6	431	1	UROK	BOVIN	350	249	6.3	328	2	Q3UEP7	MOUSE	Q3UEP7	mus musculu
278	261	6.6	969	2	Q5KQJ1	MACFA	351	249	6.3	409	1	FAS	PIG	P1E293	sus scrofa
279	260.5	6.6	264	2	Q5E0Z8	RAT	352	249	6.3	548	2	Q5MPB5	MANSE	Q5MPB5	manduca sex
280	260.5	6.6	456	2	Q7TT43	MOUSE	353	249	6.3	401	2	Q4QY73	SPAU	Q4QY73	spatue aura
281	260.5	6.6	482	2	Q6PAG2	XENLA	354	248.5	6.3	241	2	Q4RG83	TEING	Q4RG83	tetracton n
282	260.5	6.6	482	2	Q3UZ05	MOUSE	355	248.5	6.3	401	2	FAS	MOUSE	P1E294	mus musculu
283	260.5	6.6	482	2	Q3V013	MOUSE	356	248.5	6.3	459	1	Q7O137	ANOCA	Q7O137	anophelis g
284	260.5	6.6	1042	2	Q5KQJ2	MACFA	357	248.5	6.3	744	2	Q5R729	PONPY	Q5R729	pongo pygma
285	260	6.6	431	2	Q5R729	PONPY	358	248.5	6.3	876	1	NETR	GORCO	NETR	GORCO
286	259	6.6	245	1	CTRB	GADMO	359	248	6.3	259	2	Q6AZC2	BRARE	Q6AZC2	brachydanto
287	259	6.6	416	1	FAS	BOVIN	360	248	6.3	261	2	Q9W7Q4	PAROL	Q9W7Q4	parallachthy
288	259	6.6	474	2	Q8JHC8	BRARE	361	248	6.3	638	2	CTRB1	HUMAN	P17538	homo sapien
289	259	6.6	581	2	Q9XZM7	STRPU	362	248	6.3	540	2	Q800V7	MELGA	Q800V7	melleagris g
290	259	6.6	1005	2	Q5KQJ2	MACFA	363	248	6.3	638	2	KLKBL	HUMAN	P03952	homo sapien
291	258.5	6.6	255	2	Q7QC55	ANOCA	364	248	6.3	764	1	Q4WEC3	HUMAN	Q4WEC3	homo sapien
292	258.5	6.6	411	2	Q5PY49	homo sapien	365	248	6.3	775	2	Q6P550	MOUSE	Q6P550	mus musculu
293	258.5	6.6	787	1	STUB	DROME	366	248	6.3	991	2	Q6NZM2	MOUSE	Q6NZM2	mus musculu
294	258	6.5	263	2	Q5PMW6	GADMO	367	248	6.3	307	2	Q7TML0	MOUSE	Q7TML0	mus musculu
295	258	6.5	433	1	UROK	PAPCV	368	247.5	6.3	311	2	Q9W2C2	DROME	Q9W2C2	drosophila
296	258	6.5	444	2	Q5MPB9	MANSE	369	247.5	6.3	991	1	BMP1	MOUSE	P9E063	mus musculu
297	258	6.5	612	2	Q804W7	FUGRU	370	247.5	6.3	235	2	Q287J31	RABIT	Q287J31	oryctolagus
298	257.5	6.5	580	2	Q501G7	ORYLA	371	247	6.3	275	1	TRYT	CANPA	P15944	canis faml
299	257.5	6.5	607	2	Q4QRS3	XENLA	372	247	6.3	364	2	Q917V4	DROME	Q917V4	drosophila
300	257.5	6.5	1004	2	P79953	XENLA	373	247	6.3	386	2	Q81924	BOMO	Q81924	bombyx mori
301	257	6.5	273	2	Q7Q812	ANOCA	374	247	6.3	764	1	CPAB	HUMAN	P00751	homo sapien
302	257	6.5	607	2	Q5FW1	XENTR	375	247	6.3	764	1	Q5JF89	HUMAN	Q5JF89	homo sapien
303	256.5	6.5	999	2	Q5H876	CIOIN	376	247	6.3	764	2	Q5JP67	HUMAN	Q5JP67	homo sapien
304	256.5	6.5	264	2	Q9D7P8	MOUSE	377	247	6.3	764	2	Q5ST50	HUMAN	Q5ST50	homo sapien
305	256.5	6.5	264	2	Q9ER05	MOUSE	378	247	6.3	986	1	BMP1	HUMAN	P13497	homo sapien
306	256.5	6.5	453	2	Q4SUAL	TEING	379	247	6.3	235	2	Q9D960	CYNPY	Q9D960	cynops pyrr
307	256	6.5	243	2	Q7PWB3	ANOCA	380	246.5	6.2	264	2	Q9D960	MOUSE	Q9D960	mus musculu
308	255.5	6.5	268	2	Q642S8	XENTR	381	246.5	6.2	297	2	Q88781	RATRT	Q88781	rattus ratc
309	255.5	6.5	763	2	Q31430	LAMJA	382	246.5	6.2	622	2	Q53H04	HUMAN	Q53H04	homo sapien
310	255	6.5	325	2	Q15944	SARPE	383	246.5	6.2	622	2	Q53H06	HUMAN	Q53H06	homo sapien
311	255	6.5	845	2	Q6GR54	XENLA	384	246.5	6.2	347	1	HPT	ATEGE	P45417	ateles geof
312	254.5	6.5	315	2	Q7TT44	MOUSE	385	246.5	6.2	418	2	Q4RE72	MACFA	Q4RE72	macaca fasc
313	254.5	6.5	461	2	Q9SND6	PANTR	386	246.5	6.2	486	2	Q5PRA6	BRARE	Q5PRA6	brachydanto
314	254	6.4	314	2	Q9VR15	DROME	387	246.5	6.2	622	1	THRB	HUMAN	P00734	homo sapien
315	254	6.4	617	1	THRB	RAT	388	246.5	6.2	622	2	Q4QZ40	HUMAN	Q4QZ40	homo sapien
316	254	6.4	998	2	Q5H875	CIOIN	389	246.5	6.2	622	2	Q53H04	HUMAN	Q53H04	homo sapien
317	253.5	6.4	471	2	Q3UES1	MOUSE	390	246.5	6.2	622	2	Q53H06	HUMAN	Q53H06	homo sapien
318	253.5	6.4	487	2	Q9NZP8	HUMAN	391	246.5	6.2	622	2	Q7Z7P3	HUMAN	Q7Z7P3	homo sapien
319	253.5	6.4	615	2	Q6GNK4	XENLA	392	246	6.2	263	2	Q5STN8	ANOCA	Q5STN8	anophelis g
320	253.5	6.4	628	2	Q9VER6	DROME	393	246	6.2	267	2	Q5BDX8	MOUSE	Q5BDX8	mus musculu
321	253	6.4	471	1	Q4SEW1	TEING	394	246	6.2	764	1	CPAB	GORCO	Q5KXG0	xenopus tro
322	253	6.4	471	1	FAS	CHICK	395	246	6.2	764	1	PLAN	BOVIN	Q864V9	gottilla gor
323	253	6.4	616	2	Q97507	PIC	396	246	6.2	812	1	PLAN	BOVIN	P06868	bos taurus

397	245.5	6.2	265	2	Q804G1_BRARE	Q804g1 brachydanio	470	238.5	6.0	578	2	Q6Q017_BOVIN	Q6q017 bos taurus
398	245.5	6.2	467	2	Q967X8_PANAR	Q967x8 panulirus a	471	238.5	6.0	625	2	Q5NTB3_BOVIN	Q5ntb3 bos taurus
399	245	6.2	245	2	Q6GNF7_XENIA	Q6gnf7 xenopus lae	472	238.5	6.0	928	2	Q7OAH1_ANOGA	Q7oah1 anophelis g
400	245	6.2	277	2	Q7PKB8_ANOGA	Q7pkb8 anophelis g	473	238	6.0	237	1	TRYP_ASTRU	P00765 astracus flu
401	245	6.2	369	2	Q2VG86_BOMMO	Q2vg86 bombyx mori	474	238	6.0	263	1	TRT2_CANPA	P04813 canis famli
402	245	6.2	638	2	Q8R0P5_MOUSE	Q8r0p5 mus musculi	475	238	6.0	275	1	TRIT_PIG	Q9n2d1 sus scrofa
403	245	6.2	639	2	BMPH_STRPU	Bp80b6 strongyloce	476	238	6.0	283	2	Q7PEY2_ANOGA	Q7pey2 anophelis g
404	245	6.2	1167	2	Q5TEB6_HUMAN	Q5teb6 homo sapien	477	238	6.0	347	1	HPT_PONPY	Q5r5f6 pongo pygma
405	244.5	6.2	223	2	Q4QY74_SPAU	Q4qy74 sparus aura	478	238	6.0	375	1	PCF_TACTR	P21902 tachylepus
406	244.5	6.2	242	2	Q7O9W3_ANOGA	Q7o9w3 anophelis g	479	238	6.0	435	2	Q9NFY2_ANOGA	Q9nfy2 anophelis g
407	244.5	6.2	511	2	Q570Z4_MOUSE	Q570z4 mus musculi	480	238	6.0	767	2	Q9DGR2_XENIA	Q9dgr2 xenopus lae
408	244.5	6.2	608	2	Q9PTW7_STRCA	Q9ptw7 struthio ca	481	237.5	6.0	267	2	Q4QRE8_BRARE	Q4qre8 brachydanio
409	244.5	6.2	1061	1	TMPS9_RAT	P695z6 rattus norv	482	237.5	6.0	449	2	Q7PEY1_ANOGA	Q7pey1 anophelis g
410	244	6.2	263	2	Q9DC86_MOUSE	Q9dc86 mus musculi	483	237.5	6.0	475	2	Q3TZ06_MOUSE	Q3tz06 mus musculi
411	244	6.2	322	2	Q920S2_MOUSE	Q920s2 mus musculi	484	237.5	6.0	735	2	Q573B1_XENIA	Q573b1 xenopus lae
412	244	6.2	445	2	Q3U0U6_MOUSE	Q3u0u6 mus musculi	485	237.5	6.0	735	2	Q66K13_XENIA	Q66k13 xenopus lae
413	244	6.2	638	1	KLKX1_MOUSE	P26z62 mus musculi	486	237.5	6.0	810	1	PLMN_ERITU	Q2z485 erinaceus e
414	244	6.2	1806	2	Q571B7_MOUSE	Q571b7 mus musculi	487	237	6.0	237	2	Q91515_FUGRU	Q91515 fugu rubrip
415	243.5	6.2	285	2	Q8CG42_RAT	Q8cg42 rattus norv	488	237	6.0	263	1	CTRB1_RAT	P07338 rattus norv
416	243.5	6.2	435	1	SNAK_DROME	P05049 drosophila	489	237	6.0	263	2	Q6RGS4_XENIA	Q6rgs4 xenopus lae
417	243.5	6.2	555	2	Q5FVX1_XENTR	Q5fvx1 xenopus tro	490	237	6.0	963	2	Q5H874_CIOIN	Q5h874 ciona intes
418	243.5	6.2	764	1	CPAB_PONPY	Q864w1 pongo pygma	491	236.5	6.0	227	2	Q7ODP9_ANOGA	Q7odp9 anophelis g
419	243.5	6.2	877	1	NETR_PONPY	Q5g269 pongo pygma	492	236.5	6.0	251	2	Q7O9W2_ANOGA	Q7o9w2 anophelis g
420	243	6.2	261	2	Q4RHR8_TETNG	Q4rhr8 tetraodon n	493	236.5	6.0	274	1	MCPT6_RAT	P50343 rattus norv
421	243	6.2	273	1	TRYT_SHEEP	Q9x8m2 ovis aries	494	236.5	6.0	707	1	BMP1_XENIA	P98070 xenopus lae
422	243	6.2	442	2	Q804X1_FUGRU	Q804x1 fugu rubrip	495	236.5	6.0	761	2	Q99JTC_RAT	Q99jtc mus musculi
423	242.5	6.1	233	2	Q4RYI8_TETNG	Q4ryi8 tetraodon n	496	236	6.0	267	2	Q7OAX5_ANOGA	Q7oax5 anophelis g
424	242.5	6.1	279	2	Q3UN95_MOUSE	Q3un95 mus musculi	497	236	6.0	328	2	Q5BLZ2_BRARE	Q5blz2 brachydanio
425	242.5	6.1	564	2	Q5R502_PONPY	Q5r502 pongo pygma	498	236	6.0	519	2	Q5MG68_LONON	Q5mg68 lonomola obi
426	242.5	6.1	564	2	Q8MKB1_RABIT	Q8mkd1 onyctolagus	499	236	6.0	812	2	P4MN_MOUSE	P20918 mus musculi
427	242.5	6.1	574	2	Q86RL8_9CAEN	Q86rl8 llyanassa o	500	236	6.0	1550	2	Q4T392_TETNG	Q4t392 tetraodon n
428	242.5	6.1	691	2	Q57658_CHICK	Q57658 gallus gall	501	236	6.0	259	2	Q5OBF4_PDIPY	Q5obf4 culicoides
429	242.5	6.1	803	2	Q59F71_HUMAN	Q59f71 homo sapien	502	235.5	6.0	260	2	Q9W703_PAROL	Q9w703 paraclichy
430	242.5	6.1	875	1	NETR_HYLE	Q5g268 hylobates l	503	235.5	6.0	369	2	Q6AXZ6_RAT	Q6axz6 rattus norv
431	242.5	6.1	875	1	NETR_MACMU	Q5g267 meacaca mula	504	235.5	6.0	453	2	Q81Z46_MOUSE	Q81z46 mus musculi
432	242.5	6.1	1019	1	TLPS2_XENIA	Q57382 xenopus lae	505	235.5	6.0	261	2	Q4QY77_SPAU	Q4qy77 sparus aura
433	242.5	6.1	1065	1	TMPS9_MOUSE	P695z25 mus musculi	506	235	6.0	270	1	TRYT_MERUN	P50342 meriones un
434	242.5	6.1	725	2	Q4LDES_HUMAN	Q4ldes homo sapien	507	235	6.0	336	2	Q7RTY5_HUMAN	Q7rtc5 homo sapien
435	242	6.1	725	2	Q4SGT4_TETNG	Q4sgt4 tetraodon n	508	235	6.0	345	2	Q28800_PANTR	Q28800 pan troglod
436	241.5	6.1	269	2	Q4S850_TETNG	Q4s850 tetraodon n	509	235	6.0	524	2	Q7SKX8_BRARE	Q7skx8 brachydanio
437	241.5	6.1	279	2	Q3M1S4_MOUSE	Q3m1s4 mus musculi	510	235	6.0	622	2	Q5NKR9_ONCMY	Q5nkr9 oncoyrnchu
438	241.5	6.1	279	2	Q99MS4_MOUSE	Q99ms4 mus musculi	511	235	6.0	812	1	PLMN_RAT	Q5k1f6 rattus norv
439	241.5	6.1	416	2	Q86T26_HUMAN	Q86t26 homo sapien	512	235	6.0	1420	1	Q5BK36_RAT	Q5bk36 rattus norv
440	241.5	6.1	623	1	THRB_PONPY	Q5ic337 pongo pygma	513	235	6.0	259	2	Q4S849_TETNG	Q4s849 tetraodon n
441	241.5	6.1	875	1	NETR_SAGLB	Q5g265 saquinus la	514	235	6.0	271	2	Q6S1U9_BRARE	Q6s1u9 brachydanio
442	241.5	6.1	875	1	NETR_TRAPH	Q5g266 trachypithe	515	234.5	5.9	267	2	Q5R1Z2_BRARE	Q5r1z2 brachydanio
443	241	6.1	296	2	Q5FV77_XENTR	Q5fv77 xenopus tro	516	234.5	5.9	326	2	Q32PT2_BRARE	Q32pt2 brachydanio
444	241	6.1	346	1	HPT_MESAU	Q6p2a6 mesocricetu	517	234.5	5.9	375	2	Q2M1G5_DROPS	Q2m1g5 drosophila
445	241	6.1	818	2	Q6PBA6_BRARE	Q6pba6 brachydanio	518	234.5	5.9	382	2	Q7O432_ANOGA	Q7o432 anophelis g
446	241	6.1	862	2	Q7Q058_ANOGA	Q7q058 anophelis g	519	234.5	5.9	395	2	Q9BZM1_HUMAN	Q9bzm1 homo sapien
447	241	6.1	1415	2	Q8MJ16_BOVIN	Q8mj16 bos taurus	520	234.5	5.9	418	2	Q6NPO2_DROME	Q6np02 drosophila
448	240.5	6.1	266	2	Q9W706_PAROL	Q9w706 paraclichy	521	234.5	5.9	453	1	TMPS3_MOUSE	Q6nlt0 mus musculi
449	240.5	6.1	366	2	Q4QY80_SPAU	Q4qy80 sparus aura	522	234.5	5.9	453	2	Q2M1G4_MOUSE	Q2m1g4 mus musculi
450	240.5	6.1	366	2	Q27Y12_BOVIN	Q27y12 bos taurus	523	234.5	5.9	624	2	QADAT3_MOUSE	Q9ad4t mus musculi
451	240.5	6.1	422	2	Q8WVC1_HUMAN	Q8wvc1 homo sapien	524	234.5	5.9	417	1	DESC4_RAT	Q5gkx8 rattus norv
452	240.5	6.1	3548	2	Q5VTE4_HUMAN	Q5vte4 homo sapien	525	234.5	5.9	575	2	Q8IRB8_DROME	Q8irb8 drosophila
453	240	6.1	242	2	Q920J9_PARMG	Q920j9 paranocthe	526	234	5.9	3623	1	CTRA_MOUSE	Q47196 gadus morhu
454	240	6.1	1059	1	TMPS9_HUMAN	Q7z410 homo sapien	527	234	5.9	263	1	CTRA_GADMO	Q78z51 brachydanio
455	239.5	6.1	240	2	Q98THO_PTELE	Q98tho engraulis j	528	234	5.9	267	2	Q90504_BETST	Q90504 eptactretus
456	239.5	6.1	371	2	Q5MPC6_MOUSE	Q5mpc6 manduca sex	529	233.5	5.9	420	2	Q4SCLO_TETNG	Q4sclo tetraodon n
457	239.5	6.1	406	1	HPT_HUMAN	P00738 homo sapien	530	233.5	5.9	779	2	Q7O845_ANOGA	Q7o845 anophelis g
458	239.5	6.1	406	2	Q2PP15_HUMAN	Q2pp15 homo sapien	531	233.5	5.9	260	2	Q9XSM1_SHEEP	Q9xsm1 ovis aries
459	239.5	6.1	1015	1	TLI2_HUMAN	Q9y617 homo sapien	532	233.5	5.9	334	2	Q5MPC9_HANSE	Q5mpc9 manduca sex
460	239.5	6.1	1015	2	Q2M1H1_HUMAN	Q2m1h1 homo sapien	533	233	5.9	386	2	Q2LZS9_DROPS	Q2lzs9 drosophila
461	239.5	6.1	3567	2	Q9BS77_MOUSE	Q9bs77 mus musculi	534	233	5.9	445	2	Q8CJ17_RAT	Q8c1j7 rattus norv
462	239	6.1	245	1	CTRA_BOVIN	P00766 bos taurus	535	233	5.9	445	2	Q5VAN3_PAPPA	Q5van3 papio hamad
463	239	6.1	264	2	Q4QY78_SPAU	Q4qy78 sparus aura	536	233	5.9	936	2	Q8IFX2_CRAGI	Q8ifx2 crassostrea
464	239	6.1	268	2	Q7PZ03_ANOGA	Q7pzo3 anophelis g	537	233	5.9	1013	1	TLI1_HUMAN	Q43897 homo sapien
465	239	6.1	435	2	Q7QC30_ANOGA	Q7qc30 anophelis g	538	233.5	5.9	416	1	HEPS_RAT	Q05511 rattus norv
466	239	6.1	436	1	HEPS_MOUSE	Q5f582 rattus norv	539	233.5	5.9	638	1	KLKX1_RAT	P14272 rattus norv
467	239	6.1	638	2	Q5FVZ2_RAT	Q5fvz2 xenopus lae	540	232	5.9				
468	239	6.1	977	2	Q91925_XENIA	Q91925 xenopus lae	541	232	5.9				
469	238.5	6.0	268	2	Q46151_PACLE	Q46151 pacifastacu	542	232	5.9				

543	232	5.9	812	2	Q3V1T9_MOUSE	Q3V1C9 mus musculus	616	226	5.7	394	1	URTG_DESRO	P49150 deamodus ro
544	231.5	5.9	269	1	ELA2_BOVIN	Q29461 bos taurus	617	226	5.7	416	2	Q4T4R1_TETNG	Q4T4R1 tetracodon n
545	231.5	5.9	270	1	Q91039_GADMO	Q91039 gadus morhua	618	226	5.7	437	1	TMPS4_HUMAN	Q91039 gadus morhua
546	231.5	5.9	371	2	Q8C116_RAT	Q8C116 rattus norv	619	226	5.7	488	2	Q4RV82_TETNG	Q4RV82 tetracodon n
547	231.5	5.9	395	2	Q5SMW8_HUMAN	Q5SMW8 homo sapien	620	226	5.7	490	2	Q6F7D7_RAT	Q6F7D7 rattus norv
548	231.5	5.9	483	2	Q8T8X4_DROME	Q8T8X4 drosophila	621	226	5.7	625	1	FALL_HUMAN	P03951 homo sapien
549	231.5	5.9	483	2	Q9VK10_DROME	Q9VK10 drosophila	622	226	5.7	625	2	Q4W5C2_HUMAN	Q4W5C2 homo sapien
550	231.5	5.9	541	2	Q4V8T5_BRARE	Q4V8T5 brachydanio	623	225.5	5.7	217	2	Q5TXH3_ANOGA	Q5TXH3 anopheles g
551	231.5	5.9	603	2	Q5M879_RAT	Q5M879 rattus norv	624	225.5	5.7	312	2	Q7M755_MOUSE	Q7M755 mus musculus
552	231.5	5.9	624	2	Q5M8E7_RABIT	Q5M8E7 coryctolagus	625	225.5	5.7	347	1	HPT_PIG	Q84974 sus scrofa
553	231.5	5.9	664	2	Q2MOM7_DROPS	Q2MOM7 drosophila	626	225.5	5.7	410	2	Q7Q956_ANOGA	Q7Q956 anopheles g
554	231.5	5.9	666	2	Q6VPUB_DROVI	Q6VPUB drosophila	627	225.5	5.7	418	2	Q8SZK2_DROME	Q8SZK2 drosophila
555	231	5.9	242	2	Q93266_PSEAM	Q93266 pseudopieur	628	225.5	5.7	418	2	Q9VAB7_DROME	Q9VAB7 drosophila
556	231	5.9	310	2	Q2YDQ2_BRARE	Q2YDQ2 brachydanio	629	225.5	5.7	429	2	Q8VAB0_BRARE	Q8VAB0 brachydanio
557	231	5.9	1008	1	TLL1_CHICK	Q9d67 gallus gall	630	225.5	5.7	457	1	TMPS5_HUMAN	Q91039 gadus morhua
558	231	5.9	1012	1	TLL2_MOUSE	Q9vrm6 mus musculus	631	225	5.7	234	2	Q4RH74_TETNG	Q4RH74 tetracodon n
559	230.5	5.8	259	2	Q69E27_HUMAN	Q69E27 homo sapien	632	225	5.7	237	2	Q7Q056_ANOGA	Q7Q056 anopheles g
560	230.5	5.8	295	2	Q69E28_HUMAN	Q69E28 homo sapien	633	225	5.7	328	2	Q80240_RAT	Q80240 rattus norv
561	230	5.8	244	2	Q8QGW3_ANOGA	Q8QGW3 anguilla ja	634	225	5.7	347	1	HPT_PAPHA	P00744 rattus norv
562	230	5.8	265	2	Q9VVT3_DROME	Q9VVT3 drosophila	635	225	5.7	387	2	Q9XY57_CTEFE	Q9XY57 ctenocephal
563	230	5.8	318	2	Q7RTY6_HUMAN	Q7RTY6 homo sapien	636	225	5.7	393	2	Q6RX66_9DIP	Q6RX66 armigeres s
564	230	5.8	372	2	Q9Y1K6_ANOGA	Q9Y1K6 anopheles g	637	225	5.7	455	2	Q8CDR0_MOUSE	Q8CDR0 mus musculus
565	230	5.8	607	2	Q91001_CHICK	Q91001 gallus gall	638	225	5.7	490	2	Q7TN04_MOUSE	Q7TN04 mus musculus
566	229.5	5.8	374	2	HPT_CANFA	P19006 canis fami	639	225	5.7	490	2	Q920X3_RAT	Q920X3 rattus norv
567	229.5	5.8	329	1	Q9VUG2_DROME	Q9VUG2 drosophila	640	225	5.7	615	1	FA12_HUMAN	Q88301 mus musculus
568	229.5	5.8	624	1	FALL_MOUSE	Q91Y47 mus musculus	641	224.5	5.7	246	2	Q54854_RAT	Q54854 rattus norv
569	229	5.8	267	2	Q9BK47_9ECHI	Q9BK47 ludia foli	642	224.5	5.7	251	2	Q88301_MOUSE	Q88301 mus musculus
570	229	5.8	274	2	Q3UN30_MOUSE	Q3UN30 mus musculus	643	224.5	5.7	253	2	Q91Y82_MOUSE	Q91Y82 mus musculus
571	229	5.8	274	2	Q9Z4N9_MOUSE	Q9Z4N9 mus musculus	644	224.5	5.7	271	1	ELA2_RAT	P00774 rattus norv
572	229	5.8	490	2	Q3UKK3_MOUSE	Q3UKK3 mus musculus	645	224.5	5.7	274	1	TR11_ANOGA	P33035 anopheles g
573	229	5.8	722	2	Q6NUP5_XENTIA	Q6NUP5 xenopus lae	646	224.5	5.7	347	2	HPT_MOUSE	P00767 bos taurus
574	229	5.8	733	2	Q9VTV3_DROME	Q9VTV3 drosophila	647	224.5	5.7	347	2	Q3UBS3_MOUSE	Q3UBS3 mus musculus
575	229	5.8	845	2	Q9DGR1_XENTIA	Q9DGR1 xenopus lae	648	224.5	5.7	1022	1	TLL1_BRARE	Q57466 brachydanio
576	228.5	5.8	347	2	Q63927_9MURI	Q63927 mus sp. hap	649	224.5	5.7	1427	2	Q8V1B7_MESAU	Q8V1B7 mesocricetu
577	228.5	5.8	352	2	Q6VUB4_HUMAN	Q6VUB4 homo sapien	650	224	5.7	222	2	Q8AV11_ONCKE	Q8AV11 oncorhynch
578	228.5	5.8	446	2	Q2VUC1_9DIP	Q2VUC1 phlebotomus	651	224	5.7	242	2	Q7T1R8_9TELE	Q7T1R8 pargastius h
579	228.5	5.8	573	2	Q7PVS8_ANOGA	Q7PVS8 anopheles g	652	224	5.7	245	1	CTRB_BOVIN	P00767 bos taurus
580	228.5	5.8	600	2	Q17490_ANOGA	Q17490 anopheles g	653	224	5.7	248	2	Q16126_9ASCI	Q16126 bottentia vi
581	228.5	5.8	761	2	Q2K1UE_BOVIN	Q2K1UE bos taurus	654	224	5.7	261	1	KLK2_HORSE	Q61321 equus caball
582	228.5	5.8	1084	2	Q9BP40_HAIARO	Q9BP40 halocynthia	655	224	5.7	343	2	Q5RBT2_PONPY	Q5RBT2 pongo pygma
583	228.5	5.8	2516	2	Q7TQ52_MOUSE	Q7TQ52 mus musculus	656	224	5.7	484	2	Q311UE_HYLSX	Q311UE hylobates s
584	228.5	5.8	2526	2	Q7TQ51_MOUSE	Q7TQ51 mus musculus	657	224	5.7	490	1	TMPS2_MOUSE	Q911q8 mus musculus
585	228.5	5.8	2531	1	NOTC1_MOUSE	Q01705 mus musculus	658	224	5.7	1174	2	Q9VYR4_DROME	Q9VYR4 drosophila
586	228.5	5.8	2531	2	Q7TQ50_MOUSE	Q7TQ50 mus musculus	659	224	5.7	2602	2	Q9VSV8_ANOGA	Q9VSV8 anopheles g
587	228.5	5.8	2531	2	Q8K428_MOUSE	Q8K428 mus musculus	660	223.5	5.7	234	2	Q90244_ACITR	Q90244 acideser t
588	228	5.8	263	2	Q5HZD0_XENTR	Q5HZD0 xenopus tro	661	223.5	5.7	266	2	Q9W7Q0_PAROL	Q9W7Q0 paracitichy
589	228	5.8	3687	2	Q9W332_DROME	Q9W332 drosophila	662	223.5	5.7	348	1	HPTR_HUMAN	P00739 homo sapien
590	227.5	5.8	235	2	Q91004_GECGE	Q91004 gecko gecko	663	223.5	5.7	417	2	Q5R5E8_PONPY	Q5R5E8 pongo pygma
591	227.5	5.8	242	1	TR11_SALSA	P35031 salmo salar	664	223.5	5.7	1242	1	JAG1A_BRARE	Q90Y57 brachydanio
592	227.5	5.8	251	1	KLK14_HUMAN	Q9P0G3 homo sapien	665	223.5	5.7	1629	2	Q8V5I3_DROME	Q8V5I3 drosophila
593	227.5	5.8	251	2	Q6B085_HUMAN	Q6B085 homo sapien	666	223.5	5.7	201	2	Q5XUG4_OREAU	Q5XUG4 oreochromis
594	227.5	5.8	349	2	Q28802_PATR	Q28802 pan troglod	667	223	5.7	242	2	Q9W7Q7_PAROL	Q9W7Q7 paracitichy
595	227.5	5.8	418	2	Q61E15_RAT	Q61E15 rattus norv	668	223	5.7	261	2	Q56GM3_CULPI	Q56GM3 culic pipie
596	227	5.8	242	2	Q6R179_9LABR	Q6R179 taetogolabr	669	223	5.7	274	2	Q7Q299_ANOGA	Q7Q299 anopheles g
597	227	5.8	249	2	Q7PKE4_ANOGA	Q7PKE4 anopheles g	670	223	5.7	454	1	TMPS3_HUMAN	P57127 homo sapien
598	227	5.8	263	2	Q7SVS4_XENTIA	Q7SVS4 xenopus lae	671	223	5.7	539	2	Q5USC7_HUMAN	Q5USC7 homo sapien
599	227	5.8	275	2	Q7YS62_HORSE	Q7YS62 equus caball	672	223	5.7	411	2	Q5VUP0_DROME	Q5VUP0 drosophila
600	227	5.8	324	1	TEST_MOUSE	Q9Y1J7 mus musculus	673	222.5	5.6	417	2	HPTR_HUMAN	P00739 homo sapien
601	227	5.8	324	1	Q54AE4_MOUSE	Q54AE4 mus musculus	674	222.5	5.6	434	1	UROK_CHICK	P51320 gallus gall
602	227	5.8	336	2	Q80YD8_MOUSE	Q80YD8 mus musculus	675	222.5	5.6	455	1	TMPS5_MOUSE	Q9E0T4 mus musculus
603	227	5.8	372	2	Q7OKL2_ANOGA	Q7OKL2 anopheles g	676	222.5	5.6	514	2	Q2PDK2_XENTIA	Q2PDK2 ginglymocto
604	227	5.8	417	1	DESCA_MOUSE	Q8B510 mus musculus	677	222.5	5.6	757	2	Q2Y2P1_GINCI	Q2Y2P1 sus scrofa
605	227	5.8	484	2	Q311U4_MACMU	Q311U4 macaca mula	678	222.5	5.6	790	1	PLMN_PIG	P06867 sus scrofa
606	227	5.8	488	2	Q9Y1H4_SCHMA	Q9Y1H4 schistosoma	679	222.5	5.6	954	2	Q5XUG6_ACHTE	Q5XUG6 achaeiranae
607	227	5.8	1464	2	Q24132_DROME	Q24132 drosophila	680	222	5.6	203	2	Q9V942_DROME	Q9V942 drosophila
608	227	5.8	1464	2	Q9VC47_DROME	Q9VC47 drosophila	681	222	5.6	267	2	ELA2_PIG	P08419 sus scrofa
609	227	5.8	1464	1	TRV3_SALSA	P35033 salmo salar	682	222	5.6	269	1	Q921N4_MOUSE	Q921N4 mus musculus
610	226.5	5.7	371	2	Q8MS52_DROME	Q8MS52 drosophila	683	222	5.6	273	2	TRV41_HUMAN	P15157 homo sapien
611	226.5	5.7	761	1	NETR_MOUSE	Q08762 mus musculus	684	222	5.6	275	1	TRV41_HUMAN	P15157 homo sapien
612	226.5	5.7	761	1	NETR_MOUSE	Q08762 mus musculus	685	222	5.6	275	1	TRV41_HUMAN	P15157 homo sapien
613	226.5	5.7	1429	1	ATRN_HUMAN	Q75682 homo sapien	686	222	5.6	275	2	Q6B052_HUMAN	Q6B052 homo sapien
614	226.5	5.7	274	2	Q7PJO0_ANOGA	Q7PJO0 anopheles g	687	222	5.6	275	2	Q6B052_HUMAN	Q6B052 homo sapien
615	226	5.7	274	2	Q7PJO0_ANOGA	Q7PJO0 anopheles g	688	222	5.6	275	2	Q6B052_HUMAN	Q6B052 homo sapien

689	222	5.6	275	2	Q706S1_ANOGA	Q706S1 anophelies g	762	217	5.5	239	1	KLK2_CAVPO	P12323 cavia porce
690	222	5.6	276	2	Q6EUAS_HUMAN	Q6EUAS homo sapien	763	217	5.5	268	1	CLCR_HUMAN	Q99895 homo sapien
691	222	5.6	282	2	Q6NZY1_HUMAN	Q6NZY1 homo sapien	764	217	5.5	273	1	TRYBI_MOUSE	Q02844 mus musculu
692	222	5.6	363	2	Q7PXE3_ANOGA	Q7PXE3 anophelies g	765	217	5.5	275	2	Q6SRZ6_HUMAN	Q96726 homo sapien
693	222	5.6	419	2	Q4WSP3_HUMAN	Q4WSP3 homo sapien	766	217	5.5	280	2	Q6GLK1_XENLA	Q6GLK1 xenopus lae
694	222	5.6	423	1	TMILE_HUMAN	Q9U152 homo sapien	767	217	5.5	597	2	Q35727_MOUSE	Q35727 mus musculu
695	222	5.6	658	2	Q4RLS7_TETNG	Q4RLS7 tetracodon n	768	217	5.5	603	1	FA12_CAVPO	Q04962 cavia porce
696	222	5.6	761	2	Q4QRE3_BRARE	Q4QRE3 brachydantio	769	217	5.5	2703	1	NOTCH_DROME	P07207 drosophilla
697	221.5	5.6	247	2	Q547S4_BOVIN	Q547S4 bos taurus	770	216.5	5.5	235	2	Q6B4R4_BOVIN	Q6B4R4 bos taurus
698	221.5	5.6	271	2	Q803Z4_BRARE	Q803Z4 brachydantio	771	216.5	5.5	277	2	Q96899_9MYRI	Q96899 scolopendra
699	221.5	5.6	2531	1	NORCI_EAT	Q07008 rattus norv	772	216.5	5.5	346	1	HPRR_PANTR	Q28801 pan troglod
700	221.5	5.6	3620	1	CUBN_CANPA	Q9UC53 canis famil	773	216.5	5.5	365	2	Q7PWE1_ANOGA	Q7PWE1 anophelies g
701	221	5.6	320	1	TRY2_SALSA	P35032 salmo salar	774	216.5	5.5	1048	2	Q4S9J6_TETNG	Q4S9J6 tetracodon n
702	221	5.6	258	2	Q973J9_PHACE	Q973J9 phaeodon coc	775	216.5	5.5	2528	2	Q8AXP0_CYNPY	Q8AXP0 cynops pyr
703	221	5.6	264	2	Q2MOD7_DROPS	Q2MOD7 drosophilla	776	216.5	5.5	2616	1	NUDEL_DROME	P98159 drosophilla
704	221	5.6	268	1	CLCR_RAT	P55091 rattus norv	777	216	5.5	255	2	Q7NNI0_MOUSE	Q7NNI0 mus musculu
705	221	5.6	273	1	TRYBI_RAT	P27435 rattus norv	778	216	5.5	259	2	Q4KLCE_XENLA	Q4KLCE xenopus lae
706	221	5.6	273	1	Q6PEW8_RAT	Q6PEW8 rattus norv	779	216	5.5	268	2	Q3SYP2_MOUSE	Q3SYP2 mus musculu
707	221	5.6	314	2	Q6RUT2_MOUSE	Q6RUT2 mus musculu	780	216	5.5	269	2	Q9CQ52_MOUSE	Q9CQ52 m adult mal
708	221	5.6	425	2	Q4SCU6_TETNG	Q4SCU6 tetracodon n	781	216	5.5	269	2	Q9D779_MOUSE	Q9D779 mus musculu
709	221	5.6	810	2	Q5R8X6_PONPY	P91658 pongo pygma	782	216	5.5	355	2	Q7PEW0_ANOGA	Q7PEW0 anophelies g
710	221	5.6	974	2	P91658_DROME	P91658 drosophilla	783	216	5.5	376	2	Q5TU09_ANOGA	Q5TU09 anophelies g
711	221	5.6	1198	2	Q5YVW3_HUMAN	Q5YVW3 homo sapien	784	216	5.5	1218	1	JA61_MOUSE	Q94GX0 mus musculu
712	221	5.6	1299	2	Q7PIQ7_ANOGA	Q7PIQ7 anophelies g	785	216	5.5	1218	2	Q3UVN4_MOUSE	Q3UVN4 mus musculu
713	221	5.6	1347	2	Q7PNR7_ANOGA	Q7PNR7 anophelies g	786	215.5	5.5	243	2	Q9TXD8_AGEAP	Q9TXD8 agelenopsis
714	220.5	5.6	242	2	Q80VS4_MOUSE	Q80VS4 mus musculu	787	215.5	5.5	247	1	TRY2_CANPA	P06872 canis famil
715	220.5	5.6	250	2	Q8CGR5_MOUSE	Q8CGR5 mus musculu	788	215.5	5.5	247	2	Q5H7Z8_MACMU	Q5H7Z8 macaca mla
716	220.5	5.6	277	2	Q80MW7_MOUSE	Q80MW7 mus musculu	789	215.5	5.5	248	1	TRY3_CHICK	Q90629 gallus gall
717	220.5	5.6	288	2	Q7Q9W5_ANOGA	Q7Q9W5 anophelies g	790	215.5	5.5	252	2	Q3B8S6_XENLA	Q3B8S6 xenopus lae
718	220.5	5.6	360	2	Q17489_ANOGA	Q17489 anophelies g	791	215.5	5.5	253	2	Q3B8S5_MOUSE	Q3B8S5 mus musculu
719	220.5	5.6	360	2	Q7PEV7_ANOGA	Q7PEV7 anophelies g	792	215.5	5.5	254	2	Q8CGR4_MOUSE	Q8CGR4 mus musculu
720	220.5	5.6	468	2	Q9U0G3_PACLE	Q9U0G3 pacifastacu	793	215.5	5.5	269	2	Q6GNR2_XENLA	Q6GNR2 xenopus lae
721	220.5	5.6	808	2	Q7YU36_DROME	Q7YU36 drosophilla	794	215.5	5.5	317	1	BSSP4_HUMAN	Q9GZN4 homo sapien
722	220.5	5.6	814	2	Q5DVP8_ONCMY	Q5DVP8 oncorhynch	795	215.5	5.5	321	2	Q80Y38_MOUSE	Q80Y38 mus musculu
723	220.5	5.6	1004	2	Q4SRX0_TETNG	Q4SRX0 tetracodon n	796	215.5	5.5	326	2	Q9D9M0_MOUSE	Q9D9M0 mus musculu
724	220.5	5.6	1067	1	TLID_DROME	P25723 drosophilla	797	215.5	5.5	562	2	Q675X7_9UROC	Q675X7 olivoplectra
725	220	5.6	237	2	Q52V24_PONLE	Q52V24 pongo pygma	798	215.5	5.5	740	2	Q6RE78_PONPY	Q6RE78 rattus norv
726	220	5.6	260	2	Q9W7P9_PAROL	Q9W7P9 parallitichy	799	215.5	5.5	741	1	Q6MG74_RAT	Q6MG74 gadus morhu
727	220	5.6	261	2	Q96ZG7_CULPI	Q96ZG7 culic pipie	800	215	5.4	261	2	TRYX_GADMO	Q25081 hyplid
728	220	5.6	275	1	TRYBI_HUMAN	Q15651 homo sapien	801	215	5.4	256	2	Q25081_HYPLI	Q25081 hypoderma 1
729	220	5.6	275	1	Q6B0S1_HUMAN	Q6B0S1 homo sapien	802	215	5.4	260	2	Q7Q5K4_ANOGA	Q7Q5K4 anophelies g
730	220	5.6	331	2	Q80X17_MOUSE	Q80X17 mus musculu	803	215	5.4	270	2	Q7PXG5_ANOGA	Q7PXG5 anophelies g
731	220	5.6	331	2	Q8RIAE_MOUSE	Q8RIAE mus musculu	804	215	5.4	388	2	Q4RRR7_TETNG	Q4RRR7 tetracodon n
732	219.5	5.6	244	1	TRY2_XENLA	P70059 xenopus lae	805	215	5.4	389	2	Q9PVX7_XENLA	Q9PVX7 xenopus lae
733	219.5	5.6	248	2	Q7SZT1_XENLA	Q7SZT1 xenopus lae	806	215	5.4	492	2	Q4RG82_TETNG	Q4RG82 tetracodon n
734	219.5	5.6	255	2	Q961Y0_GALME	Q961Y0 galleria me	807	215	5.4	597	2	Q6PER0_MOUSE	Q6PER0 mus musculu
735	219.5	5.6	255	2	Q4QR60_XENLA	Q4QR60 xenopus lae	808	215	5.4	609	2	Q80YCS_MOUSE	Q80YCS mus musculu
736	219.5	5.6	255	2	Q6GNU2_XENLA	Q6GNU2 xenopus lae	809	215	5.4	749	2	Q9YGB8_ONCMY	Q9YGB8 oncorhynch
737	219.5	5.6	259	2	Q3ZB43_MOUSE	Q3ZB43 mus musculu	810	215	5.4	760	2	Q8JG08_TETNG	Q8JG08 tetracodon n
738	219.5	5.6	271	1	ELA2_MOUSE	P05208 mus musculu	811	215	5.4	762	2	Q4SFT0_TETNG	Q4SFT0 tetracodon n
739	219.5	5.6	347	1	HPT_MUSCR	P06574 mus caroli	812	215	5.4	810	2	PLMN_HUMAN	P00747 homo sapien
740	219.5	5.6	761	1	CPAB_MOUSE	P04186 mus musculu	813	215	5.4	810	2	Q5TEH4_HUMAN	Q5TEH4 homo sapien
741	219.5	5.6	761	2	Q3UEB6_MOUSE	Q3UEB6 mus musculu	814	215	5.4	1116	2	Q7TP05_RAT	Q7TP05 rattus norv
742	219.5	5.6	1378	2	Q3UHB0_MOUSE	Q3UHB0 mus musculu	815	215	5.4	1497	2	Q5T938_HUMAN	Q5T938 homo sapien
743	219.5	5.6	1378	2	Q6BHV2_MOUSE	Q6BHV2 mus musculu	816	214.5	5.4	195	2	Q819P3_AURAU	Q819P3 aurelia aur
744	219.5	5.6	1444	2	Q6A0S1_MOUSE	Q6A0S1 mus musculu	817	214.5	5.4	244	2	Q5EBE2_XENTR	Q5EBE2 xenopus tro
745	219	5.6	249	2	Q7OAM5_ANOGA	Q7OAM5 anophelies g	818	214.5	5.4	247	1	TRY2_BOVIN	Q22463 bos taurus
746	219	5.6	318	2	Q80UR4_MOUSE	Q80UR4 mus musculu	819	214.5	5.4	249	1	Q6DIN2_XENTR	Q6DIN2 xenopus tro
747	219	5.6	343	1	PRSS8_HUMAN	Q16651 homo sapien	820	214.5	5.4	303	2	Q4SRR0_BOMMO	Q4SRR0 bombyx mori
748	219	5.6	365	2	Q97366_HOLDI	Q97366 holotrichia	821	214.5	5.4	366	2	Q7O170_MOUSE	Q7O170 mus musculu
749	218.5	5.5	374	2	Q81862_DERVA	Q81862 dermacentor	822	214.5	5.4	505	2	Q966V4_HALRO	Q966V4 halocynthia
750	218.5	5.5	375	2	Q817W8_DERAN	Q817W8 dermacentor	823	214.5	5.4	593	1	Q7OIMT_ANOGA	Q7OIMT anophelies g
751	218.5	5.5	435	1	TMPS4_MOUSE	Q8V4S5 mus musculu	824	214.5	5.4	1130	2	Q9ANAT0_ANOGA	Q9ANAT0 anophelies g
752	218.5	5.5	787	2	Q6S1G0_NAJKA	Q6S1G0 najia kaouth	825	214.5	5.4	1322	2	Q9NAT0_ANOGA	Q9NAT0 anophelies g
753	218.5	5.5	1007	1	TLIL_XENLA	Q8J128 xenopus lae	826	214.5	5.4	1428	1	ATRN_MOUSE	Q94U60 mus musculu
754	218.5	5.5	1379	2	Q6T2S6_HUMAN	Q6T2S6 homo sapien	827	214	5.4	252	2	Q5QBG0_SDIPT	Q5QBG0 culicoides
755	218	5.5	242	2	Q7SX90_BRARE	Q7SX90 brachydantio	828	214	5.4	262	2	Q5G3K5_PYAGNE	Q5G3K5 pygathrix n
756	218	5.5	252	2	Q5W908_XENTR	Q5W908 xenopus tro	829	214	5.4	262	2	Q5G3K6_PYAGR	Q5G3K6 pygathrix n
757	218	5.5	260	2	Q7Q0G6_ANOGA	Q7Q0G6 anophelies g	830	214	5.4	262	2	Q5G3K7_PYGBI	Q5G3K7 pygathrix b
758	217.5	5.5	271	2	Q54213_STRGR	Q54213 streptomyce	831	214	5.4	275	2	Q6FFH8_HUMAN	Q6FFH8 homo sapien
759	217.5	5.5	243	2	Q7M413_MEGRE	Q7M413 megabombus	832	214	5.4	342	1	PRSS8_RAT	Q96887 rattus norv
760	217.5	5.5	269	2	Q61SUS_HUMAN	Q61SUS homo sapien	833	214	5.4	342	2	Q6G5Y8_RAT	Q6G5Y8 rattus norv
761	217.5	5.5	3570	2	Q7Q737_ANOGA	Q7Q737 anophelies g	834	213.5	5.4	241	2	Q98TG9_9TELE	Q98TG9 engraulis j

835	213.5	5.4	248	2	Q9VQ98_DROME	Q9VQ98_drosophila	908	208.5	5.3	258	2	Q28803_PANTR	Q28803_pan troglod
836	213.5	5.4	249	2	Q7QK50_ANGA	Q7QK50_anopheles g	909	208.5	5.3	311	2	Q80X23_RAT	Q80X23_rattus norv
837	213.5	5.4	251	2	Q4V675_DROME	Q4V675_drosophila	910	208.5	5.3	417	1	TM1LD_MOUSE	Q80Xk8 m transmemb
838	213.5	5.4	270	2	Q53CG5_BRABE	Q53CG5_brachydanio	911	208.5	5.3	444	2	Q9V4W6_DROME	Q9V4W6_drosophila
839	213.5	5.4	274	2	Q7PN85_ANGA	Q7PN85_anopheles g	912	208.5	5.3	464	2	Q617Z5_HAELO	Q617Z5_haemaphysal
840	213.5	5.4	381	2	Q7PN97_ANGA	Q7PN97_anopheles g	913	208.5	5.3	581	1	TMPSD_HUMAN	Q99Yez2 homo sapien
841	213.5	5.4	442	1	TM1E_MOUSE	Q5a248 mus musculu	914	208	5.3	256	2	Q25082_HYPLI	Q25082_hypoderma 1
842	213.5	5.4	543	1	TMPSD_MOUSE	Q5u405 mus musculu	915	208	5.3	271	2	Q8HYJ2_BOVIN	Q8HYJ2_bos taurus
843	213.5	5.4	2352	2	Q61240_HAIRO	Q61240_haliocythia	916	208	5.3	275	2	Q81XD7_HUMAN	Q81XD7_homo sapien
844	213	5.4	211	2	Q4SBS0_TETNG	Q4SBS0_tetradodon n	917	208	5.3	295	2	Q706S2_ANGA	Q706S2_anopheles g
845	213	5.4	355	2	Q9NFU1_ANGA	Q9NFU1_anopheles g	918	208	5.3	326	2	Q7RTY6_HUMAN	Q7RTY6_homo sapien
846	213	5.4	394	2	P91817_TACTR	P91817_tachypleus	919	208	5.3	357	2	Q4KLE1_XENLA	Q4KLE1_xenopus lae
847	213	5.4	541	2	Q4SM14_TETNG	Q4SM14_tetradodon n	920	207.5	5.3	195	2	Q8J0U6_HUMAN	Q8J0U6_homo sapien
848	213	5.4	615	2	Q81Z25_HUMAN	Q81Z25_homo sapien	921	207.5	5.3	239	2	Q91218_ONCMY	Q91218_oncorynchu
849	213	5.4	1477	2	Q4H3A4_CIOIN	Q4H3A4_ciona intes	922	207.5	5.3	256	1	TRYB_MANSE	P35046 manduca sex
850	212.5	5.4	242	2	Q7POB3_ANGA	Q7POB3_anopheles g	923	207.5	5.3	266	2	Q92077_GADMO	Q92077_gadus mortu
851	212.5	5.4	247	2	Q3SY13_HUMAN	Q3SY13_homo sapien	924	207.5	5.3	269	1	ELAZA_HUMAN	P08217 homo sapien
852	212.5	5.4	260	2	Q7RTY3_HUMAN	Q7RTY3_homo sapien	925	207.5	5.3	269	2	Q61SN8_HUMAN	Q61SN8_homo sapien
853	212.5	5.4	265	2	Q4V804_XENLA	Q4V804_xenopus lae	926	207.5	5.3	298	2	Q9NH06_HELIZE	Q9NH06_heliochis z
854	212.5	5.4	282	1	KLK11_HUMAN	Q9UBX7 homo sapien	927	207.5	5.3	900	2	Q6AX42_XENLA	Q6AX42_xenopus lae
855	212.5	5.4	339	2	Q99144_MOUSE	Q99144_mus musculu	928	207.5	5.3	1010	2	Q4SO11_TETNG	Q4SQ11_tetradodon n
856	212.5	5.4	397	2	Q7P285_ANGA	Q7P285_anopheles g	929	207.5	5.3	1282	2	Q8TER0_HUMAN	Q8TER0_homo sapien
857	212.5	5.4	420	2	Q61E14_RAT	Q61E14_rattus norv	930	207	5.2	225	2	Q5TAH7_HUMAN	Q5TAH7_homo sapien
858	212.5	5.4	693	2	Q2SHS3_9GAMM	Q2SHS3_haella che	931	207	5.2	238	1	TRY5_AEDAE	P23787 aedes aegypt
859	212.5	5.4	778	2	Q9V519_DROME	Q9V519_drosophila	932	207	5.2	240	2	Q7SYQ8_XENLA	Q7SYQ8_xenopus lae
860	212.5	5.4	849	1	POLS2_MOUSE	Q5K2P8 mus musculu	933	207	5.2	260	1	NRPN_RAT	Q88780 rattus norv
861	212	5.4	260	1	NRPN_MOUSE	Q61955 mus musculu	934	207	5.2	274	2	Q7Q2X3_ANGA	Q7Q2X3_anopheles g
862	212	5.4	274	2	Q6GNFO_XENLA	Q6GNFO_xenopus lae	935	207	5.2	426	2	Q5T6B5_HUMAN	Q5T6B5_homo sapien
863	212	5.4	340	2	Q8BUV6_MOUSE	Q8BUV6_mus musculu	936	207	5.2	1957	2	Q4SUZ8_TETNG	Q4SUZ8_tetradodon n
864	212	5.4	875	2	Q5DPTU_MOUSE	Q5DPTU_mus musculu	937	206.5	5.2	195	2	Q6SPC0_HUMAN	Q6SPC0_homo sapien
865	212	5.4	1322	2	Q9NJ55_ANGA	Q9NJ55_anopheles g	938	206.5	5.2	256	1	TRYA_MANSE	P35045 manduca sex
866	211.5	5.4	272	2	Q7PWES_ANGA	Q7PWES_anopheles g	939	206.5	5.2	269	2	Q61CT2_HUMAN	Q61CT2_homo sapien
867	211.5	5.4	401	2	Q2TRBU_BOVIN	Q2TRBU_bos taurus	940	206.5	5.2	269	2	Q96GV5_HUMAN	Q96GV5_homo sapien
868	211.5	5.4	413	2	Q5M8B7_XENTR	Q5M8B7_xenopus tro	941	206.5	5.2	269	2	Q9V923_DROME	Q9V923_drosophila
869	211.5	5.4	418	1	TM1LD_HUMAN	Q60235 homo sapien	942	206.5	5.2	270	2	Q278Z2_UCAPU	Q278Z2_uca pugilat
870	211.5	5.4	484	2	Q7QCV0_ANGA	Q7QCV0_anopheles g	943	206.5	5.2	274	2	Q7Q092_ANGA	Q7Q092_anopheles g
871	211.5	5.4	629	2	Q6AZS7_XENLA	Q6AZS7_xenopus lae	944	206.5	5.2	284	2	Q8NF86_HUMAN	Q8NF86_homo sapien
872	211.5	5.4	719	2	Q6DJ90_XENTR	Q6DJ90_xenopus tro	945	206.5	5.2	321	1	TRYQ26_HUMAN	Q91RZ7 homo sapien
873	211	5.3	237	2	Q29464_BOVIN	Q29464_bos taurus	946	206.5	5.2	359	2	Q7Q5Z6_ANGA	Q7Q5Z6_anopheles g
874	211	5.3	276	1	MCPT6_MOUSE	P21845 mus musculu	947	206.5	5.2	467	2	Q86WX2_HUMAN	Q86WX2_homo sapien
875	211	5.3	313	2	Q7PX30_ANGA	Q7PX30_anopheles g	948	206.5	5.2	476	2	Q5T5Y9_HUMAN	Q5T5Y9_homo sapien
876	211	5.3	510	2	Q7Q554_ANGA	Q7Q554_anopheles g	949	206.5	5.2	573	2	Q9V516_DROME	Q9V516_drosophila
877	211	5.3	1218	1	JAG1_HUMAN	P78504 homo sapien	950	206.5	5.2	728	2	Q7QBP4_ANGA	Q7QBP4_anopheles g
878	211	5.3	1218	2	Q4KMR2_HUMAN	Q4KMR2_homo sapien	951	206.5	5.2	741	2	Q4SIU3_TETNG	Q4SIU3_tetradodon n
879	211	5.3	2447	2	Q13148_FUGRU	Q13148_fugu rubrip	952	206.5	5.2	1065	2	Q810H2_MOUSE	Q810H2_mus musculu
880	210.5	5.3	247	1	TRYP_SIMYI	P35048 stimulum vi	953	206.5	5.2	1403	2	Q7QEB2_MOUSE	Q7QEB2_mus musculu
881	210.5	5.3	275	2	Q7PNF7_ANGA	Q7PNF7_anopheles g	954	206	5.2	238	2	Q7QKX8_ANGA	Q7QKX8_anopheles g
882	210.5	5.3	280	2	Q8N171_HUMAN	Q8N171_homo sapien	955	206	5.2	263	2	Q9NB92_AGRIP	Q9NB92_agrotis ips
883	210.5	5.3	300	2	Q5M8S2_MOUSE	Q5M8S2_mus musculu	956	206	5.2	264	2	Q4RZ78_TETNG	Q4RZ78_tetradodon n
884	210.5	5.3	342	1	PRSS8_MOUSE	Q9uedi mus musculu	957	206	5.2	269	2	Q6AZP9_XENLA	Q6AZP9_xenopus lae
885	210.5	5.3	360	2	Q9W1X6_DROME	Q9W1X6_drosophila	958	206	5.2	374	2	Q49QW1_SPOLT	Q49QW1_spodoptera
886	210.5	5.3	572	1	TMPS7_HUMAN	Q7TYE8 homo sapien	959	206	5.2	389	2	Q3UQ41_MOUSE	Q3UQ41_mus musculu
887	210.5	5.3	754	2	Q28290_CAFPA	Q28290_canis famli	960	206	5.2	395	2	Q6R559_OSTNU	Q6R559_ostriina nu
888	210.5	5.3	855	1	POLS2_HUMAN	Q5K463 homo sapien	961	206	5.2	492	2	Q7Z155_9EUCI	Q7Z155_chironantes
889	210.5	5.3	1219	1	JAG1_RAT	Q53722 rattus norv	962	206	5.2	2040	2	Q5VTD7_HUMAN	Q5VTD7_homo sapien
890	210	5.3	262	2	Q5G3K6_BUNHO	Q5G3K6_bunopithec	963	206	5.2	4548	1	ABO4_HUMAN	P08519 homo sapien
891	210	5.3	750	2	Q3SYW2_BOVIN	Q3SYW2_bos taurus	964	205.5	5.2	245	2	Q7POR3_ANGA	Q7POR3_ANGA
892	210	5.3	2437	1	NOTC1_BRAKE	Q3BYW2 brachydanio	965	205.5	5.2	257	2	Q5OBUS_SUIPT	Q5OBUS_sulicoides
893	209.5	5.3	260	2	Q3KQ12_XENLA	Q3KQ12_xenopus lae	966	205.5	5.2	269	2	Q61SM5_HUMAN	Q61SM5_homo sapien
894	209.5	5.3	280	1	TRYM_CAFPA	P19236 canis famli	967	205.5	5.2	269	2	Q61SP9_HUMAN	Q61SP9_homo sapien
895	209.5	5.3	313	2	Q8IN51_DROME	Q8IN51_drosophila	968	205.5	5.2	347	1	HPT_RAT	P06866 rattus norv
896	209.5	5.3	347	1	HPT_MOUSE	Q62558 mus saxicol	969	205.5	5.2	357	2	Q5MFC6_MANSE	Q5MFC6_manduca sex
897	209.5	5.3	423	2	Q5FBE1_HUMAN	Q5FBE1_homo sapien	970	205.5	5.2	363	2	Q2VPP0_XENLA	Q2VPP0_xenopus lae
898	209.5	5.3	875	1	POLS2_RAT	Q5K2P9 rattus norv	971	205.5	5.2	374	2	Q80YD5_MOUSE	Q80YD5_mus musculu
899	209.5	5.3	1441	2	Q7Z3G3_HUMAN	Q7Z3G3_homo sapien	972	205.5	5.2	416	2	Q8BZ13_MOUSE	Q8BZ13_m adult fem
900	209	5.3	263	2	Q632K0_XENLA	Q632K0_xenopus lae	973	205.5	5.2	416	2	Q8BZ13_MOUSE	Q8BZ13_mus musculu
901	209	5.3	279	2	Q4RGP3_TETNG	Q4RGP3_tetradodon n	974	205.5	5.2	470	2	Q5CZ10_XENTR	Q5CZ10_xenopus tro
902	209	5.3	340	2	Q21624_GLOMR	Q21624_glossina mo	975	205.5	5.2	492	1	TMPS2_HUMAN	O15393 homo sapien
903	209	5.3	384	2	Q9W630_CYRCA	Q9W630_cyprinus ca	976	205.5	5.2	492	2	Q6CTK7_HUMAN	Q6CTK7_homo sapien
904	209	5.3	401	2	Q7QKD2_ANGA	Q7QKD2_anopheles g	977	205.5	5.2	752	2	Q5R8P4_PONPY	Q5R8P4_pongo pygma
905	209	5.3	433	1	UROK_MOUSE	P06869 m urokinase	978	205.5	5.2	848	2	Q2KOC3_RHET	Q2KOC3_rhizobium e
906	209	5.3	893	1	Q613J2_CAEBR	Q613J2_caenorhabdi	979	205	5.2	220	2	Q4L114_9NEOP	Q4L114_sesamia non
907	208.5	5.3	236	2	Q9TYH3_SCHMA	Q9TYH3_schistocoma	980	205	5.2	256	1	HYPB_HYPLI	P35588 hypoderma 1

981	205	5.2	264	2	002569_CUIQU	002569_culex quing	1054	201.5	5.1	195	2	080008_HUMAN	081008_homo sapien
982	205	5.2	396	2	045Y35_TERING	045Y35 tetraodon n	1055	201.5	5.1	246	1	TRX2_MOUSE	P07146_mus musculus
983	205	5.2	492	2	096T73_HUMAN	096T73 homo sapien	1056	201.5	5.1	246	2	0792Y6_MOUSE	P07926_mus musculus
984	205	5.2	870	2	0810G6_DROME	0810G6 drosophila	1057	201.5	5.1	255	2	061S10_HUMAN	061S10_homo sapien
985	204.5	5.2	246	1	TRX2_RAT	P00763 rattus norv	1058	201.5	5.1	256	1	KIK15_HUMAN	0912T5_homo sapien
986	204.5	5.2	247	2	09C9N9_MOUSE	09C9N9 m adult mal	1059	201.5	5.1	265	1	05H2U5_XENTR	05H2U5_xenopus tro
987	204.5	5.2	247	2	09D7Y7_MOUSE	09D7Y7 mus musculi	1060	201.5	5.1	320	2	07FOX2_XENLA	07FOX2_xenopus lae
988	204.5	5.2	256	1	TRXC_MANSE	P35047 manduca sex	1061	201.5	5.1	344	2	0640F8_XENLA	0640F8_xenopus lae
989	204.5	5.2	281	2	046137_LUMRU	046137 lumbricus r	1062	201.5	5.1	383	2	07PQ72_ANOGA	07PQ72_anopheles g
990	204.5	5.2	311	2	04V3F4_DROME	04V3F4 drosophila	1063	201.5	5.1	415	2	053BE6_HUMAN	053BE6_homo sapien
991	204.5	5.2	367	2	04V3K5_DROME	04V3K5 drosophila	1064	201.5	5.1	438	2	06ZMK6_HUMAN	06ZMK6_homo sapien
992	204.5	5.2	367	2	070169_MOUSE	070169 mus musculi	1065	201.5	5.1	597	2	04SMT3_HUMAN	04SMT3_tetodon n
993	204.5	5.2	373	2	04V3X9_DROME	04V3X9 drosophila	1066	201	5.1	247	2	042608_PETMA	042608_petromyzon
994	204.5	5.2	449	2	095RA3_DROME	095RA3 drosophila	1067	201	5.1	248	2	066105_XENLA	066105_xenopus lae
995	204.5	5.2	470	2	0661F4_XENTR	0661F4 xenopus tro	1068	201	5.1	260	2	081W69_HUMAN	081W69_homo sapien
996	204.5	5.2	752	1	CO2_PONPY	086675 pongo pygma	1069	201	5.1	275	2	066UD0_SPIPT	066UD0_culicoides
997	204.5	5.2	768	2	05T146_HUMAN	05T146 homo sapien	1070	201	5.1	351	2	0816K0_HOLDI	0816K0_holothricia
998	204.5	5.2	1008	2	0336F5_HUMAN	0336F5 homo sapien	1071	201	5.1	392	2	09VMZ3_DROME	09VMZ3_drosophila
999	204.5	5.2	1497	2	08NBT9_HUMAN	08NBT9 homo sapien	1072	201	5.1	484	2	0311V4_PANPA	0311V4_pan paniscu
1000	204.5	5.2	2470	1	NOTC2_MOUSE	035516 mus musculi	1073	201	5.1	484	2	0311V5_PANTR	0311V5_pan troglod
1001	204	5.2	190	2	05TT88_ANOGA	05TT88 anopheles g	1074	201	5.1	490	2	052KE2_MOUSE	052KE2_mus musculi
1002	204	5.2	220	2	04L1L5_9NEOP	04L1L5 sesamla non	1075	201	5.1	665	2	05SPB5_BRARE	05SPB5_brachydantio
1003	204	5.2	260	1	NREN_HUMAN	060259 homo sapien	1076	200.5	5.1	148	2	053325_OREMO	053326_otrochtrontis
1004	204	5.2	395	2	06R558_OSTNU	06R558 oestinia nu	1077	200.5	5.1	231	1	TRIP_PIG	P00761_sus scrofa
1005	204	5.2	417	1	TM1LD_RAT	08V1J4 r cranembu	1078	200.5	5.1	246	2	0792Z1_MOUSE	0792Z1_mus musculi
1006	204	5.2	645	2	05RG66_BRARE	05RG66 brachydantio	1079	200.5	5.1	247	2	05H729_MACMU	05H729_macaca mlla
1007	203.5	5.2	195	2	081XB4_HUMAN	081XB4 homo sapien	1080	200.5	5.1	249	2	09W7Q1_PAROL	09W7Q1_papilio mach
1008	203.5	5.2	238	2	07QF40_ANOGA	07QF40 anopheles g	1081	200.5	5.1	281	2	06NSB4_HUMAN	06NEB4_homo sapien
1009	203.5	5.2	247	1	TRX2_HUMAN	P07478 homo sapien	1082	200.5	5.1	358	2	057434_FUGRU	057434_fugu rubrip
1010	203.5	5.2	247	2	03SY20_HUMAN	03SY20 homo sapien	1083	200.5	5.1	415	1	PCOC2_HUMAN	0914K9_homo sapien
1011	203.5	5.2	247	2	03NV56_HUMAN	03NV56 homo sapien	1084	200.5	5.1	752	1	CO2_HUMAN	P06681_homo sapien
1012	203.5	5.2	261	2	0725F3_HUMAN	0725F3 homo sapien	1085	200.5	5.1	752	2	053HP3_HUMAN	053HP3_homo sapien
1013	203.5	5.2	263	1	FA9_CAVPO	P32038 rattus norv	1086	200.5	5.1	752	2	05JP69_HUMAN	05JP69_homo sapien
1014	203.5	5.2	285	1	FA9_CAVPO	P16295 cavia porce	1087	200.5	5.1	810	1	PLMN_MACMU	P13545_macaca mlla
1015	203.5	5.2	294	2	03V068_MOUSE	03V068 mus musculi	1088	200.5	5.1	951	1	NAS35_CAREL	020176_cenothadit
1016	203.5	5.2	309	2	027083_TACTR	027083 tachypneus	1089	200	5.1	247	2	042158_PETMA	042158_petromyzon
1017	203.5	5.2	335	2	08V1F2_MOUSE	08V1F2 mus musculi	1090	200	5.1	385	1	TSBP50_HUMAN	09A138_homo sapien
1018	203.5	5.2	664	1	DLIC_BRARE	091AT6 brachydantio	1091	200	5.1	454	2	046506_PAPPA	046506_papio hamad
1019	203.5	5.2	734	2	069D12_PIG	069D12 sus scrofa	1092	200	5.1	504	2	04FMFO_DROME	04FMFO_drosophila
1020	203.5	5.2	750	2	09W633_CYPCA	09W633 cyprinus ca	1093	200	5.1	564	2	07RT21_HUMAN	07RT21_homo sapien
1021	203.5	5.2	1323	2	07Z387_HUMAN	07Z387 homo sapien	1094	200	5.1	2061	2	04SRM9_TERING	04SRM9_tetradon n
1022	203.5	5.2	1432	1	ATRN_RAT	099186 rattus norv	1095	199.5	5.1	223	2	03VB14_DROME	09Y4M4_drosophila
1023	203.5	5.2	2067	2	059ED6_HUMAN	059ED6 homo sapien	1096	199.5	5.1	243	3	05M902_XENTR	05M902_xenopus tro
1024	203.5	5.2	2655	2	05XXM3_HUMAN	05XXM3 homo sapien	1097	199.5	5.1	247	1	TRX3_RAT	P08426_rattus norv
1025	203.5	5.2	3494	2	07LCS3_HUMAN	07LCS3 homo sapien	1098	199.5	5.1	247	1	05X1Z0_BRARE	05X1Z0_brachydantio
1026	203	5.1	254	2	05MBG2_XENTR	074880 xenopus tro	1099	199.5	5.1	257	1	KIK1_MACPA	007276_macaca fasc
1027	203	5.1	255	2	07OH50_ANOGA	074880 anopheles g	1100	199.5	5.1	258	2	028508_MACMU	028508_macaca mlla
1028	203	5.1	263	2	02PEN7_XENLA	02PEN7 xenopus lae	1101	199.5	5.1	258	1	Q5VAN4_CERTO	05VAN4_carpocobus
1029	203	5.1	370	2	Q9VA44_DROME	Q9VA44 drosophila	1102	199.5	5.1	275	1	TRX3_ANOGA	P33037_anopheles g
1030	203	5.1	403	2	Q9KSO6_VIBCH	Q9KSO6 vibrlio chol	1103	199.5	5.1	348	2	086W55_HUMAN	086W55_homo sapien
1031	203	5.1	520	2	021622_GLOMR	021622 glossina mo	1104	199.5	5.1	378	2	090WFO_TRASC	090WFO_trachemys s
1032	203	5.1	833	2	09YIC5_CYPCA	09YIC5 cyprinus ca	1105	199.5	5.1	1193	2	090819_CHICK	090819_gallus galli
1033	202.5	5.1	239	2	08N1C9_HUMAN	08N1C9 homo sapien	1106	199.5	5.1	2556	1	NOTC3_HUMAN	P46531_homo sapien
1034	202.5	5.1	255	1	KIK15_SAGOE	071196 baguinus oe	1107	199.5	5.1	2653	2	025253_LUCCU	025253_lucilia cup
1035	202.5	5.1	274	2	016133_ANOST	016133 anopheles s	1108	199	5.0	191	2	05TN52_ANOGA	05TN52_anopheles g
1036	202.5	5.1	339	2	06BDAB_PENUP	06BDAB penaeus jap	1109	199	5.0	254	2	05XG53_XENLA	05XG53_xenopus lae
1037	202.5	5.1	347	2	05EBB4_RAT	05EBB4 rattus norv	1110	199	5.0	263	2	062562_PENVA	062562_penaeus van
1038	202.5	5.1	372	2	09W2C8_DROME	09W2C8 drosophila	1111	199	5.0	264	2	06GPV5_XENLA	06GPV5_xenopus lae
1039	202.5	5.1	1327	2	059ED1_HUMAN	059ED1 homo sapien	1112	199	5.0	264	2	080GR6_XENLA	080GR6_xenopus lae
1040	202.5	5.1	3623	1	CUBN_HUMAN	064949 homo sapien	1113	199	5.0	266	2	05M8V7_XENTR	05M8V7_xenopus tro
1041	202	5.1	241	1	TRY1_GADMO	P16049 gadus morhu	1114	199	5.0	268	2	051S29_MAYDE	051S29_mayetiola d
1042	202	5.1	246	1	KLK_PIG	P00752 sus scrofa	1115	199	5.0	317	2	03UMG7_MOUSE	03UMG7_mus musculi
1043	202	5.1	249	2	07O9X5_ANOGA	07O9X5 anopheles g	1116	199	5.0	401	2	06LH17_PHOPI	06LH17_photobacter
1044	202	5.1	263	2	04L1K1_9NEOP	04L1K1 sesamla non	1117	199	5.0	441	2	09XXV0_BOMMO	09XXV0_bombyx mori
1045	202	5.1	331	2	032NG3_XENLA	032NG3 xenopus lae	1118	199	5.0	1303	2	066S84_UBROC	066S84_oltopleura
1046	202	5.1	380	2	068D21_HUMAN	068D21 homo sapien	1119	198.5	5.0	237	2	017035_ANOGA	017035_anopheles g
1047	202	5.1	394	2	05MPB7_MANSE	05MPB7 manduca sex	1120	198.5	5.0	243	1	TRY1_BOVIN	P00760_bos taurus
1048	202	5.1	488	2	081UV8_HUMAN	081UV8 homo sapien	1121	198.5	5.0	260	2	07SZC3_CHICK	07SZC3_gallus galli
1049	202	5.1	605	2	05MPB8_MANSE	05MPB8 manduca sex	1122	198.5	5.0	311	1	TRYQ3_MOUSE	09BVC3_mus musculi
1050	202	5.1	743	2	09YGE7_ONCMY	09YGE7 oncohytnchu	1123	198.5	5.0	357	2	07PVQ3_ANOGA	07PVQ3_anopheles g
1051	202	5.1	797	2	0501G6_ORYLA	0501G6 oryzias lat	1124	198.5	5.0	364	2	0701D1_ANOGA	0701D1_anopheles g
1052	202	5.1	2321	1	NOTC3_HUMAN	09um47 homo sapien	1125	198.5	5.0	364	2	09NAS9_ANOGA	09NAS9_anopheles g
1053	201.5	5.1	195	2	080007_HUMAN	080007 homo sapien	1126	198.5	5.0	388	2	044330_MANSE	044330_manduca sex

1127	198.5	5.0	461	2	Q8T4N2_RH1AP	Q8c4n2_rh1cephal	1200	194.5	4.9	247	2	Q561Z7_BRARE	Q561z7_brachydantio
1128	198.5	5.0	752	1	CO2_GORGO	Q86a30_gorilla gor	1201	194.5	4.9	258	2	Q5V4N2_CERTO	Q5v4n2_cercocobus
1129	198.5	5.0	829	2	Q5T145_HUMAN	Q5t145_homo sapien	1202	194.5	4.9	261	2	Q7Z5F4_HUMAN	Q7z5f4_homo sapien
1130	198.5	5.0	829	2	Q4PPC3_MOUSE	Q4ppc3_mus musculu	1203	194.5	4.9	278	2	Q4SH19_TETNG	Q4sh19_tetracton n
1131	198.5	5.0	830	2	Q5T145_HUMAN	Q5t145_homo sapien	1204	194.5	4.9	283	2	Q5V222_9ANNE	Q5v222_lumbicue b
1132	198.5	5.0	1051	2	Q5U4U1_XENTLA	Q5u4u1_xenopus lae	1205	194.5	4.9	343	1	PLMN_SHEEP	Q54286_ovis aries
1133	198.5	5.0	1214	2	Q90YD2_XENTLA	Q90ydz_xenopus lae	1206	194.5	4.9	359	2	Q4SPG0_TETNG	Q4spg0_tetracton n
1134	198.5	5.0	1289	2	Q59FL3_HUMAN	Q59fl3_homo sapien	1207	194.5	4.9	393	2	Q5MPC5_MANSE	Q5mpc5_manduca sex
1135	198	5.0	235	1	TRYD_HUMAN	Q9b3j3_homo sapien	1208	194.5	4.9	394	2	Q5TMN0_ANOGA	Q5tmn0_anopheles g
1136	198	5.0	259	1	DERF3_DERPA	P492f5_dematophag	1209	194.5	4.9	461	2	Q4V7J4_XENTLA	Q4v7j4_xenopus lae
1137	198	5.0	261	2	Q6QX60_9MAX1	Q6q460_lepeophthei	1210	194.5	4.9	1374	2	Q9VSU0_DROME	Q9v5u0_drosophila
1138	198	5.0	268	2	Q51S8B_MAYDE	Q51s8b_mayetiola d	1211	194.5	4.9	1449	2	Q9U112_DROME	Q9u112_drosophila
1139	198	5.0	427	2	Q5D198_MANSE	Q5d198_manduca sex	1212	194.5	4.9	1450	2	Q810B8_DROME	Q810b8_drosophila
1140	198	5.0	427	2	Q6Y2X4_MANSE	Q6y2x4_manduca sex	1213	194.5	4.9	1462	2	Q9U113_DROME	Q9u113_drosophila
1141	198	5.0	760	1	CO2_MOUSE	P21180_mus musculu	1214	194.5	4.9	2382	2	Q9H119_DROME	Q9h119_drosophila
1142	198	5.0	1024	1	SE2GL_HUMAN	Q9b3h1_homo sapien	1215	194.5	4.9	2409	2	Q960G6_DROME	Q960g6_drosophila
1143	198	5.0	1128	2	Q4S6G8_TETNG	Q4s6g8_tetracton n	1216	194.5	4.9	2428	2	Q816X6_BOOMI	Q816x6_boophilus m
1144	197.5	5.0	226	1	COGS_UCAPU	P00771_uca pugilac	1217	194.5	4.9	2549	2	Q21697_CIOIN	Q21697_ciona intes
1145	197.5	5.0	242	2	Q6NTB8_HUMAN	Q6nbt8_homo sapien	1218	194.5	4.9	2786	2	Q9VSU2_DROME	Q9v5u2_drosophila
1146	197.5	5.0	246	2	Q61E66_RAT	Q61e66_rattus norv	1219	194	4.9	243	2	Q7BEF7_ANOGA	Q7bef7_drosophila
1147	197.5	5.0	248	1	KXK12_HUMAN	Q9ukr0_homo sapien	1220	194	4.9	245	2	Q42160_PETMA	Q42160_petrymazon
1148	197.5	5.0	251	2	Q7Q4H6_ANOGA	Q7q4h6_anopheles g	1221	194	4.9	247	2	Q70T74_HORSE	Q70t74_equis cabal
1149	197.5	5.0	255	2	Q96RQ0_HUMAN	Q96rq0_homo sapien	1222	194	4.9	253	2	Q9VAG3_DROME	Q9vag3_drosophila
1150	197.5	5.0	258	2	Q28805_PANTR	Q28805_pan troglod	1223	194	4.9	259	1	CFAD_PIG	Q9vags_drosophila
1151	197.5	5.0	263	2	Q6H319_PIG	Q6h319_sus scrofa	1224	194	4.9	267	1	TRY7_ANOGA	P51179_sus scrofa
1152	197.5	5.0	263	2	Q53GZ8_HUMAN	Q53g28_homo sapien	1225	194	4.9	379	2	Q4SU40_TETNG	Q4su40_choristoneu
1153	197	5.0	222	2	Q91WZ0_RAT	Q91wz0_rattus norv	1226	194	4.9	556	2	Q803D5_BRARE	Q803d5_brachydantio
1154	197	5.0	253	2	Q5Q8G3_9D1PT	Q5q8g3_culicoides	1227	194	4.9	578	2	Q3USM6_MOUSE	Q3usm6_mus musculu
1155	197	5.0	258	2	Q7QKX6_ANOGA	Q7qkx6_anopheles g	1228	194	4.9	806	1	PLMN_MACRU	Q18783_mactropus eu
1156	197	5.0	261	2	Q9VXC7_DROME	Q9vxc7_drosophila	1229	193.5	4.9	183	2	Q6FLJ7_9ERUCA	Q6flj7_femutropena
1157	197	5.0	268	2	Q51Y42_MAYDE	Q51y42_mayetiola d	1230	193.5	4.9	235	2	Q70820_ANOGA	Q70820_anopheles g
1158	197	5.0	338	1	PLMN_HORSE	P80010_equis cabal	1231	193.5	4.9	245	2	Q792Y9_MOUSE	Q792y9_mus musculu
1159	197	5.0	385	2	Q5U365_RAT	Q5u365_rattus norv	1232	193.5	4.9	246	2	Q9GUK9_MOUSE	Q9guk9_m_tespa (tr
1160	197	5.0	421	2	Q95R85_DROME	Q95r85_drosophila	1233	193.5	4.9	247	2	Q6T376_EISFO	Q6t376_eisenta foe
1161	197	5.0	585	2	Q9U0E2_TRICA	Q9u0e2_citrobolium c	1234	193.5	4.9	247	2	Q9W7Q5_PAROL	Q9w7q5_parallelchty
1162	197	5.0	745	2	Q91701_XENTLA	Q91701_xenopus lae	1235	193.5	4.9	256	2	Q27540_CHOFU	Q27540_choristoneu
1163	197	5.0	760	2	Q70350_MOUSE	Q70350_mus musculu	1236	193.5	4.9	262	2	Q70144_ANOGA	Q70144_anopheles g
1164	196.5	5.0	219	2	Q91036_GADMO	Q91036_gadus moriu	1237	193.5	4.9	263	2	Q9V5X7_DROME	Q9v5x7_drosophila
1165	196.5	5.0	231	2	Q6GYU5_STRCA	Q6gyu5_struthio ca	1238	193.5	4.9	269	2	Q5M9Z5_XENTR	Q5m9z5_xenopus tro
1166	196.5	5.0	246	2	Q4SH18_TETNG	Q4sh18_tetracton n	1239	193.5	4.9	317	2	Q9DGR3_XENTLA	Q9dgr3_xenopus lae
1167	196.5	5.0	259	2	Q81RE0_DROME	Q81re0_drosophila	1240	193.5	4.9	347	2	Q70B73_ANOGA	Q70b73_anopheles g
1168	196.5	5.0	269	1	ELA2B_HUMAN	P08218_homo sapien	1241	193.5	4.9	789	2	Q8N1B3_HUMAN	Q8n1b3_homo sapien
1169	196.5	5.0	298	2	Q8T4N2_RH1AP	Q8t4n2_rh1cephal	1242	193.5	4.9	1089	2	Q8T3A0_CIOIN	Q8t3a0_ciona intes
1170	196.5	5.0	362	2	Q566K9_XENTR	Q566k9_xenopus tro	1243	193.5	4.9	1235	2	Q610S0_HUMAN	Q610s0_homo sapien
1171	196.5	5.0	570	1	FEB3_STRPU	P49013_strongyloce	1244	193.5	4.9	2471	1	NOTC2_RAT	Q9g430_rattus norv
1172	196.5	5.0	829	2	Q6NUL0_HUMAN	Q6nul0_homo sapien	1245	193	4.9	293	2	Q30808_EISFO	Q30808_eisenta foe
1173	196.5	5.0	2030	2	Q2WBV6_PLADU	Q2wbv6_platyneris	1246	193	4.9	253	1	ELAI_CANFA	Q9xy56_canocephal
1174	196.5	5.0	2524	1	NORCH_XENTLA	P21783_xenopus lae	1247	193	4.9	268	2	Q9XV56_CTEFE	Q9xv56_canis fam1l
1175	196	5.0	248	2	Q6GPK7_XENTLA	Q6gpk7_xenopus lae	1248	193	4.9	258	1	Q9XKX7_BOVIN	Q9xkx7_bos tauru
1176	196	5.0	257	2	Q52KX8_XENTLA	Q52kx8_xenopus lae	1249	193	4.9	269	2	Q95KM7_HUMAN	Q95km7_bos tauru
1177	196	5.0	262	2	Q5XGPs_XENTLA	Q5xgPs_xenopus lae	1250	193	4.9	272	2	Q52NM5_9D1PT	Q52nm5_anopheles c
1178	196	5.0	270	1	ELA3B_HUMAN	P08861_homo sapien	1251	193	4.9	315	2	Q5MG83_LONON	Q5mg83_lonomaia odl
1179	196	5.0	275	2	Q6GUC8_9D1PT	Q6guc8_culicoides	1252	193	4.9	393	2	Q57433_FUGRU	Q57433_fugu rubrip
1180	196	5.0	400	2	Q9GRG2_TETNG	Q9grg2_tenebrio mo	1253	193	4.9	423	2	Q57430_ANOGA	Q57430_anopheles g
1181	196	5.0	418	2	Q4RJM2_TETNG	Q4rjm2_tetracton n	1254	193	4.9	447	2	Q499M3_HUMAN	Q499m3_homo sapien
1182	196	5.0	432	2	Q3KR76_RAT	Q3kr76_rattus norv	1255	193	4.9	481	2	Q9H284_HUMAN	Q9h284_homo sapien
1183	196	5.0	484	2	Q31IV3_9PRIM	Q31iv3_gotilla gor	1256	193	4.9	543	2	Q6PHN6_MOUSE	Q6phn6_mus musculu
1184	196	5.0	3623	1	CUBN_RAT	Q70244_rattus norv	1257	193	4.9	962	2	Q8C420_MOUSE	Q8c420_mus musculu
1185	195.5	5.0	247	2	Q5H730_MACMU	P51124_maca mul	1258	193	4.9	963	2	Q6P1D5_MOUSE	Q6p1d5_mus musculu
1186	195.5	5.0	257	1	GRAM_HUMAN	Q9gpd7_drosophila	1259	193	4.9	1275	2	Q41PE4_CABER	Q41pe4_caenorhabd
1187	195.5	5.0	267	2	Q9GPD7_DROME	Q9gpd7_drosophila	1260	193	4.9	2030	2	Q4RHP2_TETNG	Q4rhp2_tetracton n
1188	195.5	5.0	274	2	Q17086_ANOST	Q17086_anopheles b	1261	192.5	4.9	178	2	Q93594_DICIA	Q93594_dicentrarch
1189	195.5	5.0	276	2	Q18443_HELAM	Q18443_helicoverpa	1262	192.5	4.9	232	2	Q94508_DERRA	Q94508_dermatophag
1190	195.5	5.0	752	1	CO2_PANTR	Q8eq74_pan troglod	1263	192.5	4.9	243	2	Q5M976_XENTR	Q5m976_xenopus tro
1191	195.5	5.0	2471	1	NOTC2_HUMAN	Q04721_homo sapien	1264	192.5	4.9	245	2	Q5T189_ANOGA	Q5t189_anopheles g
1192	195.5	5.0	2471	2	Q4ADVA_SEROU	Q4adv4_seriola qui	1265	192.5	4.9	246	2	Q9Z1R9_MOUSE	Q9z1r9_mus musculu
1193	195	4.9	261	1	KXK6_MOUSE	P15547_mus musculu	1266	192.5	4.9	255	1	Q8NTH4_HUMAN	Q8nth4_choristoneu
1194	195	4.9	262	2	Q7Z0G3_9D1PT	Q7z0g3_phlebotomus	1267	192.5	4.9	267	2	Q4GRH5_BRARE	Q4grh5_brechydantio
1195	195	4.9	336	2	Q3V0Q7_MOUSE	Q3v0q7_mus musculu	1268	192.5	4.9	276	1	Q8MOY4_DROME	Q8moy4_drosophila
1196	195	4.9	432	1	UROK_RAT	P29598_r uroknae	1269	192.5	4.9	381	2	Q9H804_HUMAN	Q9h804_homo sapien
1197	195	4.9	246	1	TRY1_RAT	P00762_rattus norv	1271	192.5	4.9	438	2	Q5RDX7_PONFY	Q5rdx7_pongo pygna
1198	194.5	4.9	246	1	Q9R0T7_MOUSE	Q9r0t7_m	1272	192.5	4.9	439	2		

1273	192.5	4.9	669	2	Q4SC13_TETNG	Q4AC13_tetradon n	1346	189.5	4.8	257	2	Q27440_AEDAE	Q27440 aedes aegypti
1274	192.5	4.9	754	2	P79816_ORYIA	P79816 oryzae lat	1347	189.5	4.8	263	2	Q02570_CULOU	Q02570 culicx quin
1275	192	4.9	233	2	Q70344_ANOGA	Q70344 anopheles g	1348	189.5	4.8	263	2	Q09Y16_PENVA	Q09Y16 penaeus van
1276	192	4.9	244	2	Q42159_PETMA	Q42159 petromyzon	1349	189.5	4.8	266	2	Q27761_PENVA	Q27761 penaeus van
1277	192	4.9	246	2	Q09B17_LUMRU	Q09B17 lumbricus r	1350	189.5	4.8	271	2	Q09RS6_DROME	Q09RS6 drosophila
1278	192	4.9	249	2	Q5TWT2_ANOGA	Q5TWT2 anopheles r	1351	189.5	4.8	281	2	Q08YB5_DROME	Q08YB5 drosophila
1279	192	4.9	254	2	Q09XY10_RHYDO	Q09XY10 rhyssopetra	1352	189.5	4.8	381	2	Q09B66_DROME	Q09B66 drosophila
1280	192	4.9	256	2	Q6MYJ6_BDEBA	Q6MYJ6 bdellovibrio	1353	189.5	4.8	384	2	Q05CBV5_9D1PT	Q05CBV5 elaphie sp.
1281	192	4.9	265	2	Q4S848_TETNG	Q4S848 tetradon n	1354	189.5	4.8	385	2	Q09W52_9SAUR	Q09W52 elaphie sp.
1282	192	4.9	364	2	Q70K13_ANOGA	Q70K13 anopheles g	1355	189.5	4.8	431	2	Q4RUW3_TETNG	Q4RUW3 tetradon n
1283	192	4.9	380	2	Q09YK5_ANOGA	Q09YK5 anopheles g	1356	189.5	4.8	466	2	Q4SUA3_TETNG	Q4SUA3 tetradon n
1284	192	4.9	383	2	Q77102_MANSE	Q77102 manuca sex	1357	189.5	4.8	470	2	Q083A1_CTOIN	Q083A1 ciona intes
1285	191.5	4.9	225	2	Q5TXH2_ANOGA	Q5TXH2 anopheles g	1358	189.5	4.8	572	1	Q1MPS7_MOUSE	Q1MPS7 mouse
1286	191.5	4.9	243	2	Q5M959_XENTR	Q5M959 xenopus tro	1359	189.5	4.8	649	2	Q28657_RABIT	Q28657 oryctolagus
1287	191.5	4.9	247	1	TRV1_HUMAN	P07477 homo sapien	1360	189.5	4.8	2386	1	EGFL4_HUMAN	Q7470 homo sapien
1288	191.5	4.9	247	2	Q5NV57_HUMAN	Q5NV57 homo sapien	1361	189	4.8	181	2	Q09GSM5_CHRBE	Q09GSM5 chrysomya b
1289	191.5	4.9	247	2	Q17039_ANOGA	Q17039 anopheles g	1362	189	4.8	245	2	Q03H18_EISFO	Q03H18 eisenia foe
1290	191.5	4.9	265	2	Q6QX61_9MAXI	Q6QX61 lepeophthei	1363	189	4.8	245	2	Q09B18_LUMRU	Q09B18 lumbricus r
1291	191.5	4.9	270	2	Q4S520_TETNG	Q4S520 tetradon n	1364	189	4.8	246	1	TRVB_RAT	P34822 rattus norv
1292	191.5	4.9	281	2	Q76898_DROME	Q76898 drosophila	1365	189	4.8	246	1	Q7TT42_MOUSE	Q7TT42 mus musculu
1293	191.5	4.9	284	2	Q81RX5_DROME	Q81RX5 drosophila	1366	189	4.8	246	1	TRV4_RAT	P34822 rattus norv
1294	191.5	4.9	285	2	Q70298_ANOGA	Q70298 anopheles g	1367	189	4.8	253	1	KUK7_HUMAN	P49862 homo sapien
1295	191.5	4.9	360	2	Q08X54_DROME	Q08X54 drosophila	1368	189	4.8	405	2	QAS6F4_TETNG	QAS6F4 tetradon n
1296	191.5	4.9	385	2	Q08X51_DROME	Q08X51 drosophila	1369	189	4.8	414	2	PCOC2_MOUSE	Q46P4 mus musculu
1297	191.5	4.9	480	2	Q661T1_XENLA	Q661T1 xenopus lae	1370	189	4.8	414	1	Q3V1K6_MOUSE	Q3V1K6 mus musculu
1298	191.5	4.9	579	2	Q06D09_HUMAN	Q06D09 homo sapien	1371	189	4.8	646	1	LYAM3_BOVIN	Q42201 bos tauru
1299	191.5	4.9	713	2	Q080P0_MOUSE	Q080P0 mus musculu	1372	189	4.8	758	2	Q08C1P8_RAT	Q08C1P8 rattus norv
1300	191.5	4.9	830	1	LYAM3_HUMAN	P16109 homo sapien	1373	189	4.8	1285	1	CRUM2_HUMAN	Q51J48 homo sapien
1301	191.5	4.9	897	2	Q3V651_MOUSE	Q3V651 mus musculu	1374	189	4.8	1532	2	Q5TQGI_ANOGA	Q5TQGI anopheles g
1302	191.5	4.9	2468	2	Q080E4_BRARE	Q080E4 brachydantio	1375	188.5	4.8	182	2	Q6PPL5_9EUCA	Q6PPL5 necatridina
1303	191.5	4.9	3396	2	Q09W55_DROME	Q09W55 drosophila	1376	188.5	4.8	239	2	Q6LCU4_LUMRU	Q6LCU4 lumbricus r
1304	191.5	4.8	228	2	Q06PEJ8_HUMAN	Q06PEJ8 homo sapien	1377	188.5	4.8	246	2	Q792Y8_MOUSE	Q792Y8 mus musculu
1305	191	4.8	230	2	Q4ROD7_TETNG	Q4ROD7 tetradon n	1378	188.5	4.8	263	2	Q706S0_ANOGA	Q706S0 anopheles g
1306	191	4.8	248	2	Q5H732_MACMU	Q5H732 macaca mula	1379	188.5	4.8	266	2	Q6AZC0_BRARE	Q6AZC0 brachydantio
1307	191	4.8	254	1	KUK4_HUMAN	Q09YK2 homo sapien	1380	188.5	4.8	282	1	PA9_RAT	P16296 rattus norv
1308	191	4.8	254	2	Q4VB16_HUMAN	Q4VB16 homo sapien	1381	188.5	4.8	290	2	PRS27_HUMAN	Q09GR3 homo sapien
1309	191	4.8	254	2	Q4VB17_HUMAN	Q4VB17 homo sapien	1382	188.5	4.8	330	1	Q6IE67_RAT	Q6IE67 rattus norv
1310	191	4.8	255	2	Q25227_LUCCU	Q25227 lucilia cup	1383	188.5	4.8	382	2	Q09W14_CROTI	Q09W14 crocodilus
1311	191	4.8	256	2	Q818E5_9D1PT	Q818E5 ocellerata	1384	188.5	4.8	471	2	Q4RYT0_TETNG	Q4RYT0 tetradon n
1312	191	4.8	273	2	Q51Y40_MAYDE	Q51Y40 mayetiola d	1385	188.5	4.8	713	2	Q0962W9_PODCA	Q0962W9 podocoryne
1313	191	4.8	277	2	Q81010_DROME	Q81010 drosophila	1386	188.5	4.8	714	1	DL11_RAT	P97677 rattus norv
1314	191	4.8	282	2	Q4VB11_BRARE	Q4VB11 brachydantio	1387	188.5	4.8	1216	2	Q5T2K7_BRARE	Q5T2K7 brachydantio
1315	191	4.8	317	2	Q8K4D1_MOUSE	Q8K4D1 mus musculu	1388	188.5	4.8	2330	1	EGFL4_MOUSE	P60882 mus musculu
1316	191	4.8	317	2	Q8K4I7_MOUSE	Q8K4I7 mus musculu	1389	188	4.8	228	2	Q6FWJ3_HUMAN	Q6FWJ3 homo sapien
1317	191	4.8	415	2	Q09GRW0_HOLDI	Q09GRW0 holotrichia	1390	188	4.8	230	2	Q05U51_HUMAN	Q05U51 homo sapien
1318	191	4.8	646	2	Q29097_PIG	Q29097 sus scrofa	1391	188	4.8	235	2	Q08A4E0_HUMAN	Q08A4E0 homo sapien
1319	191	4.8	758	2	Q6MG73_RAT	Q6MG73 rattus norv	1392	188	4.8	253	1	QALIK4_9NEOP	P00746 homo sapien
1320	190.5	4.8	245	2	Q4G0C2_MOUSE	Q4G0C2 mus musculu	1393	188	4.8	254	2	KUKR_FRANA	P35824 praomys nat
1321	190.5	4.8	246	2	Q3V2G3_MOUSE	Q3V2G3 mus musculu	1394	188	4.8	263	1	Q6P326_XENTR	Q6P326 xenopus tro
1322	190.5	4.8	246	2	Q792Z0_MOUSE	Q792Z0 mus musculu	1395	188	4.8	265	2	Q6RW10_PARCM	Q6RW10 parailthode
1323	190.5	4.8	257	2	Q818E3_9D1PT	Q818E3 aedes polyn	1396	188	4.8	266	2	Q2LZD5_DROPS	Q2LZD5 drosophila
1324	190.5	4.8	317	2	Q5PMP3_XENTR	Q5PMP3 xenopus tro	1397	188	4.8	271	2	Q18487_PENVA	Q18487 penaeus van
1325	190.5	4.8	578	2	Q335M3_HUMAN	Q335M3 homo sapien	1398	188	4.8	272	2	Q5T1Y44_MAYDE	Q5T1Y44 mayetiola d
1326	190.5	4.8	579	2	Q09B79_HUMAN	Q09B79 homo sapien	1399	188	4.8	273	2	Q5T1Y44_MAYDE	Q5T1Y44 mayetiola d
1327	190.5	4.8	762	2	Q09Y1C6_CYPCA	Q09Y1C6 cyprinus ca	1400	188	4.8	273	2	Q5VXP8_DROME	Q5VXP8 drosophila
1328	190.5	4.8	762	1	LYAM3_MOUSE	Q01102 mus musculu	1401	188	4.8	276	2	Q68FNG_BRARE	Q68FNG brachydantio
1329	190.5	4.8	768	2	Q3ZMFI_MOUSE	Q3ZMFI mus musculu	1402	188	4.8	278	2	Q07K2R3_DROME	Q07K2R3 drosophila
1330	190.5	4.8	1064	1	FBP1_STRPU	P10079 strongyloce	1403	188	4.8	282	2	PLMN_CANPA	P80009 canis famli
1331	190.5	4.8	2038	2	Q70F52_ANOGA	Q70F52 anopheles g	1404	188	4.8	333	1	Q5D1S9_MANSE	Q5D1S9 manuca sex
1332	190.5	4.8	2341	2	Q4RU01_TETNG	Q4RU01 tetradon n	1405	188	4.8	383	2	Q641D3_ANTGR	Q641D3 anthromus
1333	190	4.8	239	2	Q70208_ANOGA	Q70208 anopheles g	1406	188	4.8	404	2	Q5XHT5_XENLA	Q5XHT5 xenopus lae
1334	190	4.8	243	2	Q86VJ5_HUMAN	Q86VJ5 homo sapien	1407	188	4.8	458	2	Q09W17_HOMAN	Q09W17 homatius ame
1335	190	4.8	245	2	Q6DKO3_EISFO	Q6DKO3 eisenia foe	1408	188	4.8	953	2	Q05XV75_MAYDE	Q05XV75 mayetiola d
1336	190	4.8	253	2	Q8WZB4_HUMAN	Q8WZB4 homo sapien	1409	187.5	4.8	247	2	Q5UTJ5_HUMAN	Q5UTJ5 homo sapien
1337	190	4.8	264	2	Q709S0_ANOGA	Q709S0 anopheles g	1410	187.5	4.8	247	2	Q6TISJ4_HUMAN	Q6TISJ4 homo sapien
1338	190	4.8	277	2	Q08Q44_PIG	Q08Q44 sus scrofa	1411	187.5	4.8	250	2	Q17036_ANOGA	Q17036 anopheles g
1339	190	4.8	282	2	Q25395_LUMRU	Q25395 lumbricus r	1412	187.5	4.8	250	2	Q709W4_ANOGA	Q709W4 anopheles g
1340	190	4.8	334	2	Q46507_PAPHA	Q46507 papio hamad	1413	187.5	4.8	251	2	Q08N203_HUMAN	Q08N203 homo sapien
1341	190	4.8	378	2	Q08Y50_DROME	Q08Y50 drosophila	1414	187.5	4.8	252	2	Q4HV44_GIBZE	Q4HV44 gibbeterella
1342	189.5	4.8	228	2	Q466B0_TETNG	Q466B0 tetradon n	1415	187.5	4.8	257	2	Q09B449_AEDAE	Q09B449 aedes aegypti
1343	189.5	4.8	241	2	Q09T135_RAT	Q09T135 rattus norv	1416	187.5	4.8	283	2	Q25394_LUMRU	Q25394 lumbricus r
1344	189.5	4.8	246	2	Q7M754_MOUSE	Q7M754 mus musculu	1417	187.5	4.8	283	2	Q08TUT7_LUMRU	Q08TUT7 lumbricus r
1345	189.5	4.8	255	2	Q9Y7A9_METAN	Q9Y7A9 metarhizium	1418	187.5	4.8	304	1	TRV3_HUMAN	P35030 homo sapien

1419	187.5	4.8	304	2	Q5VXV0_HUMAN	Q5VXV0_homo sapien
1420	187.5	4.8	425	2	Q4SAR5_TETNG	Q4SAR5_tetracodon n
1421	187.5	4.8	435	2	Q4SPXS_ANGCA	Q4SPXS_anopheles g
1422	187.5	4.8	625	2	Q4SCR3_TETNG	Q4SCR3_tetracodon n
1423	187.5	4.8	1008	2	Q5ZQU0_RAT	Q5ZQU0_rattus norv
1424	187.5	4.8	1216	2	Q5ZQU5_BRARE	Q5ZQU5_birchydantio
1425	187.5	4.7	246	1	TRYA_RAT	P32821_rattus norv
1426	187	4.7	256	2	Q18439_HELAM	Q18439_helicoverpa
1427	187	4.7	261	2	Q29474_CANFA	Q29474_canis famli
1428	187	4.7	271	1	CTRBI_BENVA	Q00871_penaues van
1429	187	4.7	291	1	Q2510_MANSE	Q2510_manduca sex
1430	187	4.7	449	2	Q5VXMI_HUMAN	Q5VXMI_homo sapien
1431	187	4.7	753	2	Q2Y2P2_GINCI	Q2Y2P2_gingilymosto
1432	187	4.7	1301	2	Q7PRP5_ANGCA	Q7PRP5_anopheles g
1433	187	4.7	2743	2	Q7O434_ANGCA	Q7O434_aedes albop
1434	186.5	4.7	235	2	Q9GTX7_AEDAL	Q9GTX7_aedes albop
1435	186.5	4.7	250	2	Q93265_PSEAM	Q93265_pseudopleur
1436	186.5	4.7	251	2	Q32M27_MOUSE	Q32M27_mus muscull
1437	186.5	4.7	257	2	Q818E2_AEDTR	Q818E2_aedes trile
1438	186.5	4.7	287	2	Q9VTV2_DROME	Q9VTV2_drosophila
1439	186.5	4.7	397	2	Q9W314_DROME	Q9W314_drosophila
1440	186.5	4.7	437	2	Q4QR89_RAT	Q4QR89_rattus norv
1441	186.5	4.7	569	2	Q4RWS2_TETNG	Q4RWS2_tetracodon n
1442	186.5	4.7	1254	2	Q5TZK8_BRARE	Q5TZK8_birchydantio
1443	186	4.7	181	2	Q9GSM1_CHRBE	Q9GSM1_chrysomya b
1444	186	4.7	249	2	Q92046_DISMA	Q92046_drosophilu
1445	186	4.7	275	2	Q7O494_ANGCA	Q7O494_anopheles g
1446	186	4.7	324	2	Q6BD05_DROYA	Q6BD05_drosophila
1447	186	4.7	449	2	Q9VDU8_DROME	Q9VDU8_drosophila
1448	186	4.7	721	2	Q3KN43_DROME	Q3KN43_drosophila
1449	186	4.7	1594	2	Q95218_RABIT	Q95218_oryctolagus
1450	185.5	4.7	211	2	Q8J009_HUMAN	Q8J009_homo sapien
1451	185.5	4.7	256	2	Q9XY51_CTRFE	Q9XY51_ctenoccephal
1452	185.5	4.7	261	1	DERP3_DERPT	P39675_dermatophag
1453	185.5	4.7	267	2	Q5MPC7_MANSE	Q5MPC7_manduca sex
1454	185.5	4.7	292	2	Q18438_HELAM	Q18438_helicoverpa
1455	185.5	4.7	310	1	TMSF8_MOUSE	Q9QYZ9_mus muscull
1456	185.5	4.7	439	2	Q8BHM5_MOUSE	Q8BHM5_m o day neo
1457	185.5	4.7	542	2	Q7MK55_VIBVY	Q7MK55_vibrio vuln
1458	185.5	4.7	711	1	HGFL_HUMAN	P26827_h hepatocyt
1459	185.5	4.7	711	2	Q5JGN8_HUMAN	Q5JGN8_homo sapien
1460	185.5	4.7	711	2	Q6GTN4_HUMAN	Q6GTN4_homo sapien
1461	185.5	4.7	840	2	Q7P2M9_ANGCA	Q7P2M9_anopheles g
1462	185.5	4.7	928	1	NRPI_XENLA	P28624_xenopus lae
1463	185.5	4.7	1254	2	Q9OY56_BRARE	Q9OY56_birchydantio
1464	185.5	4.7	1254	2	Q9YH02_BRARE	Q9YH02_birchydantio
1465	185	4.7	250	2	Q7P243_ANGCA	Q7P243_anopheles g
1466	185	4.7	256	1	KLKB4_MOUSE	P00757_mus muscull
1467	185	4.7	258	1	KLKI_PAPHA	Q28773_papio hamad
1468	185	4.7	287	2	Q9NH10_AGRIP	Q9NH10_agrotis ips
1469	185	4.7	308	2	Q3KNK7_MOUSE	Q3KNK7_mus muscull
1470	185	4.7	508	2	Q8DA23_VIBVU	Q8DA23_vibrio vuln
1471	185	4.7	644	2	Q5Y144_HUMAN	Q5Y144_homo sapien
1472	185	4.7	709	2	Q7ZTN9_XENLA	Q7ZTN9_xenopus lae
1473	185	4.7	767	2	Q3MIDI_RAT	Q3MIDI_rattus norv
1474	184.5	4.7	173	2	Q4Z8K5_9PERC	Q4Z8K5_celidichthy
1475	184.5	4.7	247	2	Q6EPG9_FUGRU	Q6EPG9_fugu rubrip
1476	184.5	4.7	255	2	Q210D8_SNEOP	Q210D8_ostreiria fu
1477	184.5	4.7	265	2	Q4QY81_SPAUP	Q4QY81_spartus aura
1478	184.5	4.7	265	2	Q562D3_XENTR	Q562D3_xenopus tro
1479	184.5	4.7	295	2	Q18445_HELAM	Q18445_helicoverpa
1480	184.5	4.7	295	2	Q18450_HELAM	Q18450_helicoverpa
1481	184.5	4.7	321	2	Q6GNK3_XENLA	Q6GNK3_xenopus lae
1482	184.5	4.7	427	2	Q8BQH6_MOUSE	Q8BQH6_mus muscull
1483	184.5	4.7	923	2	Q6EPAR3_MOUSE	Q6EPAR3_mus muscull
1484	184.5	4.7	1213	1	JAG1B_BRARE	Q9OY54_birchydantio
1485	184.5	4.7	1554	2	Q4SMT5_TETNG	Q4SMT5_tetracodon n
1486	184	4.7	246	2	Q6DKO3_ETSFO	Q6DKO3_eisentra fee
1487	184	4.7	246	2	Q817P0_9ANNE	Q817P0_lumbidicus b
1488	184	4.7	251	2	Q510Q6_XENTR	Q510Q6_xenopus tro
1489	184	4.7	314	1	TEST_HUMAN	Q9Y6Q6_homo sapien
1490	184	4.7	324	2	Q4SL79_TETNG	Q4SL79_tetracodon n
1491	184	4.7	325	2	Q4ST88_TETNG	Q4ST88_tetracodon n

1492	184	4.7	358	2	Q5XK88_XENLA	Q5XK88_xenopus lae
1493	184	4.7	381	2	Q7RP23_RAT	Q7RP23_rattus norv
1494	184	4.7	395	2	Q7RSK1_DROME	Q7RSK1_drosophila
1495	184	4.7	405	2	Q8SZ60_DROME	Q8SZ60_drosophila
1496	184	4.7	745	2	Q90WF9_TRISC	Q90WF9_citrakis scy
1497	184	4.7	988	2	Q81WY4_HUMAN	Q81WY4_homo sapien
1498	183.5	4.7	245	2	Q6R670_OREAU	Q6R670_oreochromis
1499	183.5	4.7	245	2	Q6R671_ORENI	Q6R671_oreochromis
1500	183.5	4.7	247	2	Q5H733_MACMU	Q5H733_macaca mula

ALIGNMENTS

RESULT 1	
Q6UXH9_HUMAN	PRELIMINARY; PRT; 720 AA.
Q6UXH9;	
AC	05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT	05-JUL-2004, sequence version 1.
DI	07-FEB-2006, entry version 11.
DE	ELG6699.
GN	ORFNames=UNQ699;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC	Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA	Chen J., Chow B., Chui C., Crowley C., Curriel B., Deuel B., Dond P.,
RA	Batou D., Foster J.S., Grimaldi C., Gu Q., Hase P.B., Heide S.,
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA	Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA	Sehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA	Vandlen R.L., Watanabe C., Wland D., Woods K., Xie M.-H.,
RA	Yanura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA	Wood W.I., Godowski P.J., Gray A.M.;
RT	"The secreted protein discovery initiative (SPDI), a large-scale
RT	effort to identify novel human secreted and transmembrane proteins: a
RT	bioinformatics assessment";
RL	Genome Res. 13:2265-2270(2003).

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EMBL; AY58346; AA088712.1; -; mRNA.

ENSEMBL; ENSG0000019090; Homo sapiens.

GO; GO:0004252; F:serine-type endopeptidase activity; IEA.

DR

GO; GO:0006508; P:proteolysis; IEA.

DR

InterPro; IPR000859; CUB.

DR

InterPro; IPR006210; EGF.

DR

InterPro; IPR00742; EGF 3.

DR

InterPro; IPR001881; EGF-Ca²⁺-bd.

DR

InterPro; IPR006209; EGF-like.

DR

InterPro; IPR013032; EGF-like-reg.

DR

InterPro; IPR001254; Peptidase S1.S6.

DR

InterPro; IPR001314; Peptidase S1A.

DR

InterPro; IPR000436; Sushi_SCR_CCP.

DR

Pfam; PF00431; CUB; 1.

DR

Pfam; PF00008; EGF; 1.

DR

Pfam; PF00084; Sushi; 2.

DR

Pfam; PF00089; Trypsin; 1.

DR

PRINTS; PR00722; CHYMOTRYPSIN.

DR

SMART; SM00032; CCP; 2.

DR

SMART; SM00042; CUB; 1.

DR

SMART; SM00181; EGF; 2.

DR

SMART; SM00020; Tryp_Spc; 1.

DR

PROSITE; PS01180; CUB; 1.

DR

PROSITE; PS00022; EGF_1; 1.

QY 421 RLGSRRCTLRGKMGSGAPSCIPICGKIENITAKTQGLRMPQAAIYRRTSGVHDSL 480
 DB 421 RLGSRRCTLRGKMGSGAPSCIPICGKIENITAKTQGLRMPQAAIYRRTSGVHDSL 480
 QY 481 HKGAMFLVCSGALVNERVTVVAHCVTDLGKVTMIKTADLKVLGKFRDDDRDEKTIQS 540
 DB 481 HKGAMFLVCSGALVNERVTVVAHCVTDLGKVTMIKTADLKVLGKFRDDDRDEKTIQS 540
 QY 541 LQISAIILHPNYDPILLADIAIILKLDKARISTVQPICLAASRDLSFPESHITVAG 600
 DB 541 LQISAIILHPNYDPILLADIAIILKLDKARISTVQPICLAASRDLSFPESHITVAG 600
 QY 601 MNVLADVSPGFKNDTLRSGVSVVDSLLCEQHEDHGI PVSVTNMFCASEPTAPSDI 660
 DB 601 MNVLADVSPGFKNDTLRSGVSVVDSLLCEQHEDHGI PVSVTNMFCASEPTAPSDI 660
 QY 661 CTAEATGIAAVSPGRASPEPRMHLMLGLVSWSYDTCSHRLSTAFKYL PFKDWIERNNK 720
 DB 661 CTAEATGIAAVSPGRASPEPRMHLMLGLVSWSYDTCSHRLSTAFKYL PFKDWIERNNK 720
 RESULT 3
 Q6N062 HUMAN PRELIMINARY; PRT; 720 AA.
 ID 06N062 HUMAN
 AC 06N062
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 11.
 DE Hypothetical protein DKFZp686N24154.
 GN Name=DKFZp686N24154;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 NC NCB1_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Colon endochei;
 RG The German cDNA Consortium;
 RA Koehler K., Beyer A., Mewes H.W., Weil B., Amlid C., Oanger A.,
 RA Fodor G., Han M., Wiemann S.;
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
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 CC License
 DB EMBL; BX640676; CAB45808.1; -; mRNA.
 DR HSSP; P00734; 1BH0.
 DR EMBL; ENSG00000149090; Homo sapiens.
 DR GO; GO:0004253; F:serine-type endopeptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis; IEA.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR006210; EGF.
 DR InterPro; IPR000742; EGF_3.
 DR InterPro; IPR001881; EGF_Ca_bd.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR013032; EGF_like_reg.
 DR InterPro; IPR001254; Peptidase_S1_S6.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR000436; Subti_SCR_CCP.
 DR Pfam; PF00431; CUB; 1.
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00084; Subti; 2.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00032; CCP; 2.
 DR SMART; SM00042; CUB; 2.
 DR SMART; SM00181; EGF; 1.
 DR SMART; SM00020; TYP_SPC; 1.
 DR PROSITE; PS00180; CUB; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR NCB1_TaxID=9606;

DR PROSITE; PS00026; EGF_3; 1.
 DR PROSITE; PS00923; SUBTI; 2.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 KM Hypothetical protein.
 SQ SEQUENCE 720 AA; 80197 MW; E98A9F948EE777D CRC64;
 Query Match 99.8%; Score 3936; DB 2; Length 720;
 Best Local Similarity 99.7%; Pred. No. 3,3e-290;
 Matches 718; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MELGCTQLGTLFQLLISLPRETYINACPAENINMRECECEDOIECVGGRRE 60
 DB 1 MELGCTQLGTLFQLLISLPRETYINACPAENINMRECECEDOIECVGGRRE 60
 QY 61 VVGVTIPCCRNENECDSCLHPGCTIPENCKSCNGSGMGTLDPFYKGFYCAECRAGW 120
 DB 61 VVGVTIPCCRNENECDSCLHPGCTIPENCKSCNGSGMGTLDPFYKGFYCAECRAGW 120
 QY 121 YGDCMRGQYLRAFKGQILLESYPLNAHCWTIHAKGFVIQLRFVNLSEFDYMCQYD 180
 DB 121 YGDCMRGQYLRAFKGQILLESYPLNAHCWTIHAKGFVIQLRFVNLSEFDYMCQYD 180
 QY 181 YVEVADGNNRQGIILKVCNERNPAPISIGSSLHLVLFHSDGSKNDFHAYEETICS 240
 DB 181 YVEVADGNNRQGIILKVCNERNPAPISIGSSLHLVLFHSDGSKNDFHAYEETICS 240
 QY 241 SSPCFHDTGVLDRKASFKKACLAGYTGRCENLLEBENCSDPGPVNNGYQKITGGPGLI 300
 DB 241 SSPCFHDTGVLDRKASFKKACLAGYTGRCENLLEBENCSDPGPVNNGYQKITGGPGLI 300
 QY 301 NGRHAKIGTVVSPFCNNSYVLSGNEKRTCOQNGEWSGKOPICIKACREPKISDLVRRVL 360
 DB 301 NGRHAKIGTVVSPFCNNSYVLSGNEKRTCOQNGEWSGKOPICIKACREPKISDLVRRVL 360
 QY 361 PMQVQSRREPLHQLYSAAFSKQKLOSAPTKPALPFGDLPNGYQHLHQLQYECISPFYR 420
 DB 361 PMQVQSRREPLHQLYSAAFSKQKLOSAPTKPALPFGDLPNGYQHLHQLQYECISPFYR 420
 QY 421 RLGSRRCTLRGKMGSGAPSCIPICGKIENITAKTQGLRMPQAAIYRRTSGVHDSL 480
 DB 421 RLGSRRCTLRGKMGSGAPSCIPICGKIENITAKTQGLRMPQAAIYRRTSGVHDSL 480
 QY 481 HKGAMFLVCSGALVNERVTVVAHCVTDLGKVTMIKTADLKVLGKFRDDDRDEKTIQS 540
 DB 481 HKGAMFLVCSGALVNERVTVVAHCVTDLGKVTMIKTADLKVLGKFRDDDRDEKTIQS 540
 QY 541 LQISAIILHPNYDPILLADIAIILKLDKARISTVQPICLAASRDLSFPESHITVAG 600
 DB 541 LQISAIILHPNYDPILLADIAIILKLDKARISTVQPICLAASRDLSFPESHITVAG 600
 QY 601 MNVLADVSPGFKNDTLRSGVSVVDSLLCEQHEDHGI PVSVTNMFCASEPTAPSDI 660
 DB 601 MNVLADVSPGFKNDTLRSGVSVVDSLLCEQHEDHGI PVSVTNMFCASEPTAPSDI 660
 QY 661 CTAEATGIAAVSPGRASPEPRMHLMLGLVSWSYDTCSHRLSTAFKYL PFKDWIERNNK 720
 DB 661 CTAEATGIAAVSPGRASPEPRMHLMLGLVSWSYDTCSHRLSTAFKYL PFKDWIERNNK 720
 RESULT 4
 Q5EBL7 HUMAN PRELIMINARY; PRT; 737 AA.
 ID 05EBL7 HUMAN
 AC 05EBL7
 DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
 DT 15-MAR-2005, sequence version 1.
 DT 07-FEB-2006, entry version 7.
 DE Regeneration associated muscle protease, isoform a.
 GN Name=DKFZp586H2123;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 NC NCB1_TaxID=9606;

[1]
 RA NUCLEOTIDE SEQUENCE.
 RC TISSUE=Chondrosarcoma Lung Metastasis;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopfins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapelton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshynki S., Carninci P., Prange C.,
 RA Raha S.S., Loguelfano N.A., Peters G.J., Abremson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Sheychenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]

RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Chondrosarcoma Lung Metastasis;
 RA Director MGC Project;
 RL Submitted (FEB-2005) to the EMBL/Genbank/DBJ databases.

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CC EMBL: BC089434; AAH89434.1; -; mRNA.
 CC Ensembl: ENSG00000149090; Homo sapiens.
 DR GO: GO:0008233; F:peptidase activity; IEA.
 DR GO: GO:0004252; F:serine-type endopeptidase activity; IEA.
 DR GO: GO:0006508; F:proteolysis; IEA.
 DR InterPro: IPR000859; CUB.
 DR InterPro: IPR006210; EGF.
 DR InterPro: IPR00742; EGF_3.
 DR InterPro: IPR001861; EGF_Ca bd.
 DR InterPro: IPR006209; EGF-like.
 DR InterPro: IPR013032; EGF-like_reg.
 DR InterPro: IPR001254; Peptidase_S1_S6.
 DR InterPro: IPR001314; Peptidase_S1A.
 DR InterPro: IPR000436; Sushi_SCR_CCP.
 DR Pfam: PF00431; CUB; 1.
 DR Pfam: PF00008; EGF; 1.
 DR Pfam: PF00084; Sushi; 2.
 DR Pfam: PF00089; Trypsin; 1.
 DR PRINTS: PRO0722; CHYMOTRYPSIN.
 DR SMART: SM00032; CCP; 2.
 DR SMART: SM00042; CUB; 1.
 DR SMART: SM00181; EGF; 2.
 DR SMART: SM00020; TYP_SPC; 1.
 DR PROSITE: PS00180; CUB; 1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS00026; EGF_3; 1.
 DR PROSITE: PS09923; SUSH1; 2.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 KM Protease.
 SQ SEQUENCE 737 AA; 81943 MW; FD3BACF84778FE CRC64;

Query March 99.5%; Score 3926.5; DB 2; Length 737;
 Best Local Similarity 97.7%; Freq. NO. 1.8e-289;
 Matches 720; Conservative 0; Mismatches 0; Indels 17; Gaps 1;

QY 1 MELGCMVQLGLTFLPOLLITSLPREYVINEACPGAEKNNINCRCECEYDOIECVCPGKRE 60
 DB 1 MELGCMVQLGLTFLPOLLITSLPREYVINEACPGAEKNNINCRCECEYDOIECVCPGKRE 60

QY 61 VVGYYTIPCCRNENECDSCLIHPGCTIFENCKSCRNGSWGTLDDPYVNGFYCAECRAG 120
 DB 61 VVGYYTIPCCRNENECDSCLIHPGCTIFENCKSCRNGSWGTLDDPYVNGFYCAECRAG 120
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 DB 121 YGGDCRCQGVYRAKRGQILLESYPLNACWNTIHAKEPVYQLAFWMLSLFPDYWCYD 180
 QY 181 YVEVDGDNRRDQIIRKVCNGNERPAPISIGSSLHYLFFSDSGKPFDPGFAIYEETIACS 240
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 QY 241 SSPCFHDGTCLVDKAGSYKACLAGYTGRCENL-----LEERNCSDP 283
 DB 241 SSPCFHDGTCLVDKAGSYKACLAGYTGRCENL-----LEERNCSDP 283
 QY 284 GGPVNGYQKITGPGILNGRAHAKITGVVSFFCNNSYVLSGNEKRTCCONGENSGQIPCI 343
 DB 284 GGPVNGYQKITGPGILNGRAHAKITGVVSFFCNNSYVLSGNEKRTCCONGENSGQIPCI 343
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 DB 344 KACREPKISDLVRRRVLPMQVQSRETPHQLYSAAFSKOKQSAPTKKPALEPGDPMGY 403
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 DB 404 OHHTQLOVEICISPPYRRLGSSRRTCLRTGKWSGAPSCIPICGKINITAPKTGLAMP 463
 QY 464 WQAAIYRRRTSGVHDSLHKGMFLVCSGALVNERVVAACVVDLGVYTMKTADLVK 540
 DB 464 WQAAIYRRRTSGVHDSLHKGMFLVCSGALVNERVVAACVVDLGVYTMKTADLVK 540
 QY 524 LKGFYRDDDRDEKTIQSLOISAIILHPNVDPILDDADIAIKLDDKARISTRVQPICLAA 583
 DB 524 LKGFYRDDDRDEKTIQSLOISAIILHPNVDPILDDADIAIKLDDKARISTRVQPICLAA 583
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 DB 541 LKGFYRDDDRDEKTIQSLOISAIILHPNVDPILDDADIAIKLDDKARISTRVQPICLAA 600
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 DB 584 SRDLSTFSQESHITVAGNVLADVRSPPGKNDTLRSGVSVSDSLICEQHEHDHGPVSV 643
 QY 601 SRDLSTFSQESHITVAGNVLADVRSPPGKNDTLRSGVSVSDSLICEQHEHDHGPVSV 660
 DB 601 SRDLSTFSQESHITVAGNVLADVRSPPGKNDTLRSGVSVSDSLICEQHEHDHGPVSV 660
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 DB 644 TDNMFCAWEPAPABDICTAETGIAAASPPGRASPEPRMLMGVSVSYKTGCHRLST 703
 QY 661 TDNMFCAWEPAPABDICTAETGIAAASPPGRASPEPRMLMGVSVSYKTGCHRLST 720
 DB 661 TDNMFCAWEPAPABDICTAETGIAAASPPGRASPEPRMLMGVSVSYKTGCHRLST 720
 QY 704 AFTKVLPEKDWIERNMK 720
 DB 704 AFTKVLPEKDWIERNMK 720
 QY 721 AFTKVLPEKDWIERNMK 737
 DB 721 AFTKVLPEKDWIERNMK 737

RESULT 5
 ID Q96JW2 HUMAN PRELIMINARY; PRT; 737 AA.
 AC Q96JW2-
 DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
 DT 01-DEC-2001, sequence version 1.
 DE CDNA FLJ14935 f18, clone PLAC81009992, weakly similar to LIMULUS
 DE CLOTTING FACTOR C (BC 3.4.21.84).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Placenta;
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahata K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Nagatsuna M., Shitatori K.,
 RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

RA Takehashi M., Kanda K., Yokoi T., Furuya T., Kikawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 RA Niimiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tani H., Kimeta M., Watanabe M., Hirooka S., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hotta T., Kusano J.,
 RA Kanohi K., Takehashi-Fuji A., Hara H., Tanase T.-O., Nomura Y.,
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Mueshino K., Yunki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
 RA Moriya S., Montama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Omori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togeishi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shitai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuo Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isegaki T., Sugano S.,
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RL Nat. Genet. 36:40-45(2004).

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 CC -----
 CC EMBL; AK027841; BAB55404.1; -; mRNA.
 DR HSSP; P00736; IGPZ.

DR MEROPS; S01.998; -;
 DR Ensembl; ENSG00000149090; Homo sapiens.

DR GO; GO:0004253; F:serine-type endopeptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis; IEA.

DR InterPro; IPR000859; CUB.
 DR InterPro; IPR006210; EGF.

DR InterPro; IPR000742; EGF_3.
 DR InterPro; IPR001881; EGF_Ca_bd.

DR InterPro; IPR006209; EGF_Like.
 DR InterPro; IPR013032; EGF_Like_reg.

DR InterPro; IPR001254; Peptidase_S1_S6.
 DR InterPro; IPR001314; Peptidase_S1A.

DR InterPro; IPR000436; Sushi_SCR_CCP.
 DR Pfam; PF00431; CUB; 1.

DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00084; Sushi; 2.

DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.

DR SMART; SM00032; CCP; 2.
 DR SMART; SM00042; CUB; 1.

DR SMART; SM00181; EGF; 2.
 DR SMART; SM00020; TRYP_SPC; 1.

DR PROSITE; PS00180; CUB; 1.
 DR PROSITE; PS00022; EGF_1; 1.

DR PROSITE; PS00186; EGF_2; 1.
 DR PROSITE; PS00026; EGF_3; 1.

DR PROSITE; PS00923; SUSHI; 2.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.

DR PROSITE; PS00240; TRYPSIN_DOM; 1.
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 DR PROSITE; PS00240; TRYPSIN_DOM; 1.

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 DR PROSITE; PS00240; TRYPSIN_DOM; 1.

DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.

QY 121 YGDCMRGCVLRAKQGIILLESYPLNAHCEWTTHAKRGFVQLRFVMLSEFDYMCYD 180
 Db 121 YGDCMRGCVLRAKQGIILLESYPLNAHCEWTTHAKRGFVQLRFVMLSEFDYMCYD 180
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 Db 181 YVEVDGDNRRDQIIKRVCGNERPPPIOSIGSLHVLTHSDGSKNPDGHAHYEETACS 240
 QY 241 SSPCHDGTGCVLDKAGKACACLAGYTGORCNL-----LEENRNSDP 283
 Db 241 SSPCHDGTGCVLDKAGKACACLAGYTGORCNLLEAGKSKTKASEDSLSVLEENRNSDP 300
 QY 284 GSPVNGYKITEGPGELINGRHAKITGVSPFCNNSYVLSEGEKRTCOQNGEMSGKQPTCI 343
 Db 301 GSPVNGYKITEGPGELINGRHAKITGVSPFCNNSYVLSEGEKRTCOQNGEMSGKQPTCI 360
 QY 344 KACREPKISDLVRRVLPVQVOSRRTPLHOLYSAAPSKQKQASAPTKKPALPFGDLPNGY 403
 Db 361 KACREPKISDLVRRVLPVQVOSRRTPLHOLYSAAPSKQKQASAPTKKPALPFGDLPNGY 420
 QY 404 OHLHTOLYECISPEYRBLGSSRRCTLRGKMSGAPSCIPICGKIENITAPKTQGLRMP 463
 Db 421 OHLHTOLYECISPEYRBLGSSRRCTLRGKMSGAPSCIPICGKIENITAPKTQGLRMP 480
 QY 464 WQAAIYRRTSQVHDSGLHKGAMFLVCSGALVVERTVVAACVTDLGKVTMTKTDLKV 523
 Db 481 WQAAIYRRTSQVHDSGLHKGAMFLVCSGALVVERTVVAACVTDLGKVTMTKTDLKV 540
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 QY 644 TDNMFCAWEPAPAPDICTAETGTAIAVSPGRASPPEPRMHLGLVMSYDXTCSHRLST 703
 Db 661 TDNMFCAWEPAPAPDICTAETGTAIAVSPGRASPPEPRMHLGLVMSYDXTCSHRLST 720
 QY 704 AFTKVLPEKDWIERNMK 720
 Db 721 AFTKVLPEKDWIERNMK 737

RESULT 6
 ID QSRD11_PONPY PRELIMINARY; PRT; 720 AA.
 AC QSRD11;
 DT 21-DEC-2004, integrated into UniProtKB/TrEMBL.
 DT 21-DEC-2004, sequence version 1.
 DT 07-FEB-2006, entry version 5.
 DE Hypothetical protein DKFP468N1810.
 GN Name=DKFP468N1810;
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Pongo.
 OC NCBI_TaxID=9600;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC Tissue=Heart;
 RA The German cDNA Consortium;
 RA Ottenweider B., Obermaier B., Deutschenbaur S., Schaipp A.,
 RA Mewes H.W., Weil B., Amdt C., Osanger A., Fobo G., Han M., Wiemann S.,
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
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 CC -----
 CC EMBL; CR857928; CAH90176.1; -; mRNA.
 DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis; IEA.

DR InterPro: IPR000859; CUB.
 DR InterPro: IPR006210; EGF.
 DR InterPro: IPR000742; EGF_3.
 DR InterPro: IPR001881; EGF_Ca_bd.
 DR InterPro: IPR006209; EGF_like.
 DR InterPro: IPR013032; EGF_like_reg.
 DR InterPro: IPR001354; peptidase_S1_s6.
 DR InterPro: IPR001254; peptidase_S1A.
 DR InterPro: IPR000436; Sushi_SCR_CCP.
 DR Pfam: PF00431; CUB; 1.
 DR Pfam: PF00008; EGF; 1.
 DR Pfam: PF00084; Sushi; 2.
 DR Pfam: PF00089; Trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00032; CCP; 2.
 DR SMART: SM00042; CUB; 1.
 DR SMART: SM00181; EGF; 2.
 DR SMART: SM00020; Tryp_Spc; 1.
 DR PROSITE: PS01180; CUB; 1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS50026; EGF_3; 1.
 DR PROSITE: PS50923; SUSH1; 2.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR Hypothetical protein.
 SQ SEQUENCE 720 AA; 80041 MW; 3F83E2DAD41FA117 CRC64;

Query Match Score 3898; DB 2; Length 720;

Best Local Similarity 98.8%; Pred. No. 2,6e-287;

Matches 709; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 MELGCMTQGLTFLQLLLISSLPREYTVINACPGAEWNNIMCECEYDIETCVGPKRE 60
 DB 1 MELGCMTQGLTFLQLLLISSLPREYTVINACPGAEWNNIMCECEYDIETCVGPKRE 60
 QY 61 VVGYYITPCCRNEENECDSCLIHGCTIFENCKSCNGSGGTLDDPYKGFCAECRAGW 120
 DB 61 VVGYYITPCCRNEENECDSCLIHGCTIFENCKSCNGSGGTLDDPYKGFCAECRAGW 120
 QY 121 YGGDCMRGQVLRARQGLLESYPNLNHCWNTIAKQGFVQLRFWMLSLFEDWMCQYD 180
 DB 121 YGGDCMRGQVLRARQGLLESYPNLNHCWNTIAKQGFVQLRFWMLSLFEDWMCQYD 180
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 DB 181 YVEVADGNDRDQGLIKRYCGNERPAPIQISGSLHVLPHSDGSKNPFDFGHAYEEITACS 240
 QY 241 YVEVADGNDRDQGLIKRYCGNERPAPIQISGSLHVLPHSDGSKNPFDFGHAYEEITACS 240
 DB 241 YVEVADGNDRDQGLIKRYCGNERPAPIQISGSLHVLPHSDGSKNPFDFGHAYEEITACS 240
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 DB 241 SSPCFHDTGCVLDKXASYKCACTAGYTCQRCENILLEERNCSDDPGSPVNGYQKITGAPGLI 300
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 DB 361 PMQVQSRPTPLHQLYSAFSAFKQKQSAATPKKPAFPGLPMGVOYHLHTQLQYECISPFYR 420
 QY 421 FLGSSRRTCCLRTGKMGSAFSCIPICGKIENITAPKTOGLRMPWQAIIYRTSGVHDSGL 480
 DB 421 FLGSSRRTCCLRTGKMGSAFSCIPICGKIENITAPKTOGLRMPWQAIIYRTSGVHDSGL 480
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 DB 481 HKGAMFLVCSALVNERTVVAAHCVTDLGKVTMTKTADLVKLVGKFRDDRDREKKTQS 540
 QY 541 LQISAILIHPVNDPLLDADIATLKLDKARISTVQPICLAASDLSTSFQESHITVAG 600
 DB 541 LQISAILIHPVNDPLLDADIATLKLDKARISTVQPICLAASDLSTSFQESHITVAG 600
 QY 601 WNVLDVRSPEGFKNDTLRSGVSVVDSLLCEQHEHDGIPVSVTDNMCASWEPTAPSDI 660
 DB 601 WNVLDVRSPEGFKNDTLRSGVSVVDSLLCEQHEHDGIPVSVTDNMCASWEPTAPSDI 660

DB 601 WNVLDVRSPEGFKNDTLRSGVSVVDSLLCEQHEHDGIPVSVTDNMCASQDPTAPSDI 660
 QY 661 CTAETGTAIVAFPPRASPEPRWHLMGVSWSYDTCGSHRISTARTKYLPPKDWIERNNK 720
 DB 661 CTAETGTAIVAFPPRASPEPRWHLMGVSWSYDTCGSHRISTARTKYLPPKDWIERNNK 720

RESULT 7
 Q5E9P5_BOVIN PRELIMINARY; PRT; 720 AA.
 AC Q5E9P5;
 DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
 DT 15-MAR-2005, sequence version 1.
 DT 07-FEB-2006, entry version 5.
 DE Regeneration associated muscle protease isoform b.
 GN Name=DKRZP564H2123;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Pooled;
 RX MEDLINE=21180013; PubMed=11282978; DOI=10.1101/gr.170101;
 RA Smith T.P.L., Grose W.M., Freking B.A., Roberts A.J., Stone R.T.,
 RA Casas E., Wray J.E., White J., Cho J., Fahrenkrug S.C., Bennett G.L.,
 RA Heaton M.P., Laegreid W.W., Rohrer G.A., Chitko-Mckon C.G.,
 RA Perera J.W., Holt I., Karameycheva S., Liang F., Quackenbush J.,
 RA Keefe J.W.;
 RT "Sequence evaluation of four pooled-tissue normalized bovine cDNA
 RT libraries and construction of a gene index for cattle.";
 RL Genome Res. 11:626-630(2001).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Pooled;
 RA Hatnay G.P., Sonstegard T.S., Clawson M.L., Heaton M.P., Keefe J.W.,
 RA Snelling W.M., Weidmann R.T., Smith T.P.L.;
 RT "Sequencing and analysis of Bos taurus full-length insert cDNA
 RT clones.";
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivs license
 CC -----
 DR EMBL: BT020875; AAX08892.1; -. mRNA.
 DR GO: GO:0008233; F:peptidase activity; IEA.
 DR GO: GO:0004252; F:serine-type endopeptidase activity; IEA.
 DR GO: GO:0006508; P:proteolysis; IEA.
 DR InterPro: IPR000859; CUB.
 DR InterPro: IPR006210; EGF.
 DR InterPro: IPR000742; EGF_3.
 DR InterPro: IPR001881; EGF_Ca_bd.
 DR InterPro: IPR006209; EGF_like.
 DR InterPro: IPR013032; EGF_like_reg.
 DR InterPro: IPR001254; peptidase_S1_s6.
 DR InterPro: IPR001354; peptidase_S1A.
 DR InterPro: IPR000436; Sushi_SCR_CCP.
 DR Pfam: PF00431; CUB; 1.
 DR Pfam: PF00008; EGF; 1.
 DR Pfam: PF00084; Sushi; 2.
 DR Pfam: PF00089; Trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00032; CCP; 2.
 DR SMART: SM00042; CUB; 1.
 DR SMART: SM00181; EGF; 2.
 DR SMART: SM00020; Tryp_Spc; 1.
 DR PROSITE: PS01180; CUB; 1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS50026; EGF_3; 1.
 DR PROSITE: PS50923; SUSH1; 2.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.

KM Proclease. 720 AA; 80057 MW; 69DA098FF95037E1 CRC64;
 SQ SEQUENCE
 Query Match 91.7%; Score 3616; DB 2; Length 720;
 Best Local Similarity 90.6%; Pred. No. 7.1e-266;
 Matches 652; Conservative 30; Mismatches 38; Indels 0; Gaps 0;

1 MELGCMWGLTFLQLLISSLPREYTVNEACPGAMNIMRECEYQDIECVCKGKE 60
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 301 NGRHAKITGVVFFCNNSVYLSGNERTCQNGEWSGKPCITKACREPKISDLYRRRL 360
 361 PMQVRSRETPHLQYSAAPSKOKLOSAPTKKAPLPGDLPWGVOHLTQLOECISPFYR 420
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 421 RLGSRRRTCLRTKXSGRAPSCIPICGKIENTAPKQGLRMPWOAAYRTSRYHDSGL 480
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 481 HKGMFLVCSGALVNERVVAHAHCVTDLGKTMKTADLKVLLGKFRYDRDRDKTIOS 540
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 541 LOISAIILHPNYPDPLLDADIAILKLDKARISTVOPICLAASRDLSTSPESHITVAG 600
 541 LRISAIILHPNYPDPLLDADIAILKLDKARISTVOPICLAASRDLSTSPESHITVAG 600
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 601 WNVLDVDSRPGKNDTLRSGVSVVDSLLCEQHEHDHGIPIVSVTDNMFCASMEPTAPSDI 660
 661 CTAAETGGAIAVSPGRASPEPRMHLGLVSYDTCSHRLSTATTCTKLPFDOMIERNMK 720
 661 CTAAETGGAIAVSPGRASPEPRMHLGLVSYDTCSHRLSTATTCTKLPFDOMIERNMK 720

RESULT 8
 Q8BU25_MOUSE PRELIMINARY; PRT; 720 AA.
 Q8BU25_MOUSE PRELIMINARY; PRT; 720 AA.
 AC Q8BU25;
 DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2003, sequence version 1.
 DT 07-FEB-2006, entry version 25.
 DE 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched
 DE library, clone:R430002G05 product:hypothetical EGF-like domain, CUB
 DE domain, Sushi domain / SCR repeat / CCP module and Serine proteases,
 DE trypsin family domain containing protein, full insert sequence.
 GN Name:R430002G05R1K;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Thymus; STRAIN=NOB;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Methods Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOB; TISSUE=Thymus;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Fritch M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Bremner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilming L.G., Aldonis V., Allen J.E.,
 RA Ambesi-Impombato A., Apweiler R., Aurali R.N., Bailey T.L.,
 RA Banal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chiu K.P., Choudhary V., Christoffele A., Clutebuck D.R.,
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
 RA Guscinich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 RA Hill D., Hummel L., Iacono M., Ikeno K., Iwama A., Ishikawa T.,
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kitano H., Kojima G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsumura H., Matsuzawa S., Miki H., Mignone F., Miyake S., Moritz K.,
 RA Mottagui-Tabar S., Mulder N., Nakano N., Nakaguchi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlowski V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Roest B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 RA Schonbach C., Sekiguchi K., Sempole C.A., Sene S., Sessa L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K.,
 RA Tamura K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yang K.,
 RA Yamashita H., Zdobych E., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Wahlestedt C., Weisberg J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Kono H., Nakano K., Ninomiya N.,
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563 (2005).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOB; TISSUE=Thymus;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RA RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the PANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566 (2005).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOB; TISSUE=Thymus;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi T., Bono H., Kondo S.,
 RA Nishio T., Ohtsuka N., Saito R., Suzuki H., Yamashita I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schmitt L.M., Kanapin A., Matsumura H., Batalov S., Beisel K.W.,
 RA Blake J.A., Brad D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Guscinich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Maglocz D.R., Malais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pereira G.,
RA Petrovskaya T., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravello T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sadelin A., Schneider C., Sempie C.A., Seton M., Shimada K.,
RA Sulana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilting L.G., Wymshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hizzone-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Maki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
[5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ND; TISSUE=Thymus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Pleischmann W., Gaasterland T., Glass C., King B., Koichiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schiml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,
RA Norcone P., Rung B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wymshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690 (2001).
[6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ND; TISSUE=Thymus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugihara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes";
RL Genome Res. 10:1617-1630 (2000).
[7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ND; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsuina T., Teshiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama S., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasaiwa K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka K., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "Riken integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multichannel sequencing";
RL Genome Res. 10:1757-1771 (2000).
[8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ND; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hizzone T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kankawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohnato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai K., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RT Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
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CC
DR EMBL: AK088017; BAC40098.1; -, mRNA.
DR HSSP: P00736; IGP2.
DR MEROPS: S01.998; -.
DR Ensembl: ENSMUSG00000027188; Mus musculus.
DR MGI: MGI:2445082; E430002G05Rik.
DR GO: GO:0005615; Cytoplasmic space; RCA.
DR GO: GO:0004263; F-tyrosinase activity; RCA.
DR GO: GO:0004295; F-tyrosinase activity; RCA.
DR GO: GO:0006508; P:proteinase; RCA.
DR InterPro: IPR000859; CUB.
DR InterPro: IPR006210; EGF.
DR InterPro: IPR000742; EGF_3.
DR InterPro: IPR001881; EGF_Ca_bd.
DR InterPro: IPR006209; EGF-like.
DR InterPro: IPR013032; EGF-like reg.
DR InterPro: IPR001254; Peptidase_S1_S6.
DR InterPro: IPR001314; Peptidase_S1A.
DR InterPro: IPR000436; Sushi_SCR_CCP.
DR Pfam: PF00431; CUB; 1.
DR Pfam: PF00008; EGF; 1.
DR Pfam: PF00084; Sushi; 2.
DR Pfam: PF00089; Trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00032; CCP; 2.
DR SMART: SM00042; CUB; 1.
DR SMART: SM00181; EGF; 2.
DR SMART: SM00020; Tryp_SPC; 1.
DR PROSITE: PS01180; CUB; 1.

Query Match 91.6%; Score 3612; DB 2; Length 720;
Best Local Similarity 90.1%; Pred. No. 1.4e-265;
Matches 649; Conservative 33; Mismatches 38; Indels 0; Gaps 0;

QY 1 MELGCTWGLTFLQLLISSLPREYVYNACPGABNNINCECEYDOIECVCPGRRE 60
DB 1 MELDRMAGLVFLQLLISSLPREYVYNACPGABNNINCECEYDOIECVCPGRKE 60
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DB 421 RLGSRRRTCLRTGKMSGRAPSCIPICGKIENITAPKTQGLRWPMQAAIYRRRTSGVHDSL 480

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Db 421 RLGSRRRLCLRTGKMGSRAPSCIPICGKIESPSPKTOGTMPQOALYRRTSGVHDCGL 480
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Db 481 HKGAMFLVCSGALVNERVTVAHAHCVTLGKTKMTKTDLKVYLGKFRDDDRDKTKIOS 540
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Qy 720 CTAEFGIAVSPFRASPERPMHLMGLVSVSYDTCGSHRSLATATKYLFPDQWIERMVK 720
Db 720 CTAEFGIAVSPFRASPERPMHLMGLVSVSYDTCGSHRSLATATKYLFPDQWIERMVK 720

RESULT 9
Q8K2B8_MOUSE PRELIMINARY; PRT; 720 AA.
ID Q8K2B8_MOUSE
AC Q8K2B8;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE Regeneration associated muscle protease.
OS Mus musculus (Mouse).
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RX NUCLEOTIDE SEQUENCE.
RC STRAIN-CZECH II; TISSUE=Mammary tumor metastasized to lung. Tumor
arose spontaneously.
RA MEDLINE=22388357; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Schenfer C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
Dietchenko L., Marnett L., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Wozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
Rach G., Schein J.E., Jones S.J.M., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
NUCLEOTIDE SEQUENCE.
RC STRAIN-CZECH II; TISSUE=Mammary tumor metastasized to lung. Tumor
arose spontaneously.
RA Strauberg R.L.;
Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
[3]
NUCLEOTIDE SEQUENCE.
RC STRAIN-CZECH II; TISSUE=Mammary tumor metastasized to lung. Tumor
arose spontaneously.
RA Director MGC Project;
Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
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CC EMBL: BC031841; AAH1841.1; -; mRNA.
DR EMBL: BC057685; AAH57685.1; -; mRNA.
DR HSSP: P00736; 1GP2.
DR MEROPS: S01.998; -.
DR Ensemble: ENSMUSG00000027188; Mus musculus.
DR MGI: MGI:2445082; E430002G05Rik.
DR GO: GO:0005615; C:extracellular space; RCA.
DR GO: GO:0004263; F:chymotrypsin activity; RCA.
DR GO: GO:0004295; F:trypsin activity; RCA.
DR GO: GO:0006508; P:proteinolysis; RCA.
DR InterPro: IPR000859; CUB.
DR InterPro: IPR006210; EGF.
DR InterPro: IPR000742; EGF_3.
DR InterPro: IPR001881; EGF_Ca_bd.
DR InterPro: IPR006209; EGF_like.
DR InterPro: IPR013032; EGF_like_reg.
DR InterPro: IPR01254; Peptidase_S1_S6.
DR InterPro: IPR001314; Peptidase_S1A.
DR InterPro: IPR000436; Sushi_SCR_CCP.
DR Pfam: PF00431; CUB; 1.
DR Pfam: PF00008; EGF; 1.
DR Pfam: PF00084; Sushi; 2.
DR Pfam: PF00089; Trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00032; CCP; 2.
DR SMART: SM00042; CUB; 1.
DR SMART: SM00181; EGF; 2.
DR SMART: SM00020; Tryp_Spc; 1.
DR PROSITE: PS01180; CUB; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS50026; EGF_3; 1.
DR PROSITE: PS50923; SUSH1; 2.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
KW Protease.
SQ SEQUENCE 720 AA; 80378 MW; 717287F1E690FD0E CRC64;
Query Match 91.6%; Score 3612; DB 2; Length 720;
Best Local Similarity 90.1%; Pred. No. 1,4e-265;
Matches 649; Conservative 33; Mismatches 36; Indels 0; Gaps 0;
Qy 1 MELGWQLGLTPIQLLISLPREYTYINRACPGAEINIMRCECEYDQIECVCPGRKE 60
Db 1 MELDRWAGLVFQLDLISLPREYTYINRACPGAEINIMRCECEYDQIECVCPGRKE 60
Qy 61 VVGYYTIPCCRNENECDSCLIPGCTIFENCKSCRNCGSGTLDFFVYKGFYCAECRAGW 120
Db 61 VVGYYTIPCCRNENECDSCLIPGCTIFENCKSCRNCGSGTLDFFVYKGFYCAECRAGW 120
Qy 121 YGGDCMRGCVLRAPKQGIILLESYPLNACGWTTHAKGFYIQLRFLWMLSLFEDMCOYD 180
Db 121 YGGDCMRGCVLRAPKQGIILLESYPLNACGWTTHAKGFYIQLRFLWMLSLFEDMCOYD 180
Qy 121 YGGDCMRGCVLRAPKQGIILLESYPLNACGWTTHAKGFYIQLRFLWMLSLFEDMCOYD 180
Db 121 YGGDCMRGCVLRAPKQGIILLESYPLNACGWTTHAKGFYIQLRFLWMLSLFEDMCOYD 180
Qy 181 YVEVADGNRGGQIIRKQGNRERAPLQISGLHLVLRHSGSKVDFGFHAYEETACS 240
Db 181 YVEVADGNRGGQIIRKQGNRERAPLQISGLHLVLRHSGSKVDFGFHAYEETACS 240
Qy 241 YVEVADGNRGGQIIRKQGNRERAPLQISGLHLVLRHSGSKVDFGFHAYEETACS 240
Db 241 YVEVADGNRGGQIIRKQGNRERAPLQISGLHLVLRHSGSKVDFGFHAYEETACS 240
Qy 241 SSPCFHDTGVLDKRAASYKACLAGYTGRCENLLEBRNCSDPGPVGNGYQKITGGPGLI 300
Db 241 SSPCFHDTGVLDKRAASYKACLAGYTGRCENLLEBRNCSDPGPVGNGYQKITGGPGLI 300
Qy 301 NGRHAKIGTVVSPFNNNSYVLISGNEKRTQONGEWSGKOPICIRACREPKISDLVRRVYL 360
Db 301 NGRHAKIGTVVSPFNNNSYVLISGNEKRTQONGEWSGKOPICIRACREPKISDLVRRVYL 360
Qy 361 PMOVOSRETPVHOLYSAFSSKQIQAAPTAKKPAIPGGLPMVGOYHLHTQLYBECISPFYR 420
Db 361 PMOVOSRETPVHOLYSAFSSKQIQAAPTAKKPAIPGGLPMVGOYHLHTQLYBECISPFYR 420
Qy 421 RLGSRRRLCLRTGKMGSRAPSCIPICGKIENITAPKTGRLMPQOALYRRTSGVHDCGL 480
Db 421 RLGSRRRLCLRTGKMGSRAPSCIPICGKIENITAPKTGRLMPQOALYRRTSGVHDCGL 480

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QY 719 MK 720
DB 721 MK 722

RESULT 11
Q7199 HUMAN PRELIMINARY; PRT; 417 AA.
AC Q7199
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE FP938.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
NCBI_TaxID=9606;
RX Nucleotide sequence.
RA Huang Y., Zhou X.M., Zhang P.P., Jiang H.Q., Qin W.X., Zhao X.T.,
RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
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CC
CC EMBL: AF370388; AAQ15224.1; -, mRNA.
DR HSSP; P00734; 1B80.
DR Ensembl; ENSG00000149090; Homo sapiens.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR001354; Peptidase_S1_S6.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00084; Sushi; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS50923; SUSHI; 1.
DR PROSITE; PS50240; TRYPsin_DOM; 1.
DR PROSITE; PS50240; TRYPsin_DOM; 1.
SQ SEQUENCE 417 AA; 46703 MW; 2546A52A3697C1C4 CRC64;

Query Match 52.2%; Score 2059; DB 2; Length 417;
Best Local Similarity 95.6%; Pred. No. 8, 5e-148;
Matches 389; Conservative 1; Mismatches 17; Indels 0; Gaps 0;

QY 314 FCNNSYVLSGNEKRTCOQNGEMSGKQPICTIKAREPKISDLVRRVLPVQVQSRETPHQ 373
DB 11 FVTTPMFLVAMRKELASMERMSGKQPICTIKAREPKISDLVRRVLPVQVQSRETPHQ 70
QY 374 LYSAAFSKQKQASAPTKKPPALPFGDLPMGYOHLATOLQYECISPPYRRISGSRRTCLRTG 433
DB 71 LYSAAFSKQKQASAPTKKPPALPFGDLPMGYOHLATOLQYECISPPYRRISGSRRTCLRTG 130
QY 434 KMSGRAPSCIPICGKINVTAPKTOGLRPMQAAIYRRSTSGHNDLSIKGAMFLYCSGL 493
DB 131 KMSGAPSCIPICGKINVTAPKTOGLRPMQAAIYRRSTSGHNDLSIKGAMFLYCSGL 190
QY 494 VNERVVAACHCVDLIGKVTMIKTADLKVLGKFPYRDDRDDEKTIQSLQISAIILHPYND 553
DB 191 VNERVVAACHCVDLIGKVTMIKTADLKVLGKFPYRDDRDDEKTIQSLQISAIILHPYND 250
QY 554 PILDADIALILKLDKARISTRVQICLAASRDLSSTFOESHIITVAGMVLADVSPGFK 613
DB 251 PILDADIALILKLDKARISTRVQICLAASRDLSSTFOESHIITVAGMVLADVSPGFK 310
QY 614 NDLTASGVSVVDLICEQHEHDGIPVSVTDNMFCASMEPPAPSDICAEFGIAAVSF 673
DB 311 NDLTASGVSVVDLICEQHEHDGIPVSVTDNMFCASMEPPAPSDICAEFGIAAVSF 370
QY 674 PGRASPEPRMHLMLGLVSWSYDKTCSHRLSTAFTKVLPFKDWIERNMK 720

DB 371 PGRASPEPRMHLMLGLVSWSYDKTCSHRLSTAFTKVLPFKDWIERNMK 417

RESULT 12
Q4SAF4_TESTING PRELIMINARY; PRT; 1009 AA.
AC Q4SAF4;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Chromosome 13 SCAP14688, whole genome shotgun sequence.
GN ORFNames=GSTENG0002148001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphi; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
NCBI_TaxID=99883;
RX Nucleotide sequence.
RA Jallion O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bouteau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicud S., Jaffe D., Fisher S., Luitalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka J., Vercherie B.,
RA Blemont C., Skalli Z., Catrolicio L., Poulat J., de Baradins V.,
RA Cruaud C., Duprat S., Broctier P., Coutanceau J.-P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Landet V., Schachter V., Queller F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissenbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype."; Nature 431:946-957(2004).
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope, Whitehead Institute Centre for Genome Research;
RL Submitted (Feb-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC
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CC
CC EMBL: CAE01014688; CAG02378.1; -, Genomic DNA.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000742; EGF_3.
DR InterPro; IPR013032; EGF_like_reg.
DR InterPro; IPR01354; Peptidase_S1_S6.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00084; Sushi; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00042; CUB; 3.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 1.
DR PROSITE; PS50923; SUSHI; 3.
DR PROSITE; PS50240; TRYPsin_DOM; 1.
DR PROSITE; PS50240; TRYPsin_DOM; 1.
SQ SEQUENCE 1009 AA; 11811 MW; 60082897CA808BD7 CRC64;

Query Match 39.7%; Score 1566; DB 2; Length 1009;

Best Local Similarity 38.4%; Pred. No. 86-110;
Matches 321; Conservative 109; Mismatches 174; Indels 232; Gaps 14;

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OY 100 GGTLDDEYKGFYCAECRAGWYGDGCMRGQYLBARPKQIILESYPLNHCMTIHAHKG 159
DB 108 GRPRDDFFISGYSCEBRCRPGMGGDCMKCGVHKHKGHLVLESIPNNARCEWITQVDRP 167
OY 160 FVIQRLPFWLLEFPYMCQYDYVEVRDGNRDGQIIKRVCGNERPAPISGSSLHVLP 219
DB 168 FAVELRFMWLLEFHNHSCQYDYVEVRDGSISSRVIGFCGNSRPPVYSSGSSLHVLPV 227
OY 220 SPGSKNPFQFAHYEITACSSPCFHDTCVLDKAGSKYKACIAGYTQRCENLLEEN 279
DB 228 SDGYKNPQGFATFQEIISG-TSSPCFHDTCILDSHTYRACAGTGYSKNCHEHVERV 286
OY 280 GSDPGPVNGYQKINGPGF----- 298
DB 287 CVLPKPKDGHDFLYVGGPVDVLIQLCYQPELSTGTSQRTCLSNNTWMSGNPVCTKEL 346
OY 299 LINGRH----- 304
DB 347 QVNGRDRDPKVGPNPTKLRVAGVEVENTVEAFNTDYTENNTVTFETKERQSNNSIRSPD 406
OY 305 -----AKT-----GTV----- 310
DB 407 KRVVPAVVVVTQYTYMVRAGBESGGTVNLSLKEDNKEKDPTEDEGRRELEKEDKAKESER 466
OY 311 -----VSFFCNNSYVLGSGNEKRTCOONGEMSGK 338
DB 467 EANESFREKSCPPRLHLHGHGRVYPGAKPBAVEFFCNHSTYLSGDLALRSCSDGTWSCR 526
OY 339 QPICKACREPKISDLVRRRVLPQVOSRETPHLQLYSAFSGKQLQSAFTPKPALPFGD 398
DB 527 QPVCVBARCPKPSVSELVQRVLPQAPFKCTVHKLKYSGLSPNLSQSDSHTKGPAL--SS 584
OY 399 LPMGQHLHTQYQICISPFYRRLSSRRTCLRTGKWSGRASCIPIGCKINITAPKTQ 458
DB 585 LPOGHQYTHLEYSQSYQYHFPSSSRRTCLKTGKWSGRHSCSPVCGKHETPDERPA 644
OY 459 GLRMPQAAIYRT-----SGVHDSLHKGAFVLCGAL 493
DB 645 DSHWMLAIIYRKSNNRVGKKTSGDGGTGLKTTDGGAGSGVRD--LESMDQLCSGVL 701
OY 494 VNERVVAHCVTDLQKVTMIKTADLKVVLGKFPYRDDRDDEKTIQSLQISAIIILHPYD 553
DB 702 VNORSVVVAHCVTELKGYKPLETAKLKVVVGKHPREDRDEKGRHRLVDSIAVHENYD 761
OY 554 PILDADIAILKLDKARISTVVOFICLAAGR-DLSTFQESHITVAGNNVLADVRSFGF 612
DB 762 PHVLDSDAVAVIRLIDKAKIGEKVAPLCISDSQEDLETTSBOGLVT--GMSPPVD--PSL 816
OY 613 -KNIDTREGVSVVNSLCEBOHBDGIPVSVTDNMFCSMPEPTAPSDICTAETGIAV 671
DB 817 GPEEKARVGLVHNLAVPCEQYARNGVPVSTDMCLCASQKPDYGSNICEPDMGILIL 876
OY 672 -----SPEGRASPEBRMLMGLVSWSYDK-TCSHRLSTAFKTVLPFKDM 714
DB 877 PPLTDSRTSRHSPSGKGDGKGRWLLGLVSGYDQGEDPDLVYVYTHVANFDM 932

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RESULT 13
QASHDA.TETNG PRELIMINARY; PRT; 488 AA.
AC QASHDA.
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DE Chromosome 5 SCAP14581, whole genome shotgun sequence. (Fragment).
GN ORFNames=GSTERG00018208001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

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OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX Pubmed=15496914; DOI=10.1038/nature03025.
RA Jallion O., Aury J.-M., Brunet F., Petit J.-L., Strange-Thomann N.,
RA Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicad S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dastila C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Caetelli V., Kacinka M., Vacherie B.,
RA Bieumont C., Skalli Z., Catolico L., Poulain J., De Bernardis V.,
RA Cruaud C., Duprat S., Brotier P., Coutanceau J.-P., Gouzy J.,
RA Parra G., Bardier G., Chapple C., McKernan K.J., McSwen P., Bosaek S.,
RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Landet V., Schachter V., Queller F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.,
RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype."
RT Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope, Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC Distributed under the Creative Commons Attribution-NonDerivative License
CC -----
DR EMBL; CAAB01014581; CAF99948.1; -; Genomic DNA.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR InterPro; IPR000436; Subst_SCR_CCP.
DR Pfam; PF00084; Subst_1.
DR Pfam; PF00431; CUB; 1.
DR SMART; SMO0042; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS09923; SUBST_1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR Kluhl.
FT NON TER
FT NON TER
FT NON TER
SQ SEQUENCE 488 AA; 54137 MW; 871FDD9B36BD90A6 CRC64;
Query Match 28.5%; Score 1122.5; DB 2; Length 488;
Best Local Similarity 38.3%; Pred. No. 1.7e-76;
Matches 220; Conservative 89; Mismatches 155; Indels 111; Gaps 11;
OY 31 EACPGAENINCRCECEYDOIECVCPGKREYVGTIPCCRBENBCSCLHPGCTIPEN 90
DB 1 DRCPSSRNAMCRPCCEYQOLIQCRCPSKGLKVGITVPCRNALMQDCPLIPPGCSLPEN 60
OY 91 CKSGRNGSWGTLDPFYKGFYCAECRAGWYGDGCMRGQYLBARPKQIILESYPLNHC 150
DB 61 KCTCHNGTMRAN-DDFPIKNGKCTDCRGSGMGGCKTCGGVLYQRAQHIALDSYPTNARC 119
OY 151 EWTTHAKGPVYQLRFVWLLEFPYMCQYDYVEVRDGNRDGQIIKRVCGNERPAPIS 210
DB 120 EMTVHVERGVIEIRFLILLSLSDHSQYDYVEVRDGGGLNSPVIIGFCGDLPPPIKSS 179
OY 211 GSSILHVLFPSPGSKNPGFAHYEITACSSPCFHDTCVL---DKAGSKYKACIAGYT 267
DB 180 GSALRIFFSSDGVNPNFVLIIFQESAGSST---HOQSTVCTPREPRRLFAACLA-T 234
OY 268 GORCENLLEBRNCSGDPGVNGYQKITGPGELINGRAHAKIGTVVSPFCNNSYVLGNEKR 327
DB 235 GQAC----- 238
OY 328 TCGONGEMSGKQPIKICACREPKISDLVRRRVLPQVOSRETPHLQLYSAFSGKQLQSA 387

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Db 239 -----SSCRQPRVSELVKQKVVKQLTSRDPKPKKPSRLSKLQGBDA 282
Qy 388 PTKKRALPGDLPMGYQHHTOLOQECISPFYRLGSSRRTLRTGKSGRAPSCIPICG 447
Db 283 -----SIVLPGLPFLPVNTVIEYKSCASPLYEHAGSSRRTLKSGKWSGRHVSCTPYCG 335
Qy 448 KIENITAKTQGLBPMQCAIYRRTSG-----VHDSLHKA-WPLVCSGA 492
Db 336 KFTNFSPLNKTQMPHVAVTIRSPDPSPTARPPGCDMFVQGDSEBSTFWVLACSGA 395
Qy 493 LVNERTVVAAACVYDLGKVTMIKTADLKVYLGEYRDDDERK-----TIQSLQISAI 546
Db 396 LLSQGSILVAAGCVVDGKQGLQPAQVRVWG-VHDTQSSQGRSLRHRTYPHLLVNI 454
Qy 547 ILHPNYDPLLDADIAILKLDKARISTRVOPICL 581
Db 455 LVHPDFH-FGASNVAVLKLRDKAKISERVLPVCL 488

RESULT 14
Qy432 HUMAN PRELIMINARY; PRT; 181 AA.
AC Qy432;
DT 01-NOV-1999, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1999, sequence version 1.
DT 07-FEB-2006, entry version 26.
DE Hypothetical protein DKFZ586H2123 (Fragment).
GN Name=DKFZ586H2123;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE-Uterus;
RA Anorge W., Winkler U., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DDJ databases.
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CC -----
DR EMBL; AL050214; CAB43317.1; -. mRNA.
DR PIR; T08805; T08805.
DR HSSP; P00736; 1MD7.
DR MEROPS; S01.998; -.
DR Ensemble; ENSG00000149090; Homo sapiens.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR Pfam; PF00089; Trypsin; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 181 AA; 19962 MW; ABC793BBE82D439 CRC64;

Query Match 24.1%; Score 949; DB 2; Length 181;
Best Local Similarity 99.4%; Pred. No. 7.2e-64;
Matches 180; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Qy 720 K 720
Db 181 K 181

RESULT 15
Qy8951 TACTR PRELIMINARY; PRT; 1019 AA.
AC Qy8951;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE Factor C precursor.
OS Tachyples tridentatus (Japanese horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Tachyples.
OX NCBI_TaxID=6853;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21955715; PubMed=11958140;
RA Wang D., Liu J., Chen L., Wang L., Yang G., Wu X., Zhang W.;
RT "Cloning and expression of Tachyples tridentatus factor C.";
RL Acta Biochim. Biophys. Sin. 34:77-82(2002).
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CC -----
DR EMBL; AF467804; AAL75577.1; -. mRNA.
DR HSSP; P00746; 1FDP.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR000742; EGF_3.
DR InterPro; IPR013111; EGF_extrace11.
DR InterPro; IPR013032; EGF_like_reg.
DR InterPro; IPR004043; LCCL.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF03815; LCCL; 1.
DR Pfam; PF00059; Sushi_SCR_CCP.
DR Pfam; PF00084; Sushi_C_1.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00032; CCP; 5.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS50041; C_Type_Lectin_2; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS50026; EGF_3; 1.
DR PROSITE; PS50820; LCCL; 1.
DR PROSITE; PS50923; SUSI; 5.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Signal.
FT SIGNAL 1
FT CHAIN 26 1019 Potential. factor C.
SQ SEQUENCE 1019 AA; 112249 MW; B8E51730AB595993 CRC64;

Query Match 17.2%; Score 678; DB 2; Length 1019;
Best Local Similarity 25.6%; Pred. No. 2.7e-42;
Matches 223; Conservative 117; Mismatches 308; Indels 222; Gaps 37;
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Qy 34 PGAENINM-----CCECCYDQIE---CVCPRKREVVGTIFCCNNEHCSCSLHPCST 86
Db 184 PNGQWSPFPKCIHBCAVSSPEHGKVTAPSGNMIEGATL-----RFSQDS---PHYL 233
Qy 87 IFENCKSCR-NGSWGTL----- 103
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Db 234 IGQETLTGQNGWGGQIPQCKKLVFCRDLDPVNAHQVKIGVBOXYGQPPQGETVYTT 293
Qy 104 --DDEYKGFYCAEGR--AGMYG--DCMR-----CGOYLK--APKG 137
Db 294 CSGNYFLMGFNTLKCNDGWSGSGQPSGVKAVDREVDGSKAVDPLDDVGEFVRTHCPAG 353
Qy 138 QILLES-----YPLNAHCEWTIHA---KPGVI-----Q 163
Db 354 CSLTAGTWGTAIYHELSSVCRAAIHAGCLPNSGGAVHVNNGPYSDFLGSDLNGIKSEB 413
Qy 164 LRFVWLSEFDYM-----CQDYVAVRD-----GDNRDQGIKRYCGN--ERAP 206
Db 414 LKSLARSFRFDVSSSTAGSGCPDGEVEENCYVYTSKQAWERAQGCCTNMAARLAV 473
Qy 207 IQS--IGSSLHVLFPKSDG--SKNFDGFH-----AIYEITACSSPCF 245
Db 474 LDKDVIPISSLTALMGKGLTTTWIGLHRLDAKFPFWELMDRSNVYLDNLTFMAGSEBG 533
Qy 246 HDGTCV-LDKAGS---YKCACTAGYTGRCENLLEBN--CSDPGPVNGYQKITGAP 297
Db 534 NETNCVYLDIRDQLPVWMTKSCFQPSFACWMDLSDRYKAKCDDPGSLENGHATLHGQS 593
Qy 298 GLINGRHAKIGTVVSPFCNNSVYLSGENKRTQONGEWSGKOPICIK--ACREPKISDLV 355
Db 594 --IDGFYA--GSSIRYSCVHLVYLSGTETVCTTGTGWSAPPKRCIKVITCQNPVPSYG 649
Qy 356 RRRVLPMQVQSRREPLHOLYSAFASKOKLQ--SAPTKKALPFGD-----LP 400
Db 650 SVEIKP---PSRTNISRVGSPFLRLPLPLABAAPPPKPRSSQPSYVDLASKVLFP 706
Qy 401 MGYOHLHTQLOYECISPFYRRLGSSRRTCRLTKWNGRAPSCIPICGKIENITAP---- 455
Db 707 EGHYVVGSRATYTCESRYELLGSGRCDSNGMWSGRPASCIPVCGRSDSPRSPFINWG 766
Qy 456 -KTQGLRPMQAAIYRTSGVHDGSLHKGAMFLVCSGALVNERTVVVAACHCTDLGKVTM 514
Db 767 NSTEIGQMPWQAGISRWLA-----DHNMPLOCGGSLNEKWIVTAAHCVTYSATAEI 819
Qy 515 IKTDLKVVLGKFYRDDDDREKTIQSLQISATILHPNYDPIILDADIAILKLLDKARIST 574
Db 820 IDPGQFKIYLGKYYDDSRDDYVQVREALEIHVNPNDPGNLNFDIALIQKTPVTYLT 879
Qy 575 RVQPICLASRDLSFQESH-----TVAGMVLADVRSPPGNDTLRSGVSVVDSL 628
Db 880 RVQPICLPT--DITT---REHLKEGTLAVVTGWC---LNENNTYSEMIQQAFLPVVAAS 930
Qy 629 LCEBOHEHDHGIPIVSTDMFCASWEPTAPSDICTAETGIAAVSPGRASPEPRNHLMLGL 688
Db 931 TCEBGYKEADLPLVTYTEMFCAGYK-KGRYDACSGDSGG--PLVPADSDRTERRWVLEGI 987
Qy 689 VSMGYDKTCSH-RLSTAFKVLFPKWIET 717
Db 988 VSMGSPSCGKANOYGGFTKVNVLFWIRQ 1017

Search completed: July 15, 2006, 06:55:57
Job time : 346 secs